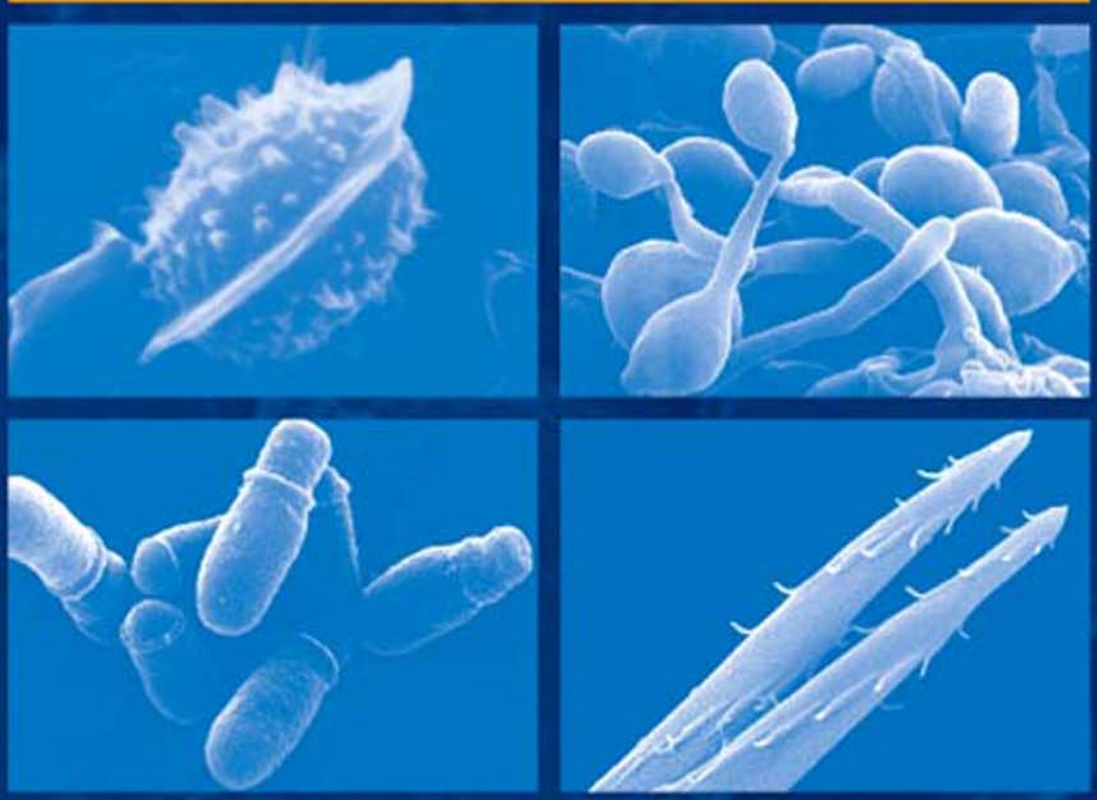
THE YEASTS

A TAXONOMIC STUDY

FIFTH EDITION



VOLUME 1

EDITED BY
C.P. KURTZMAN • J.W. FELL • T. BOEKHOUT

The Yeasts, a Taxonomic Study

Volume 1

This book is dedicated to the memory of

Robert J. Bandoni
Helen R. Buckley
Nellie J. W. Kreger-van Rij
Martin W. Miller
Herman J. Phaff
Wilhelmina Ch. Slooff
Isabel Spencer-Martins

The Yeasts, a Taxonomic Study

Volume 1

Fifth Edition

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Preface

The importance of yeasts is underscored by our often daily consumption of bread and fermented beverages. Recent advances in biotechnology have increased our reliance on yeasts for pharmaceuticals and for bulk biochemicals such as citric acid. Furthermore, clinically important yeasts are commonplace, especially as numbers of immunosuppressed patients increase, and biologists are continuing to discover the importance of yeasts in the ecosystem and their application in the biocontrol of plant pests. All of these areas of science and technology have a common need: the rapid and accurate identification of yeasts. The goal of this book is to provide that information.

This book, the fifth edition of *The Yeasts*, *a Taxonomic Study*, represents a continuation of the monographic series begun by J. Lodder and N.J.W. Kreger-van Rij (1st edn, 1952), J. Lodder (2nd edn, 1970), N.J.W. Kreger-van Rij (3rd edn, 1984) and C.P. Kurtzman and J.W. Fell (4th edn, 1998). In the fourth edition (1998), 100 genera and over 700 species were described. In the present edition, there are 149 genera and nearly 1500 species. The application of gene sequence analysis is largely responsible for the increase in the number of taxa presented in this edition. In 1998 and in 2000, diagnostic gene sequences were published for essentially all known yeasts. This advance allowed rapid, accurate species identification for the first time, and the method has been widely adopted by the yeast community to catalogue new species. Sequence analysis has also demonstrated that genera were often polyphyletic, and from such analyses many genera are now phylogenetically circumscribed. There is still much to do to understand phylogenetic relationships among species and genera, but a good start has been made.

In this edition, a large array of fermentation and growth tests is reported for each species. These tests can be used for species identification, but as this is now commonly done from gene sequences, their major value is to provide information for the selection of biotechnologically important species, to understand how metabolism affects species ecology and for the selective isolation of taxa. Many of the species are illustrated by photographs or line drawings because it is important to know the species morphology and the method of growth.

This edition includes chapters on the importance of yeasts and the current methods used for their identification and classification. We hope readers will find these chapters useful, and that they will provide a starting point for more extensive studies with a fascinating group of fungi that we know as the yeasts.

Cletus P. Kurtzman
Jack W. Fell
Teun Boekhout

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Use of this Book

1. INTRODUCTORY CHAPTERS

With the widespread use of gene sequences for yeast identification, the number of known species has doubled since publication of the fourth edition of this book in 1998. As a result, the book has grown from one to three volumes. As in previous editions, the book begins with introductory chapters that discuss the definition of yeasts, their importance and the means for their characterization and classification. Thus in Volume 1, Part I discusses the current definition of yeasts, their classification and the rules for their nomenclature. Part II focuses on yeasts that are human and plant pathogens, those that cause food and beverage spoilage, species used for biocontrol of plant pests, their applications in biotechnology, and an overview of yeast ecology. Part III provides chapters on phenotypic characterization, chemotaxonomy, ultrastructure and molecular biological characters that are used to identify yeasts and to develop a phylogenetic framework for their classification. Volume 2 is devoted to the ascomycetous yeasts, and Volume 3 includes the basidiomycetous yeasts, along with the genus *Prototheca*.

The format of this edition differs from previous editions in the placement of the all-species key, summary table of species characteristics, glossary, and indexes to taxa and literature references in Volume 1 with the introductory chapters, rather than at the back of the book as was done previously. Because we now have three volumes, we reasoned that it would be more convenient, while looking for taxa and their references or keying species, to have these sections in a separate volume from the species descriptions, thus avoiding the need to flip between the front to back of a single volume while looking for the information. We hope that readers will find this format to be a convenient choice for a multi-volume taxonomic work.

2. DESCRIPTIONS OF GENERA AND SPECIES

Genera are arranged alphabetically within four groups: teleomorphic ascomycetes, anamorphic ascomycetes, teleomorphic basidiomycetes and anamorphic basidiomycetes. The introductory chapters for both ascomycetes and basidiomycetes include discussions of genera and their phylogenetic placement. These discussions also note relationships between teleomorphic and anamorphic genera. Each chapter begins with a narrative description of the genus, a phylogenetic tree that depicts species relationships within the genus, and a key to species based on growth characteristics, which is followed by a table that includes the key characters. Each species description begins with a designation of the anamorph or teleomorph, where known, followed by a listing of synonyms. The characterization proceeds to morphological and physiological descriptions. Representative species for each genus are illustrated by either drawings or photographs, which include a scale bar and growth conditions. Noteworthy information for the species is given in sections entitled Systematics, Ecology, Biotechnology, Agriculture and food, and Clinical importance.

Abbreviations used throughout the text are standard. For mol% G+C of nuclear DNA, the method for determination is included and abbreviated as follows: T_m, thermal melt; BD, buoyant density; HPLC, high-pressure liquid chromatography.

The following symbols are used for the fermentation and assimilation reactions given with species descriptions:

+	positive
l	latent (rapid development of a positive reaction after a lag period)
+/l	positive or latent
s	positive but slow
w	weak
ws	weak and slow
+/w	positive or weak
w/−	weak or negative
lw	latent but weak (rapid development of a weak reaction after a lag period)
−/l	negative or latent
v	variable
−	negative
n	no data

3. YEAST-LIKE TAXA

Some microbial taxa that could be mistaken as yeasts are briefly discussed. For example, species of the dimorphic euascomycete genus *Aureobasidium* are commonly isolated, and often appear white to light pink in color and yeast-like on isolation plates. Consequently, *Aureobasidium pullulans* is included in the all-species key. Similarly, the achlorophyllic algal genus *Prototheca* is often misidentified as a yeast, and for this reason a chapter on the genus is included.

4. SPECIES SUMMARY TABLE AND KEY TO ALL TAXA

A summary table of fermentation and assimilation reactions and certain key biochemical characteristics is placed near the end of Volume 1. Taxa are listed alphabetically, first by genus and then by species. A key using the physiological data in the table includes all species of ascomycetes, basidiomycetes and the genus *Prototheca* for which data are available. The following abbreviated symbols are used in the table and for the key:

+	+, s, l, +/l, +/w , w, ws, lw
−	−
v	v, w/−, −/l
n	no data or not applicable

5. GLOSSARY

A glossary has been provided that includes morphological, genetic and molecular biological terms.

6. INDEXES TO TAXA

There are two indexes to taxa. The first lists genera followed by assigned species and their synonyms. Validly accepted combinations are in bold type. The second index alphabetically lists all species and variety names followed by all genera to which the species and varieties were assigned. Validly accepted genera are in bold type.

7. REFERENCES

The references for all chapters have been consolidated into a single list. This saved sufficient space to allow inclusion of titles which would have been omitted if each chapter had a reference list.

Part I

Classification of Yeasts

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Chapter 1

Definition, Classification and Nomenclature of the Yeasts

Cletus P. Kurtzman, Jack W. Fell and Teun Boekhout

1. DEFINITION AND CLASSIFICATION OF THE YEASTS

The English word yeast and its equivalents in many other languages are based on words meaning "foam" and "to rise", direct references to the fermentation processes that produce beer and bread. For this reason, yeasts are often thought of as fermentative ascomycetous fungi similar to *Saccharomyces cerevisiae*. In fact, it is not uncommon in some areas of molecular biology to treat the words "yeast" and "*Saccharomyces*" as synonyms. The discovery that some taxa are basidiomycetes has broadened our perception of the nature of yeasts. As a consequence, we have come to view yeasts as fungi that asexually reproduce by budding or fission, which results in growth that is comprised mainly of single cells.

An imprecise distinction has been made between yeasts and those dimorphic filamentous fungi that often produce abundant yeast-like growth. Yeasts can be defined as those fungi whose asexual growth predominantly results from budding or fission, and which do not form their sexual states within or upon a fruiting body. For ascomycetous yeasts, this distinction has been substantiated by molecular comparisons, which demonstrate that budding and fission yeasts are phylogenetically distinct from one another and from the euascomycetes (Pezizomycotina) (see Chapter 13). One exception is the genus *Eremascus*, which has unenclosed asci, but budding cells are not formed. A similar distinction can be made for basidiomycetous yeasts, which are often phylogenetically separate from the mushrooms and other taxa that form complex fruiting bodies (see Chapter 100). In summary, yeasts, whether ascomycetes or basidiomycetes, are generally characterized by budding or fission as the primary means of asexual reproduction, and have sexual states that are not enclosed in fruiting bodies.

2. TAXONOMY

Rules for taxonomy of the yeasts and other fungi fall under the authority of the International Code of Botanical Nomenclature. The most recent version of the Code (McNeill et al. 2006) was adopted at the Seventeenth International Botanical Congress, Vienna, Austria, 2005 (http://ibot.sav.sk/icbn/main.htm). The following is a brief discussion of the Botanical Code as it applies to yeasts.

2.1. Description of New Taxa

2.1.1. Species

Publication of new species must include a description of essential characters as well as a diagnosis that distinguishes the taxon from previously described species. Since January 1, 1935, the description and/or diagnosis must be given in Latin. Failure to comply with this requirement results in an invalidly described species termed a *nomen invalidum* (*nom. inval.*). A *nomen invalidum* also results if publication is not in a recognized scientific journal, e.g., as in a patent or a trade magazine. If the new species is designated without a description or a diagnosis, it is invalid and termed a *nomen nudum* (*nom. nud.*). Names of taxa must be given in Latin or modified in such a way that they follow the rules of Latin derivation including appropriate gender designations. If a name has been incorrectly crafted, it may be treated as an "orthographic error" and corrected. An example is *Pichia membranifaciens* for which the 1888 spelling "*membranaefaciens*" has been corrected. The authority name does not change due to the spelling correction. Other requirements for valid publication include deposition of type material in a publicly accessible herbarium. This material must be an original specimen of the organism, and it is to be dead and dried. The 1994 Code (Greuter et al. 1994) changed the requirements to allow lyophilized specimens to be valid type material (holotype) and that living cultures derived from the lyophilized material are considered *ex typo*, i.e., from the type. It seems that once the original material is exhausted, there is no longer type material available. A possible solution to this problem would be to lyophilize new material and designate it as a neotype, a convention permitted when the original type material is lost or destroyed and the species can be otherwise recognized. This discussion leads to the recognition that a majority of presently accepted yeast species are technically invalid because legitimate type material has not been preserved. A portion of presently lyophilized stocks of the holotype that are maintained in culture collections should be withheld from distribution and designated as type. Consequently, the designation of "Type strain" given for each cultivatable species described in this book can, at best, represent an ex-type. The 1994 Code recognized the need for living cultures in the practice of modern taxonomy and stated in Recommendation 8B.1:

> *"Whenever practicable a living culture should be prepared from the holotype material of the name of a newly described taxon of fungi or algae and*

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deposited in at least two institutional culture or genetic resource collections. (Such action does not obviate the requirement for a holotype specimen under Art 8.2)."

The 1994 Code further states in Recommendation 8B.2:

"In cases where the nomenclatural type is a culture permanently preserved in a metabolically inactive state (see Art. 8 Ex. 1), any living isolates obtained from that should be referred to as 'ex-type' (ex typo)*, 'ex-holotype'* (ex holotypo)*, 'ex-isotype'* (ex isotypo)*, etc., in order to make it clear they are derived from the type but are not themselves the nomenclatural type."*

From these recommendations, it is clear that the Code strongly encourages scientific cooperation and communication through active sharing of published taxonomic specimens. A listing of commonly used yeast culture collections is given in Chapter 7.

From gene sequence comparisons, strains that represent new species are usually easily recognized (Chapter 10). Nonetheless, some would argue against description of a new species based on a single strain. The argument is that a single strain does not reflect the genetic variation that might be found in a species, and that little can be learned of the ecology of a species when only a single strain is available. However, nearly one-third of described yeast species are based on a single strain. If these species had not been described, much less would be known about the phylogenetic diversity of the yeasts. From the perspective of understanding diversity among the yeasts, description of single-strain species is to be supported, although descriptions based on multiple strains are preferred. Further, it is recommended that the description should be based on multigene analysis to lessen the possibility that the strain represents a hybrid of known species.

2.1.2. Genera, Families, Orders

The rules for describing new genera, families and orders are similar to those for describing new species. The taxa must be based on a validly described species and provided with a Latin description and diagnosis. The rules of priority are briefly described below, but one exception is that orders are exempt from priority usage.

2.2. Basionyms, Synonyms, Priority of Usage

Because of the inexact art of species characterization, as well as the occasional situation in which two independent investigators describe the same new species, the Botanical Code has provided a set of rules to reconcile resulting problems. The following example should prove helpful to the reader, but the Code needs to be consulted for full details.

1. *Saccharomycopsis fibuligera* (Lindner) Klöcker (1924)

   Synonyms:

2. *Endomyces fibuligera* Lindner (1907)
3. *Endomycopsis fibuligera* (Lindner) Dekker (Stelling-Dekker 1931)
4. *Pichia fibuligera* (Lindner) Boidin, Pignal, Lehodey, Vey & Abadie (1964)
5. *Endomyces lindneri* Saito (1913)
6. *Saccharomycopsis lindneri* (Saito) Klöcker (1924)
7. *Endomycopsis fibuligera* (Lindner) Dekker var. *lindneri* Dekker (Stelling-Dekker 1931)
8. *Endomyces hordei* Saito (1914)
9. *Saccharomycopsis hordei* (Saito) Klöcker (1924)
10. *Endomycopsis fibuligera* (Lindner) Dekker var. *hordei* (Saito) Dekker (Stelling-Dekker 1931)
11. *Candida lactosa* Dwidjoseputro & Wolf (1970)

In the example, *Saccharomycopsis fibuligera* (1) is the currently accepted name. The species was originally described by Lindner in 1907 as *Endomyces fibuligera* (2) and transferred to *Saccharomycopsis* by Klöcker in 1924. Other authors transferred the species to *Endomycopsis* (3) and to *Pichia* (4), but in all cases, the original author, Lindner, is listed in parentheses. The other species listed (5–11) are misidentified strains of *S. fibuligera*. The genus assignments for these "species" were also changed before it was recognized that they were conspecific with *S. fibuligera*. In the context of the Code, *Endomyces fibuligera* (2) is the basionym or basal name for the species. Synonyms 2, 3 and 4 are nomenclatural or obligate synonyms of *S. fibuligera* because they are all based on the same type strain. Synonyms 5–11 are termed taxonomic or facultative synonyms because they are based on different type strains. Species 6 and 7 represent obligate synonyms of *Endomyces lindneri*, hence the listing of synonyms is ordered by priority of publication date of obligate synonyms followed by publication date of facultative synonyms and their own obligate synonyms. The Code requires, with few exceptions, that the first described name has priority of usage. Thus, *Endomyces fibuligera* Lindner (1907) is the basionym, and personal preference for another name to serve as basionym, e.g., *Endomyces lindneri* Saito (1913), is generally not allowed. Arguments for exceptions might include uncertain names and the substitution of economically or medically important names for an older but obscure basionym.

The following publications provide examples of descriptions of new taxa and the conservation of older names, but the most recent edition of the Botanical Code should be consulted as well.

New species and genera

Fell, J.W., A.C. Statzell, I.L. Hunter and H.J. Phaff. 1969. *Leucosporidium* gen. n., the heterobasidiomycetous stage of several yeasts of the genus *Candida.* Antonie van Leeuwenhoek 35, 433–462.

New combinations

Kurtzman, C.P. 1995. Relationships among the genera *Ashbya, Eremothecium, Holleya* and *Nematospora* determined from rDNA sequence divergence. J. Ind. Microbiol. 14, 523–530.

Conservation of taxa

Fell, J.W., C.P. Kurtzman and K.J. Kwon-Chung. 1989. Proposal to conserve *Cryptococcus* (fungi). Taxon 38, 151–156.

2.3. Teleomorphs, Anamorphs and Holomorphs

Fungi are unique among living organisms because they may have two valid names. The primary name is based on the sexual state or teleomorph, but a second valid name may be based on the asexual state or anamorph. This redundancy of names developed because teleomorphs have not been found for many fungi, or it has not been clear that a particular teleomorph is the same species as a particular anamorph. If a teleomorph is unknown, a species can be described in an anamorphic genus, e.g., genera 86–99 and 135–162 in this book. Use of gene sequence comparisons has made the connection between teleomorphs and anamorphs for some species, but for many, the teleomorphic states are unknown. When both teleomorph and anamorph are known for a species and are part of the same type specimen, the combination is termed the holomorph. In the descriptions of teleomorphic yeasts presented in this book, the anamorph name is given if it exists.

Various possibilities have been offered to limit fungal species to just one name. Anamorphic species that are members of a teleomorph clade might be renamed to the teleomorph genus. For example, *Candida pseudolambica*, a member of the *Pichia* clade, might be renamed "*Pichia pseudolambica*" and the assignment to *Candida* would then be considered an invalid name. One disadvantage would be the incorrect implication that an ascosporic state has been found for *C. pseudolambica*.

Article 59.7 of the Vienna Code (2006) states

"Where a teleomorph has been discovered for a fungus previously known only as an anamorph and for which there is no existing legitimate name for the holomorph, an epitype exhibiting the teleomorph stage may be designated for the hitherto anamorphic name even when there is no hint of the teleomorph in the protologue of that name."

Guided by Article 59.7, use of an anamorphic genus name for a teleomorphic state would be straightforward if the particular clade had no teleomorphic species. For example, the anamorphic genus *Trichosporon* has no described teleomorphs, and if one were found, it could be named *Trichosporon*. However, it appears contrary to the Code to preferentially select an anamorph genus name and discard the teleomorphic genus name. An example of this would be to use *Cryptococcus neoformans* (anamorph) rather than *Filobasidiella neoformans* (teleomorph), because the name *Cryptococcus neoformans* is more often found in publications. In this book, both anamorphic and teleomorphic names have been maintained, but this may change in the future.

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Part II

Importance of Yeasts

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Chapter 2

Yeasts Pathogenic to Humans

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1. INTRODUCTION TO THE MEDICALLY IMPORTANT YEASTS

Prior to global emergence of the human immunodeficiency virus (HIV), which is the causative agent of the acquired immunodeficiency syndrome (AIDS), approximately 200 fungal pathogens were recognized from among the more than 100,000 then-known fungal species (Kwon-Chung and Bennett 1992, Rippon 1988). About 50 of these species were regularly associated with fungal disease (mycosis). Since then, there has been a concurrent dramatic increase in both the number of known fungal species and the incidence of mycoses that they cause. Moreover, the spectrum of pathogenic fungi has changed radically. Though HIV infection has been noted to be a significant factor in these changes, it is only one of many diseases that have encompassed the dynamic transformation of human affairs over the past several decades. The developments that have played noteworthy roles in the increased frequency of mycoses include the relative ease of international travel, an expanding and aging population, a breakdown in public health measures, rising immigration rates, heightened awareness of disease, industrialization, prolongation of life due to medical advances, and, sadly enough, politics (Cooper 2002, Lederberg et al. 1992, Smolinski et al. 2003). The collective result of these changes markedly influenced the diversification of etiological agents by permitting virtually any fungus capable of growing at or near body temperature (37°C) to eclipse a critical first hurdle in ascending to the level of pathogen.

Yeasts are among the most prominent of the disease-causing fungi, especially *Candida* spp., *Cryptococcus* (*Cr.*) *neoformans*, and *Cr. gattii*. There also exists a spectrum of unicellular fungi that have emerged as significant infectious agents (Table 2.1). Moreover, while the term "yeast infection" tends to elicit an image of an agent that exists mainly in a monomorphic state, other fungi also produce yeast cells or yeast-like forms *in vivo*. These include several thermally dimorphic fungi that exist as saprotrophic molds when grown at moderate temperatures (22°C–28°C), but convert to a yeast phase upon tissue invasion or *in vitro* culture at 37°C. In addition, a number of members grouped within the form-family Dematiaceae exhibit a yeast form both in culture and *in vivo*. Moreover, the enigmatic fungus *Lacazia loboi*, the agent of lobomycosis, presents chains of yeasts in tissue although this organism has yet to be isolated from nature. Hence, in medical mycology, the above examples support using the term "yeast" to strictly define a morphological feature without ascribing a taxonomic significance. However, many clinicians commonly use this term to refer mainly to the pathologies designated as candidiasis and cryptococcosis.

As an introduction to this text, the present review is meant to serve as a brief, descriptive compendium of mycoses caused by yeasts. Yet, it is not the author's intent to suggest that yeast biologists will regularly encounter the organisms described below. In fact, many medical mycologists spend entire careers without direct clinical exposure to many of these fungi. Rather, the purpose of this review is to enlighten the non-medical mycologist as to the diversity of yeast and mold species regularly associated with human and animal disease that also, at least in part, present a unicellular mode of growth *in vivo*.

The following descriptions present a concise overview of the key biological and clinical features of these fungi. Where appropriate, references to recent reviews of particular disease agents and their pathologies are provided. For a global perspective of fungal diseases, including in-depth clinical discussions of specific pathologies, diagnoses, and treatments, the reader is referred to several outstanding and recently published texts (Anaissie et al. 2003, Dismukes et al. 2003, Kauffmann 2006a, Merz and Hay 2005). In addition, brief summaries of mycotic diseases and their etiological agents, including currently accepted binomials for these fungi, can be found on the Internet web page; Doctor Fungus (www.doctorfungus.com). Moreover, the narratives below provide brief taxonomic descriptions for each species and, if known, its teleomorph. In some instances, the particular classification of the sexual state was retrieved from the National Library of Medicine (www.ncbi.nlm.nih.gov/genomes/static/euk_o.html). Finally, of those fungi presented below, with the possible exception of *Histoplasma*, all can be handled using Biosafety Level 2 practices (www.cdc.gov/od/ohs/biosfty/bmbl4/bmbl4s7b.htm).

2. ASCOMYCETOUS YEASTS OF CLINICAL SIGNIFICANCE

Overall, ascomycetous yeasts comprise the largest group of pathogenic fungi. Most of these pathogens are members of the anamorphic genus *Candida*. To a far lesser extent, fungi classified within the genera *Saccharomyces, Pichia* (including species formerly assigned to *Hansenula*), and *Magnusiomyces* (formerly *Dipodascus, Blastoschizomyces*) also cause human infections.

2.1. *Candida*

A number of *Candida* species exist in a commensal relationship with humans as normal residents of the gastrointestinal tract, mucocutaneous tissues, and skin. The most notable of these species is *Candida albicans*. However, being opportunistic pathogens, *Candida* spp. can exploit local or systemic weaknesses in host resistance, to cause disease in virtually any part of the body. Such infections, termed candidiasis, have become increasingly common during the past several decades for a number of reasons, which include the use of immunosuppressive therapies for other diseases as well as the unfortunate

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TABLE 2.1 Selected Yeast and Yeast-Like Pathogens for Humans and Animals

Anamorph	Known Teleomorph
Ascomycetous Fungi	
Candida albicans	None
Candida dubliniensis	None
Candida glabrata	None
Candida nivariensis	None
Candida bracarensis	None
Candida guilliermondii	*Meyerozyma* (*Pichia*) *guilliermondii*
Candida krusei	*Pichia kudriavzeii*
Candida lusitaniae	*Clavispora lusitaniae*
Candida parapsilosis	None
Candida metapsiloisis	None
Candida orthopsilosis	None
Candida tropicalis	None
—	*Saccharomyces cerevisiae*
—	*Saccharomyces boulardii*
—	*Wickerhamomyces* (*Pichia*) *anomalus*
—	*Ogataea* (*Pichia*) *polymorpha*
Blastoschizomyces capitatus	*Dipodascus capitatus*
Basidiomycetous Fungi	
Cryptococcus neoformans var. *neoformans*	*Filobasidiella neoformans*
Cryptococcus neoformans var. *grubii*	*Filobasidiella neoformans*
Cryptococcus gattii	*Filobasidiella bacillispora*
Malassezia spp.	None
Trichosporon spp.	None
Rhodotorula spp.	None
Sporobolomyces spp.	None
Pseudozyma spp.	*Ustilago* spp.

prevalence of HIV infection. Other factors, such as increased awareness and improved diagnostic tools, have contributed to the sense that candidiasis has risen in importance as an affliction of humans and animals.

Evidence supporting the significance of *Candida* spp. as infectious agents might be readily noted by the number of publications cited in the medical literature that document case studies and research reports featuring these fungi. Using the words "*Candida albicans*", the present author searched for citations in the PubMed database supported by the National Center for Biotechnology Information (www.ncbi.nlm.nih.gov). From 1970 through 1974, 1124 publications included the topic "*Candida albicans*". Over the next 30 years, this number rose by more than 334% with exponential increases from 1985 to 2004. Data for the past 2 years suggest that such publications will continue to proliferate exponentially over the next several years. Therefore, if the number of citations is indeed representative of the significance of *C. albicans* to public health, and by extrapolation to other *Candida* spp. as well, it is clear that these yeasts and the infections they cause have commanded much attention from clinical and experimental mycologists.

In addition to the human body, *Candida* spp. can be found in a wide variety of environmental habitats. Like those typically considered non-pathogenic, disease-causing species can be recovered from many of the same sources including air, water, foodstuffs, clothing, toothbrushes, etc. However, the environmental isolation of *Candida* spp. that are regularly associated with infections is often the result of contamination by humans or animals rather than a reflection of a true primary habitat for such fungi. This is a particularly disturbing fact that coincides with reports showing health care facilities to be a major location for contracting candidiasis (Jarvis 1995). Collectively, *Candida* spp. are the fourth most common cause of hospital-acquired (nosocomial) infections in North America.

A detailed description of the various clinical manifestations of candidiasis, as well as clinically relevant biological investigations of *Candida* spp., can fill entire books. Indeed, several books (Bodey 1993, Calderone 2002, Odds 1988, Segal and Baum 1994), chapters within medical mycology texts (Anaissie et al. 2003, Dismukes et al. 2003, Heitman 2006, Kauffmann 2006a, Kwon-Chung and Bennett 1992, Merz and Hay 2005), and numerous reviews (Pappas 2006, San-Blas and Calderone 2004, Sims et al. 2005, Spellberg et al. 2006) have been published over the past two decades covering these topics. As such, the reader is referred to these resources. The remainder of the present discussion will focus on brief portrayals of the more significant pathogenic species of *Candida*. Suffice to note, however, candidiasis encompasses a broad range of infections. Mucocutaneous forms of the disease (e.g., vaginitis) are very common and rarely life threatening to the immune competent host. Rather, such mucosal and superficial skin infections are typically troublesome in terms of physical comfort, cosmetic concern, and occasional relapse of the condition. In contrast, mucocutaneous candidiasis in immunocompromised hosts (e.g., HIV-infected individuals with esophageal candidiasis) is more serious and subject to frequent relapses. The more serious cases of systemic candidiasis, either in immune compromised persons or others with predisposing conditions (e.g., burn patients), can produce a multitude of symptoms and involved organ systems. Highly significant mortality rates accompany these forms of candidiasis.

As yeasts, *Candida* spp. are generally small, ovoid, thin-walled fungi that reproduce mainly by budding. Relatively few species are routinely isolated from human and animal infections (Table 2.1). Clinical isolates are often distinguished from one another by using one of several simple methods. For example, as discussed below, yeast cells of several etiological agents of candidiasis produce germ tubes in serum at 37°C, thereby reducing the number of possible identifications. Also, only a few species produce chlamydospores, again restricting identification to a few yeasts. Perhaps one of the quickest means to a presumptive identification is the use of CHROMagar *Candida* media. Based upon the color and morphology of colonies growing on this proprietary medium, the clinical mycologist can distinguish among yeasts of *C. albicans*, *C. krusei*, *C. tropicalis*, *C. glabrata*, and other non-*C. albicans* species (Jabra-Rizk et al. 2001, Odds and Bernaerts 1994, Pfaller et al. 1996). However, the traditional method of employing commercially available carbohydrate fermentation and assimilation assays (e.g., API 20C, Vitek 2 ID-YST, etc.) remains key to making more precise identifications when ambiguous or equivocal phenotypic results are obtained. Hopefully, some of the ambiguity will be resolved as progress is made in the development and application of molecular methods in which DNA-based technology will provide the means to more rapidly and accurately identify pathogenic yeasts. For a review of traditional and commercial yeast identification methods, as well as a capsule summary of genotypic techniques, the reader is referred to a recent publication by Pincus et al. (Pincus et al. 2007).

The following discussions are limited to those species that are well-documented *Candida* pathogens. Regarding the taxonomy of these species, to note that this topic has been a source of tremendous study would be a gross understatement. For a comprehensive review of the taxonomic aspects of these fungi, the reader is referred to the pertinent sections of the present publication. To summarize, the following fungi are considered ascomycetes due to the teleomorphic state exhibited by some species as well as other cellular and molecular properties. Physiologically, these yeasts fall within Group VI

described by Meyer et al. (Meyer et al. 1998), in that all grow at 40°C, but they do not assimilate nitrate, erythritol, or *myo*-inositol.

2.1.1. Candida albicans

This fungus is the most common cause of candidiasis, but is not readily isolated from the environment. This apparent absence from the environment may be due to its adaptation to a parasitic life cycle with the concomitant loss of the properties permitting it to easily survive outside a host. In addition to a yeast phase, *C. albicans* produces true hyphae and pseudohyphae when it is cultured on the appropriate media and incubated under suitable environmental conditions. *In vivo*, both hyphal-like elements and yeast cells can be observed. The hyphae generate grape-like clusters of blastoconidia. The latter can grow as budding yeasts or germinate as hyphae. Also, *C. albicans* is well known for the ability to form thick-walled entities, termed chlamydospores, at the terminal ends of hyphae. This structure is often used as a diagnostic feature for this species, although *C. dubliniensis* also produces chlamydospores. An additional diagnostic feature of *C. albicans* is the ability of yeasts grown at 37°C in serum to form germ tubes. These hyphal initials differ from the outgrowth of other *Candida* spp. in that a constriction is absent at the germ tube base. Finally, on CHROMagar *Candida*, this species produces distinctive green colonies.

A true teleomorph of *C. albicans* has yet to be established although recent advances have demonstrated that this yeast possesses mating type genes (Hull and Johnson 1999). Genetically modified strains provided evidence of "mating" within a mammalian host (Hull et al. 2000). In the laboratory setting, appropriate strains can undergo a type of cytoplasmic fusion followed by karyogamy that strongly resembles that exhibited by *Saccharomyces cerevisiae* (Bennett and Johnson 2005, Miller and Johnson 2006, Soll 2006). A key difference is that the mating strains are naturally diploid and the daughter cell product of this mating is a tetraploid. Subsequent loss of chromosomes during asexual growth of the daughter cell eventually results in the re-establishment of a diploid state. This entire process is highly regulated and is associated with a genetically controlled morphological phenomenon known as phenotypic switching.

2.1.2. Candida dubliniensis

In 1995, a new species of *Candida* was isolated from the oral cavity of HIV-infected patients. This new species was designated as *C. dubliniensis*. Subsequently, like *C. albicans*, *C. dubliniensis* proved to be readily recovered from HIV-positive patients across the world. This yeast has also been isolated from bone marrow transplant patients and those persons on broad-spectrum antibiotics. A recent review highlights the status of this pathogen since its discovery (Sullivan et al. 2005).

Candida dubliniensis is morphologically similar to *C. albicans* in that it forms germ tubes and chlamydospores. These two properties are only exhibited by these two species among all members of the genus *Candida*. However, a published report suggests that Staib agar supports chlamydospore formation only by *C. dubliniensis*, thereby providing a possible diagnostic tool for differentiating these species (Staib and Morschhauser 1999). A more recent study suggests that the regulatory signals that control chlamydospore formation differ between *C. dubliniensis* and *C. albicans* (Staib and Morschhauser 2007). Such data may help decipher the biological function of this curious structure. In addition to the morphological and developmental resemblance of *C. dubliniensis* and *C. albicans*, both of these species are physiologically similar bearing only subtle differences. However, the two species can be distinguished from one another by incubating strains at 45°C. At this temperature, *C. dubliniensis* will not grow, whereas *C. albicans* readily forms colonies under the same conditions. On CHROMagar *Candida*, *C. dubliniensis* also forms green colonies like *C. albicans*, though on newer formulations of the medium the colonies are darker. There are differences in karyotypes and rDNA sequences, but the applications that would be employed to assess these characteristics are usually beyond the purview of a typical clinical laboratory.

2.1.3. Candida glabrata

From a medical viewpoint, the significance of this species of *Candida* can be found in its increased incidence worldwide, compounded by an apparent increase in its resistance to commonly applied antifungal agents. *Candida glabrata* is the second most common cause of bloodstream infections following *C. albicans*, with the upsurge in frequency being due to the larger population of immunocompromised individuals and the widespread use of antimycotics. This species is also one of the most prevalent isolates from cases of oral infections and vaginitis. For further information regarding the biological and clinical properties of this yeast, the reader is referred to recently published reviews (Bialkova and Subik 2006, Kaur et al. 2005).

Isolates of *C. glabrata* can be readily recovered from clinical specimens using routine medical mycological media. A presumptive identification can be made using CHROMagar *Candida* media upon which colonies of *C. glabrata* appear purple to pale pink. Recent clinical findings, however, suggest that some diagnoses of *C. glabrata* infections may be missed since the growth of particular isolates is dependent upon exogenously supplied cholesterol (Bard et al. 2005, Hazen et al. 2005, Rezusta et al. 2007). Routine isolation media that are not supplemented with a source of cholesterol will not support the growth of these strains, which appear to have arisen from lipid-enriched therapies associated with the antifungal treatment. Apparently, these isolates are able to scavenge and use exogenous cholesterol in place of ergosterol for their plasma membrane structure. Because the mode of action of certain antifungals used to treat *C. glabrata* infections is related to the production of ergosterol (e.g., terbinafine, fluconazole, etc.) or its presence in the plasma membrane (e.g., amphotericin B) (see selected chapters within Anaissie et al. 2003, Dismukes et al. 2003, Merz and Hay 2005), the antifungal drug may have facilitated the selection of cholesterol-dependent strains following their acquisition of spontaneous mutations in ergosterol biosynthesis (Bard et al. 2005). Recently, an amphotericin B-resistant, cholesterol-dependent isolate of *C. glabrata* has been recovered (Rezusta et al. 2007). Isolating such strains might have been predicted based upon the mechanism of action of amphotericin B. Moreover, this observation further suggests that cholesterol-dependent isolates of *C. glabrata* that are simultaneously resistant to certain azole drugs might be encountered in the near future.

The taxonomy of this species had been one of controversy for a number of years. The primary argument focused on the inability of *C. glabrata*, previously designated as *Torulopsis glabrata*, to form pseudohyphae as opposed to *Candida* spp. that are characteristically noted to possess this property. However, the use of pseudohyphal formation as a diagnostic tool was demonstrated to be unreliable (Odds et al. 1997). Both molecular and phenotypic observations clearly support placing this species within the genus *Candida* (Fidel et al. 1999). In addition, laboratory investigations indicate that *C. glabrata* undergoes a mating process, similar to that recently discovered in *C. albicans*, and apparently analogous to that of *S. cerevisiae* (Brockert et al. 2003, Dodgson et al. 2005, Soll 2006, Srikantha et al. 2003). Recently, two additional species, *C. nivariensis*

and *C. bracarensis*, have been isolated from clinical specimens and these species are closely related to *C. glabrata*. However, analyses of 26S rRNA gene sequences support the differentiation of these two organisms as separate species (Alcoba-Flórez et al. 2005, Correia et al. 2006, Wahyuningsih et al. 2008).

2.1.4. Candida guilliermondii

This yeast species (teleomorph *Meyerozyma* (*Pichia*) *guilliermondii*) has been isolated from a wide number of environmental sources, e.g., fresh and salt water, soil, sand, amphibians, birds, and humans. It is also a noted source of nosocomial infections. Overall, the incidence of infections due to *C. guilliermondii* is low, but cases of candidemia, endocarditis, and invasive disease have been recorded (Girmenia et al. 2006).

Morphologically, pseudohyphal formation varies in abundance from strain to strain. True hyphae, however, are not produced by this species. The blastoconidia of *C. guilliermondii* may be found in short chains or clusters. Colonies of *C. guilliermondii* appear pink to lavender on CHROMagar *Candida*.

2.1.5. Candida krusei

This species (teleomorph *Pichia kudriavzevii*) is the fifth most common cause of candidemia, but probably is most noteworthy for its innate resistance to the antifungal agent fluconazole in addition to somewhat reduced susceptibility to other drugs (Pelletier et al. 2005). Most commonly isolated from neutropenic patients, *C. krusei* has sometimes been inadvertently selected as a pathogen in some patients receiving prophylactic fluconazole therapy. This yeast, which is commonly recovered from various environmental sources, is a significant etiological agent of vaginitis although it is not typically recovered from mucosal surfaces of healthy persons.

The blastoconidia of *C. krusei* are typically elongate reaching up to 25 μm in length. These cells often take on a "match-stick" like appearance. In stationary liquid cultures *C. krusei* forms a pellicle on the surface of the medium, and on agar media the colonies often appear wrinkled and flat. Physiologically, *C. krusei* can grow on vitamin-free media and differs from other *Candida* spp. in a number of properties. Colonies of *C. krusei* appear pink and have a rough texture on CHROMagar *Candida*.

2.1.6. Candida lusitaniae

Studies have shown *C. lusitaniae* (teleomorph *Clavispora lusitaniae*) to be part of the normal mycobiota of animals, though its prevalence among isolates from clinical samples is low. In health care settings, the possible transmission of this yeast from hospital personnel can lead to nosocomial colonization of the digestive and urinary systems. However, the medical importance of *C. lusitaniae* resides in the intrinsic resistance of some strains to the polyene antifungal agent, amphotericin B (Hawkins and Baddour 2003). Acquired resistance by *C. lusitaniae* to this drug has also been noted. Serious infections by *C. lusitaniae* typically involve patients with hematological malignancies as well as other types of individuals being treated in intensive care units.

Strains of *C. lusitaniae* produce pseudohyphae upon which chains of blastoconidia develop. Colonies of this species appear pink to lavender on CHROMagar *Candida* and some produce a waxy texture on this medium.

2.1.7. Candida parapsilosis

This yeast is one of the most common causes of candidemia, especially in neonatal intensive care units (Bendel 2003, Chapman 2003). Patients with intravenous catheters and prosthetic devices are frequently at risk of infection by *C. parapsilosis*. This fungus produces an adhesive slime layer that enables the transmission to patients from environmental sources and hospital personnel.

In culture, *C. parapsilosis* produces long, branching pseudohyphae that present a "pine forest" appearance. However, the degree of pseudohyphal formation varies among strains. On CHROMagar *Candida*, colonies of this species appear ivory to pink to lavender and some are wrinkled.

To date, no teleomorph for *C. parapsilosis* has been documented. Within this species, though, a variety of previous typing studies was able to discern three different groups of isolates, designated I, II, and III. Using a multilocus typing scheme, however, investigators established two new species, *C. orthopsilosis* and *C. metapsilosis*, to replace the existing designations of *C. parapsilosis* groups II and III, respectively (Tavanti et al. 2005a).

2.1.8. Candida tropicalis

As a frequent isolate from blood cultures, *C. tropicalis* mainly afflicts individuals suffering from leukemia, prolonged neutropenia, or extended hospitalization in intensive care units. This yeast is also found to be a frequent isolate from the oral cavities of asymptomatic persons. Like many other cases of candidiasis, infections due to *C. tropicalis* can be endogenous, i.e., from within the normal mycobiota of the patient, or transmitted from hospital personnel. On CHROMagar *Candida*, steel blue to dark gray colonies are formed by *C. tropicalis* that also often exhibit a brown to purple halo. No documented teleomorph has been observed for *C. tropicalis*.

2.2. *Saccharomyces*

This genus is comprised of eight species. One, *S. cerevisiae*, has been documented to cause human infection (Enache-Angoulvant and Hennequin 2005, Munoz et al. 2005). Strains of *S. cerevisiae* appear to be more pathogenic, especially when used as a probiotic preparation in immune compromised patients. However, with appropriate treatment, such individuals tend to have a better prognosis than persons infected by other routes.

Commonly known as baker's or brewer's yeast, *S. cerevisiae* may colonize the mucosal surfaces of persons with underlying illness. Such infections tend to be superficial (e.g., thrush, esophagitis, vaginitis). Conceivably, cases of vaginitis caused by *S. cerevisiae* may be mistakenly attributed to *C. albicans* due to their similar symptoms. This may result in empirical treatment without performing a culture. In addition, serious invasive infections and fungemia due to *S. cerevisiae* have been recorded. Typically, such patients possess profoundly compromised immunity and infections are often associated with risk factors such as surgery, burns, malignancies, central catheters, hyperalimentation, and broad-spectrum antibiotic use. Because *S. cerevisiae* is a common colonizing fungus, histopathological examination of tissues is necessary to diagnose and confirm infection.

Most individuals tend to think of *S. cerevisiae* as being solely monomorphic. However, it does form pseudohyphae and chains of budding yeasts under the appropriate conditions. For example, nitrogen-poor media induces pseudohyphal growth in *S. cerevisiae* (Gagiano et al. 2002). This alternate growth form of *S. cerevisiae* is the result of a well-developed nutritional sensing mechanism that impacts cellular morphogenic programs (Gimeno et al. 1992).

2.3. *Pichia* and Derived Genera

Many medical mycology texts and journal publications cite two species formerly classified in the genera *Hansenula (H.)* and *Pichia* as

causes of human infection. One, *Wickerhamomyces anomalus (H. anomala)*, is encountered more than the second, *Ogataea polymorpha (H. polymorpha*). The following brief description will employ the current binomials *W. anomalus* and *O. polymorpha*, respectively.

The incidence of mycoses due to *W. anomalus* and *O. polymorpha* has been relatively small. Documented infections include pediatric pneumonia, endocarditis, urinary tract infection, fungemia, and a "thrush-like" condition. One case of invasive disease was associated with chronic granulomatous disease in a child. In all cases, the predisposing factors to infection appear to coincide with those most often associated with encouraging colonization by opportunistic fungi. Clinical distinction between disease caused by *W. anomalus* and *O. polymorpha* is not well established. Isolates of these two species are distinguished from similar yeasts by their sugar fermentation patterns.

2.3.1. Magnusiomyces (Dipodascus) capitatus (Blastoschizomyces capitatus = Geotrichum capitatum)

Dipodascus capitatus is the teleomorph of the fungus commonly known as *Blastoschizomyces capitatus* and occasionally as *Geotrichum capitatum*. This species has been routinely isolated from the environment, particularly woody areas and from poultry feces. However, an environmental source is often not associated with infections. Infections can involve a single organ or multiple organs. Fungemia is common. Disseminated disease is similar in pathology to that evoked by infections due to *Candida* species. Most disease occurs in individuals with hemotologic abnormalities including leukemia and neutropenia (Anaissie et al. 2003, Christakis et al. 2005, Dismukes et al. 2003, Gadea et al. 2004, Levy et al. 2006, Martino et al. 2004, Merz and Hay 2005, Pimentel et al. 2005). Cultures of *D. capitatus* grow as hyaline mycelia that are septate and produce arthroconidia.

3. BASIDIOMYCETOUS YEASTS OF CLINICAL SIGNIFICANCE

The following section provides a brief review of those basidiomycetous yeasts that have been isolated from diseased individuals. The major pathogenic genera, *Cryptococcus* and *Malassezia*, afflict significantly more persons on a regular basis than those yeasts belonging to the genera *Sporobolomyces, Rhodotorula, Trichosporon*, and *Ustilago*. Nonetheless, the latter are included to provide a broad view of the spectrum of infectious fungi. For in-depth descriptions beyond that presented below, the reader is referred to several clinical mycology texts (Anaissie et al. 2003, Dismukes et al. 2003, Kauffmann 2006a, Merz and Hay 2005).

3.1. *Cryptococcus*

The genus *Cryptococcus* is comprised of at least 70 species that have been isolated from various habitats and animals on every continent. Though the species *Cryptococcus (Cr.) laurentii, Cr. curvatus,* and *Cr. albidus* have caused occasional infections, termed cryptococcosis, only two species, *Cr. neoformans* and *Cr. gattii*, have been routinely documented as pathogenic for humans. The biology and clinical significance of these two species have been recently reviewed (Campbell and Carter 2006, Chayakulkeeree and Perfect 2006, Lin and Heitman 2006, Perfect 2006).

Cryptococcosis is caused by basidiomycetous yeasts within the "*Cr. neoformans* species complex" (Lin and Heitman 2006). Phenetic, biologic, and phylogenetic analyses suggest that this complex is comprised of two distinct species, *Cr. neoformans* and *Cr. gattii* (Kwon-Chung et al. 2002, Kwon-Chung and Varma 2006). Both are encapsulated yeasts, but *Cr. gattii* colonies on agar media tend to be more mucoid. Also, subtle morphological differences exist between the yeast cells of *Cr. neoformans* and *Cr. gattii*. For example, *Cr. neoformans* produces colonies of ovoid to spherical cells. In contrast, *Cr. gattii* yeasts tend to be more ellipsoid in appearance. Also, these two species can be differentiated via their biochemical differences. Most notable is that *Cr. gattii* reacts positively on CGB agar, whereas *Cr. neoformans* does not. Furthermore, *Cr. neoformans* appears to consist of two varietal states (var. *neoformans* and var. *grubii*), whereas *Cr. gattii* seems to be a distinct species possessing pronounced intraspecific genetic diversity. Not all taxonomists agree with this position, however. Different experts have championed the establishment of up to eight distinct species within the *Cr. neoformans* species complex (Coenjaerts 2006, Lin and Heitman 2006). Much of this debate has been prompted by advances in the development and application of molecular epidemiological methods as well as the phylogenetic and genotypic analyses of various clinical, environmental, and hybrid isolates (Boekhout et al. 1997, 2001, 2007, Bovers et al. 2006, 2007, Campbell et al. 2005, Diaz et al. 2000, Escandon et al. 2006, Kidd et al. 2004, Meyer et al. 2003, Meyer et al. 1999, Trilles et al. 2003). The collective data from these various studies show that the *Cr. neoformans* species complex is highly divergent at the genomic level and comprises at least nine molecular types. Taken alone, the genotypic variation supports the contention that the complex is in the process of evolving new species. However, what is not clear is at which point does this genotypic variation define the emergence of separate species, particularly if phenetic and biologic information is not considered. Hence, based upon a species concept involving phenetic and biologic evidence, in addition to cladistic data, Kwon-Chung and Varma (2006) argued for two distinct species within the *Cr. neoformans* species complex. The following is a brief summary of this argument.

Prior to 1950, cryptococcosis was considered to be a mycosis caused by the single, homogeneous species, *Cr. neoformans*. However, investigations of the polysaccharide capsule of this species revealed the existence of four capsular epitopes which were designated A, B, C, and D. Apparent hybrid strains possessing serotype AD were also noted. Subsequently, in 1975, heterothallism in *Cr. neoformans* was demonstrated in laboratory experiments (Kwon-Chung 1975, 1976a). To date, the teleomorph of *Cr. neoformans* has not been observed in nature. Laboratory crosses of appropriate mating type strains produce dikaryotic hyphae that form true clamp connections characteristic of basidiomycetous fungi. Some hyphal apices differentiate into basidia wherein meiosis occurs followed by the formation of uninucleate basidiospores. From matings attempted with the various different serotypes, two different biological species were defined. Both can be distinguished on the basis of basidiospore morphology. One species, designated *Filobasidiella neoformans*, produced spherical basidiospores. This teleomorph was initially observed between compatible serotype D strains and later demonstrated between appropriate strains bearing serotypes A and D. Correspondingly, the anamorphic strains comprising these serotypes were designated *Cr. neoformans*. In contrast, mating of suitable strains exhibiting serotypes B and C produced meiospores that are ovoid and bacilliform. Therefore, based upon the morphological differences, the teleomorph resulting from the serotype B and C crossings was defined as a second species, *Filobasidiella bacillispora*. Concomitantly, the anamorphic strains of the B and C serotypes were given a new epithet, *Cr. bacillisporus*, which was later changed to *Cr. gattii* (Kwon-Chung et al. 2002). Subsequent biochemical analyses, e.g., glycine metabolism, canavanine resistance, etc. (Kwon-Chung et al. 1982, Min and Kwon-Chung 1986, Polacheck and Kwon-Chung 1980, 1986)

further supported the phenetic distinction of *Cr. neoformans* and *Cr. gattii* as separate species. Moreover, with the development of molecular methodologies, phylogenetic analysis using nucleotide sequences from ribosomal RNA genes, various housekeeping genes, and virulence-associated genes demonstrated the genetic relatedness of all serotypes (Butler and Poulter 2005, Diaz et al. 2000, 2005, Diaz and Fell 2005a, Fan et al. 1995, Fell et al. 2000, Litvintseva et al. 2003, Xu et al. 2000). That is, serotypes A, D, and AD tended to cluster together as did serotypes B and C. Such observations are consistent with the phenetic and biological analyses that demonstrate the existence of two species.

With regard to pathogenesis, *Cr. neoformans* and *Cr. gattii* tend to afflict different types of individuals. Infections by *Cr. neoformans* are markedly more frequent in immunocompromised individuals, such as HIV-infected patients, with var. *grubii* (= serotype A) being the major etiological agent. In contrast, *Cr. gattii* appears to more commonly cause disease in persons with competent immune systems. Moreover, these species appear to differ in their ecological niches. Whereas *Cr. neoformans* appears to be distributed worldwide, *Cr. gattii* tends to be found mainly in tropical and subtropical regions. However, a recent and ongoing outbreak of *Cr. gattii* infections in Vancouver, Canada and the Northwestern region of the US suggests that this species has disseminated beyond those artificial boundaries (Hoang et al. 2004, Kidd et al. 2004, 2007a, 2007b, Lindberg et al. 2007, MacDougall and Fyfe 2006, MacDougall et al. 2007, Upton et al. 2007).

Cryptococcosis can present a number of clinical manifestations (Chayakulkeeree and Perfect 2006). Infection presumably begins with the inhalation of the fungus via the aerosolization of particles (e.g., basidiospores) from bird dung (Sukroongreung et al. 1998). Such infections may cause asymptomatic lung colonization or a range of symptomatic pulmonary afflictions up to and including fulminant disease resulting in respiratory failure. In immune competent individuals, a coordinated cellular immune response eliminates the fungus or induces a quiescent state within pulmonary foci and lymph nodes. Subsequent debilitation of the immune system may permit such latent organisms to spread to other body locations. In immune compromised persons, however, colonization of the airways by *Cr. neoformans* typically leads to dissemination from the lungs to the central nervous system causing subacute or chronic meningitis. In a significant number of infected individuals, especially HIV-infected patients, skin manifestations occur. Less common are infections of the bone and other organs.

Various attributes of *Cr. neoformans* and *Cr. gattii* contribute to their virulence, including the presence of a polysaccharide capsule, the ability to synthesize melanin, thermotolerance, and the secretion of various metabolites (e.g., mannitol) and enzymes (e.g., proteases). In addition, host response via cellular immunity plays a crucial role in determining if infection is limited to transient colonization of the airways or subsequent establishment of diverse clinical manifestations. Also, the capsule serves as a diagnostic feature that is readily visible when specimens are stained with India ink. The presence of encapsulated yeasts from normally sterile body locations (e.g., spinal fluid) is a presumptive identifying characteristic for cryptococcosis.

Determining the ecological niches of *Cr. neoformans* and *Cr. gattii* may help to identify crucial factors involved in virulence as well as in the dissemination of cryptococcosis. The source of *Cr. neoformans* in the environment has often been associated with pigeon droppings and infected soils. However, guano from other types of birds (e.g., chickens, parrots, turkeys, and canaries), and the soils contaminated by it, has also yielded *Cr. neoformans* upon culture. Both var. *neoformans* and var. *grubii* have been isolated from these sources worldwide. Prior speculation had suggested that bird (pigeon) guano actually selected for the growth *of Cr. neoformans* var. *neoformans* and var. *grubii* since *Cr. gattii* has never been cultured from this source. Nonetheless, it was recently demonstrated that media prepared from pigeon guano does support the growth of both *Cr. neoformans* and *Cr. gattii*, but only *Cr. neoformans* exhibits robust sexual reproduction and basidiospore formation under the same culture conditions (Nielsen et al. 2007). The results of these investigations help explain the cosmopolitan distribution of cryptococcosis due to *Cr. neoformans*, given pigeon migratory patterns and evidence that infection begins via the inhalation of basidiospores. In contrast, *Cr. gattii* is most often found in a unique and restricted habitat. This species has been regularly isolated from gum trees (*Eucalyptus spp*.) located in numerous tropical and subtropical areas across the world. Correspondingly, a significant number of cryptococcosis cases in areas harboring these trees have been due to *Cr. gattii* strains. Other trees in tropical areas may also be niches for this species. Hence, the localized nature of the ecological niche provided by eucalypts and other types of vegetation, which grow mainly in tropical and subtropical regions, helps to clarify the restricted endemicity of infections due to *Cr. gattii*. Curiously, however, the ongoing outbreak of cryptococcosis in the temperate zones of Vancouver, Canada and the Northwestern US appears to be caused by a genetic subset of *Cr. gattii* strains (Kidd et al. 2004, 2007b, MacDougall et al. 2007). These strains appear to have developed the ability to grow in soil and thereby have expanded or altered the ecological niche in which they exist. Subsequently, dispersal of the organism was shown to be anthropogenic (via footwear and the wheels of vehicles) (Kidd et al. 2007a) suggesting that *Cr. gattii* infections will continue to reach beyond this geographical area.

3.2. *Malassezia*

Malassezia spp. are considered part of the normal skin mycobiota of humans and animals (Ashbee 2006, Batra et al. 2005, Chen and Hill 2005, Crespo-Erchiga and Florencio 2006). They have, however, garnered a great deal of attention over the years mainly for their association with various dermatological afflictions. Among these conditions are pityriasis versicolor, seborrhoeic dermatitis, atopic eczema/dermatitis syndrome, psoriasis, dandruff, folliculitis, and otitis. However, members of this genus have also been associated with invasive disease. The following discussion briefly highlights some of the salient features of this fungus.

The taxonomy of the genus *Malassezia* has been, and continues to be, an area of intense investigation. No teleomorph is known for this genus. However, the basidiomycetous affinity of the genus *Malassezia* has been demonstrated phylogenetically using ribosomal RNA gene sequence analysis (Begerow et al. 2000, Fell et al. 2000). Collectively, the species used in these studies formed a separate clade (Malasseziales) within the class Ustilaginomycetes. Presently, physiologic and molecular methods have established the 13 species listed in the following studies (Ashbee 2006, Batra et al. 2005, Cabañes et al. 2007). All species of *Malassezia*, except *M. pachydermatis*, require an exogenous source of lipids for growth. The particular lipid requirements appear to vary among species. However, all grow as yeasts that bud in a repetitive, unipolar fashion. The buds are generated enteroblastically, usually forming a wide base between parent cell and buds. *Malassezia* species can also produce a mycelial form.

Malassezia species are known to produce a diverse range of metabolites, including lactones that give rise to the fruity smell when the fungus is cultured (Ashbee 2006, Labows et al. 1979). These organisms also synthesize compounds (e.g., pityriarubins) that interfere with the respiratory burst of host immune cells (Kramer et al. 2005a). In addition, *Malassezia* species generate azelaic acid

that inhibits reactive oxygen species (Akamatsu et al. 1991). These latter two compounds may be factors that contribute to the survival of the fungus within the harsh environment of the host skin. Moreover, melanin production by *Malassezia* species has been documented *in vivo* (Gaitanis et al. 2005a). Melanin is a known fungal virulence factor that enhances survival of the invading organism on or within the host (Nosanchuk and Casadevall 2003). Hence, melanin formation may be another attribute that contributes to the ability of *Malassezia* species to colonize and survive on the skin.

Although considered to be generally benign members of the normal skin mycobiota, *Malassezia* spp. can pose clinical problems (Ashbee 2006, Batra et al. 2005). Under certain conditions, they initiate a superficial skin infection that, due to their lipid requirements, most often occurs in the sebum-rich areas of the body, i.e., face, forehead, scalp, back and trunk. The major clinical conditions arising from *Malassezia* infections include pityriasis versicolor, seborrhoeic dermatitis, and dandruff. Additional types of superficial pathologies attributed to *Malassezia* include atopic eczema/dermatitis syndrome, otitis, folliculitis, and psoriasis among others. Traditionally, diagnosis of infection was based upon histopathological examination as well as biochemical and phenotypic characterization of clinical isolates. However, the advent of molecular biology has prompted the development of a number of nucleic acid-based methods for the diagnosis of *Malassezia* infection as well as the identification of the specific species involved, including techniques that are culture independent (Boekhout et al. 1998a, Cafarchia et al. 2007, Diaz et al. 2006a, Gaitanis et al. 2002, Gemmer et al. 2002, Guillot and Guého 1995, Guillot et al. 2000, Morishita et al. 2006, Sugita et al. 2001e, Takahata et al. 2007, Theelen et al. 2001).

Perhaps one of the more notable clinical conditions caused by *Malassezia* species is pityriasis versicolor. This dermatologic manifestation is a chronic superficial infection characterized by round to oval lesions on the arms, trunk, and back. The lesions can be hypo- or hyperpigmented. Presumably, pityriasis versicolor occurs when the *Malassezia* species colonizing the skin converts to a mycelial form that subsequently invades the stratum corneum. Hypopigmentation of the lesions may result from the destruction of skin melanocytes caused by the release of malassezin by the invading fungus (Kramer et al. 2005b). Histopathological examination will confirm infection by noting the presence of characteristic yeast and mycelial forms in what is commonly referred to as "spaghetti and meatballs". Studies have suggested that *M. globosa* is the major pathogen causing this condition (Crespo-Erchiga et al. 2000, Crespo-Erchiga and Florencio 2006), although *M. sympodialis* may also be a significant causative agent of this condition (Gupta et al. 2001a, 2004a,b). Two other conditions noted above, seborrhoeic dermatitis and dandruff, are frequently associated with *Malassezia* spp. It has been suggested that seborrhoeic dermatitis, and likely dandruff as well, are caused by an abnormal host response to the yeasts on the skin rather than overgrowth of the pathogen. The major species involved in these conditions appear to be *M. restricta* and *M. globosa*. Similarly, atopic eczema/dermatitis syndrome appears to result from the chronic inflammation of the skin due to various allergens released by *Malassezia*, perhaps in conjunction with other microbiota.

Finally, *Malassezia* spp. have been isolated as agents of deep-seated and systemic infections, including abscesses, mastitis, and peritonitis. Usually, solid organ involvement does not occur. However, the most commonly reported systemic infection is fungemia, particularly in those patients receiving lipid infusions via a catheter. These cases have most often occurred in neonatal units in hospitals, but adult infections have been recorded (Ashbee 2006, Batra et al. 2005, Cannizzo et al. 2007, Chryssanthou et al. 2001, Curvale-Fauchet et al. 2004, Devlin 2006, Giusiano et al. 2006, Rosales et al. 2004). Left untreated, the fungus can disseminate to the lungs and brain. If the infection appears catheter related, simply removing this line helps alleviate the condition although antifungal treatment should still be considered in certain situations.

3.3. Less Common Basidiomycetous Yeast Pathogens

A number of other yeasts with basidiomycetous affinities have been observed to cause mycoses. These include *Trichosporon* spp., *Rhodotorula* spp., and *Sporobolomyces* spp. In addition, two cases of infection due to the corn smut fungus, *Ustilago*, have been recorded (Patel et al. 1995, Teo and Tay 2006). Collectively, these fungi do not cause large numbers of infections, yet they are often difficult to treat due to the condition of the patient or the low susceptibility of the etiological agent to antifungal regimens. A brief review of these fungi is provided below. For further details, the reader is referred to various clinical mycology texts and reviews (Anaissie et al. 2003, Boekhout and Guého 2003, Bouza and Munoz 2004, Dismukes et al. 2003, Girmenia et al. 2005, Groll and Walsh 2001, Kauffmann 2006a, Kiken et al. 2006, Martino et al. 2004, Merz and Hay 2005).

Infections caused by members of the genus *Trichosporon* can be either superficial or deep. There is a variety of species within this genus, but the most well known pathogens are *T. cutaneum* and *T. asahii*. The superficial colonization of hair shafts, termed "white piedra", is caused by several species of *Trichosporon*, but is primarily due to *T. cutaneum* (Anaissie et al. 2003, Dismukes et al. 2003, Kiken et al. 2006, Merz and Hay 2005). Deep-seated infections caused by *Trichosporon* are being reported with increasing frequency (Chowdhary et al. 2004, Girmenia et al. 2005, Rodrigues Gda et al. 2006, Tokimatsu and Kadota 2006). The most common etiological agent is *T. asahii*. Most afflicted patients possess predisposing conditions such as catheterization, steroid use, immunosuppressive therapy, chemotherapy, granulocytopenia, surgical procedures, continuous ambulatory peritoneal dialysis, and HIV infection. Hypersensitivity pneumonitis due to *T. asahii* and *T. mucoides* has also been recorded (Ono et al. 2007, Sugiyama et al. 2005, Tokimatsu and Kadota 2006). The genus is characterized by septate hyphae that produce abundant arthroconidia. Budding cells are also produced but are less common.

The genus *Sporobolomyces* encompasses several species of yeast-like fungi commonly found in various environments. In culture, colonies are pink-orange in color much like *Rhodotorula rubra*. However, *Sporobolomyces* often can be discerned from other yeasts by formation of reproductive ballistoconidia. To date, only seven cases of disease have been recorded due to *Sporobolomyces* spp. (Anaissie et al. 2003, Bergman and Kauffman 1984, Dismukes et al. 2003, Merz and Hay 2005, Morris et al. 1991, Morrow 1994, Plazas et al. 1994, Sharma et al. 2006). These cases included dermatitis, formation of nasal polyps, skin blisters, eumycetoma, and endophthalmitis. Two others involved disseminated disease in two HIV-infected patients indicating the potential of this genus to produce invasive infection in immune compromised hosts.

Finally, *Rhodotorula* is another common environmental yeast that has been documented to cause infection (Anaissie et al. 2003, Dismukes et al. 2003, Merz and Hay 2005). However, like *Sporobolomyces*, the number of cases is small. The most common condition is fungemia, but other conditions have been described, including peritonitis, meningitis, endocarditis, and eye infections. A number of cases have occurred in HIV-infected patients (Kaur et al. 2007, Merkur and Hodge 2002). *Rhodotorula* grows as orange-pink colonies in culture and characteristically does not produce hyphae. Among the various species, some represent the anamorph of the teleomorphic genus *Rhodosporidium*.

4. MEDICALLY-IMPORTANT DIMORPHIC FUNGI

The dimorphic fungi that cause disease in humans typically exist as saprotrophic molds in nature (Anaissie et al. 2003, Dismukes et al. 2003, Kauffmann 2006b, Merz and Hay 2005) (Table 2.2). Upon tissue invasion, many, but not all, undergo a morphological transition to a yeast form. To the non-medical mycologist this can lead to confusion, particularly when culture of clinical specimens results in growth of a mold form.

Another curious feature common to many of the clinically significant dimorphic fungi is their endemic nature. As described below, most of the infections caused by a particular species are geographically restricted. Nonetheless, diseases by these fungi are regularly diagnosed outside their endemic area. In some cases, infections are diagnosed in indigenous people from the region who have traveled outside its boundaries, whereas others have developed in non-native persons subsequent to visiting a particular endemic area.

The descriptions of the dimorphic fungi presented below mainly focus on their anamorphic state. In some cases, the teleomorphs of particular fungi have been demonstrated and each falls within the Ascomycota. For the remaining dimorphic fungi described below, despite the absence of a teleomorph, genetic and morphological evidence strongly suggests that all possess an ascomycetous nature.

4.1. *Histoplasma capsulatum*

The most common endemic disease in the United States is histoplasmosis caused by the fungus *Histoplasma (Histo.) capsulatum* var. *capsulatum*. A second variety, *Histo. capsulatum* var. *duboisii*, is restricted to portions of the African continent. A third variety, *Histo. capsulatum* var. *farciminosum*, is a pathogen of mules and horses in parts of Asia and Africa. Although the latter variety is also thermally dimorphic, it will not be included in the present discussion. For more detailed information regarding histoplasmosis and the biology of *Histoplasma*, including virulence attributes, the reader is referred to recent reviews (Couppie et al. 2006, Wheat 2006, Woods 2006).

Briefly, *Histo. capsulatum* var. *capsulatum* mainly resides in the Mississippi and Ohio River valleys of the United States and in portions of Central and South America, whereas *Histo. capsulatum* var. *duboisii* is most often found between the Tropic of Cancer and the Tropic of Capricorn in Africa. Sources of exposure for both varieties include caves, decaying and rotting organic matter, and bird roosts or chicken coops. Moreover, the pathologies of these two etiologic agents are distinct. For further details, see Couppie et al. (2006), Wheat (2006), and Woods (2006). Morphologically, both varieties are indistinguishable in their mold phase. Yet the yeast forms *of Histo. capsulatum* var. *capsulatum* and *Histo. capsulatum* var. *duboisii* are different. The former species appears as tiny budding yeasts (2–4 μm) and are typically found residing within macrophages *in vivo*. By comparison, the budding yeast form of *Histo. capsulatum var. duboisii* is significantly larger (8–15 μm), having thick walls and a prominent bud scar. In addition, this latter variety often appears as short chains of yeasts within infected tissue. The ascosporic state of *Histo. capsulatum* var. *capsulatum* is *Ajellomyces capsulatus* (Class Eurotiomycetes, Order Onygenales, Family Ajellomycetaceae). Interestingly, although an ascosporic state for var. *duboisii* has not been observed, strains of this variety will mate with the *capsulatum* variety and form cleistothecia that are indistinguishable from those produced by *A. capsulatus*. The ascospores in this cross-variety mating do not germinate *in vitro*, but they will grow and cause disease in mice.

4.2. *Blastomyces dermatitidis*

Blastomyces dermatitidis is the causative agent of the fungal disease termed blastomycosis (Bradsher et al. 2003, Bromel and Sykes 2005, Kauffman 2006b). This mycosis is endemic to the eastern half of North America, thus earning it the ethnocentric name of North American blastomycosis. However, the disease has been documented in the continent of Africa as well as portions of central India.

Infection by *B. dermatitidis* is initiated via the inhalation of conidia. If suspected, diagnosis of blastomycosis can be readily made due to the relative ease of culture. The mold phase that grows at 25°C readily produces macroconidia, but these are quite similar to those formed by many other types of fungi. Instead, observation of the yeast phase of *B. dermatitidis*, either *in vitro* or *in vivo*, is a key diagnostic feature. Microscopically, yeast cells of this fungus are large (8–12 μm in diameter), multinucleate, and have a thick wall, often described as a "double wall". The most prominent attribute of the yeast form is that budding cells exhibit a wide base of attachment between a cell and its bud, i.e., broad-based budding. The ascosporic state of *B. dermatitidis* is *Ajellomyces dermatitidis* (Class Eurotiomycetes, Order Onygenales, Family Ajellomycetaceae).

4.3. *Paracoccidioides brasiliensis*

Paracoccidioidomycosis is the clinical pathology caused by the dimorphic fungus, *Paracoccidioides (Para.) brasiliensis* (San-Blas et al. 2002, Visbal et al. 2005). This fungus has exhibited no known teleomorph. However, based upon phylogenetic comparisons of rRNA gene sequences, *Para. brasiliensis* belongs to the order Onygenales, family Onygenaceae. The geographic distribution of *Para. brasiliensis* ranges from Mexico to South America, but it is more prevalent mainly on the southern continent rather than Central America.

Like other endemic fungi, infection begins through breathing in an infectious propagule that may or may not result in a symptomatic

TABLE 2.2 Selected Dimorphic Fungi Pathogenic for Humans and Animals

Anamorph	Known Teleomorph	*In Vivo* Morphology
Histoplasma capsulatum var. *capsulatum*	*Ajellomyces capsulatus*	Small (2–4 μm) ovoid, budding yeasts
var. *duboisii*	*Ajellomyces capsulatus*[a]	Larger (8–15 μm), thick-walled budding yeasts with a prominent bud/birth scar
Blastomyces dermatitidis	*Ajellomyces dermatitidis*	Large (8–15 μm), broad-based budding yeasts
Paracoccidioides brasiliensis	None	Multiply budding yeasts ("Pilot's Wheel", 15–30 μm)
Sporothrix schenckii	None	Round to ovoid yeasts (4–6 μm, cigar-shaped)
Penicillium marneffei	None	Small (3–5 μm), globose to elongated fission yeast

[a]*Variety* duboisii *will mate with an appropriate strain from var.* capsulatum *and form a teleomorph indistinguishable from* A. capsulatus.

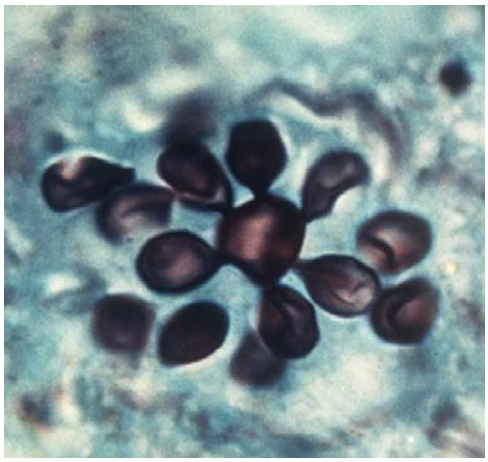


FIGURE 2.1 Multiple budding yeast form of *Paracoccidioides brasiliensis* in tissue. Gomori Methenamine Silver stain. Bar = 10 μm. Figure adapted from image provided through the courtesy of www.doctorfungus.org © 2007.

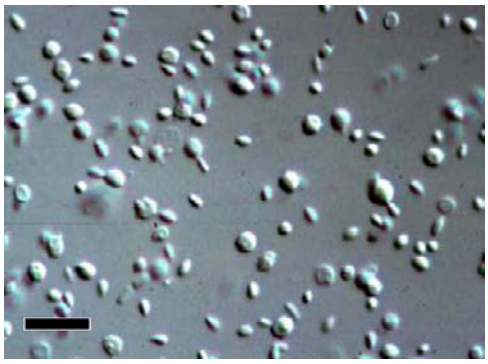


FIGURE 2.2 Budding yeast cells of *Sporothrix schenckii* grown in a 37°C broth culture. Differential interference contrast optics. Bar = 12 μm. Figure adapted from image provided through the courtesy of www.doctorfungus.org © 2007.

response. Once established in the lungs, however, *Para. brasiliensis* undergoes a morphological transformation that gives rise to the yeast phase that is decidedly characteristic for the mycosis caused by this fungus. At 37°C or *in vivo*, spherical yeast cells develop over a wide range of sizes (3–30 μm in diameter). From attachment points all along the surface of a central yeast cell, lemon-shaped buds (2–10 μm in diameter) develop that are connected to the parent cell through a narrow-based, isthmus-like connection. In simple terms, this entity is often referred to as a "pilot's wheel" or "mariner's wheel" (Fig. 2.1).

4.4. *Sporothrix schenckii*

The etiological agent of sporotrichosis, *Sporothrix schenckii*, causes a cosmopolitan disease that probably ranks as the world's most frequent subcutaneous mycosis (Bustamante and Campos 2001, Kauffman 2006b, Pang et al. 2004). Sporotrichosis occurs in many areas of the world, but is most frequently encountered in the United States, Central and South America, Africa, and Japan. Most cases are sporadic, although rare epidemics have been well documented.

Transmission of *S. schenckii* typically occurs through traumatic implantation, such as a prick from a rose thorn or pine needle. In several documented epidemics, implantation was directly related to small skin injuries due to handling pine seedlings, shrubs, or other types of vegetation. However, several cases of sporotrichosis have been reported that resulted from non-implantation means of infection. Many of these were laboratory-acquired infections (Cooper et al. 1992). In addition, pulmonary disease has been traced to the inhalation *of S. schenckii* conidia.

Like the other dimorphic fungi described above, *S. schenckii* grows as a mold at room temperature forming unicellular, tear-shaped to clavate conidia that are darkly pigmented. When incubated at 37°C, though, this fungus undergoes mold-to-yeast conversion. The yeast phase is distinctive in that the budding yeast cells (4–6 μm in diameter) tend to exhibit a "cigar shaped" appearance (Fig. 2.2). Curiously, however, the yeast phase of this fungus is rarely seen in clinical specimens. Finally, a few sporotrichosis infections have been caused by *S. schenckii* var. *luriei*. This variety differs from *S. schenckii* in that the yeast form, which can exist at 25°C, is large and thick-walled.

No known sexual phase has been observed for *S. schenckii* though evidence suggests it may be closely related to the genus *Ophiostoma*. In addition to *S. schenckii*, which is classified within the ascomycetous family Ophiostomataceae (Class Sordariomycetes, Order Ophiostomatales), cases of sporotrichosis have been ascribed to a far less common species, *S. cyanescens*. This species does not readily convert to a yeast phase *in vitro* and possesses septal structures consistent with basidiomycetous fungi. Recently, this species was transferred to the basidiomycetous genus *Fugomyces* (Sigler and Verweij 2003).

4.5. *Penicillium marneffei*

Infections by *Penicillium s*pp. (penicilliosis) are rare with one exception – those caused by *Penicillium (Pen.) marneffei* (Cooper 1998, Cooper and Haycocks 2000, Cooper and Vanittanakom 2008, Vanittanakom et al. 2006, Viviani and Vanittanakom 2005). The ability of this fungus to cause disease is directly associated with its formation of a yeast phase *in vivo*. This species emerged in the early 1980s as a significant pathogen of HIV-infected individuals residing or having traveled in Southeast Asia, the endemic region of disease caused by this fungus. Prior to this time, infections by *Pen. marneffei* were relatively rare. Penicilliosis due to *Pen. marneffei* typically disseminates systemically in immunocompromised patients and, left untreated, is universally fatal.

Infection by *Pen. marneffei* is presumably initiated by the inhalation of conidia that are subsequently phagocytized by pulmonary histiocytes. There, the fungus grows as a small yeast ($2–3 \times 2–7$ μm) and is approximately the same size as yeast cells of *Histo. capsulatum* (Fig. 2.3). This may have been the factor by which many of the early cases were misdiagnosed as histoplasmosis. The distinguishing feature of *Pen. marneffei* yeast cells is that they divide by fission as opposed to the budding yeasts of *Histo. capsulatum*. Cultures of *Pen. marneffei* incubated at 37°C also reproduce as fission yeasts.

Taxonomic studies have placed this fungus within the Phylum Ascomycota (Class Eurotiomycetes, Order Eurotiales, Family Trichocomaceae) (LoBuglio and Taylor 1995, Vanittanakom et al. 2006, Woo et al. 2003). Although no ascosporic state has been observed for *Pen. marneffei*, experimental studies have noted potential heterothallism in this fungus by documenting the existence of mating-type-like genes in its genome (Woo et al. 2006). Other studies have suggested that the profound asexual nature of this fungus has led it to develop a niche-adapted genotype, thus perhaps explaining its endemic nature (Fisher et al. 2005).



FIGURE 2.3 *Penicillium marneffei* growing as a fission yeast in a broth culture incubated at 37°C. Differential interference contrast optics. Bar = 5 μm.

5. OTHER YEAST-LIKE MYCOTIC AGENTS

The following brief descriptions cover three distinct types of fungi that are not often given consideration as medically important yeasts. One, the dematiaceous (phaeoid) fungi, can exhibit growth as budding yeasts both *in vitro* and *in vivo*. A second, *Lacazia loboi*, is a non-cultureable fungus that elicits keloidal lesions containing yeast cells often in chains. The remaining organism, *Pneumocystis*, is a major opportunistic pathogen of HIV-infected patients and for years was considered to be protozoan-like in nature, but is presently considered to belong to the Ascomycota (see Chapter 58, *Pneumocystis*).

5.1. Dematiaceous (Phaeoid) Fungi

The dematiaceous fungi represent a heterogeneous collection of darkly pigmented organisms (Cooper 2005). The term "dematiaceous", though not an appropriate description based upon its Greek root, has been used for so many years that it has found nearly complete acceptance in the mycological literature. Still, a better term to describe these pigmented fungi is "phaeoid". Both terms will be used interchangeably in the following discussion.

The dematiaceous fungi exist either as monomorphic or pleomorphic organisms capable of causing a wide range of mycoses (Anaissie et al. 2003, Dismukes et al. 2003, Merz and Hay 2005). It is the pleomorphic nature of some of these fungi that presents many challenges to the clinical mycologist. Some species can grow in a variety of forms, among which includes mold, yeast, and pseudohyphal phases. To further complicate this issue, some species growing as molds can exhibit more than one type of conidium generated by different modes of conidiogenesis. In essence, a significant number of the phaeoid fungi express multiple synanamorphs. Of the most intriguing synanamorphs are those designated "black yeasts".

The phaeoid yeasts are anamorphs of certain darkly pigmented molds. They mainly reproduce by budding. However, not all dematiaceous molds produce a yeast phase. Of those that do, most exhibit ascomycetous characteristics, but a few appear more basidiomycetous in nature. Moreover, not all black yeasts are associated with human disease. Those that do cause infection represent two distantly related phylogenetic groups within the Ascomycota (de Hoog 1993, de Hoog et al. 2003, Matos et al. 2003, Spatafora et al. 1995, Uijthof 1996). Most of the infections caused by these fungi can be grouped into the pathological condition known as phaeohyphomycosis, but they can also elicit other conditions (Anaissie et al. 2003, Dismukes et al. 2003, Merz and Hay 2005).

Clinical specimens of black yeasts can present a challenge in their identification (Dixon and Polak-Wyss 1991). Complicating this effort is that taxonomy of the phaeoid fungi appears to be in continual flux, thereby prompting seemingly constant nomenclatural changes. For an up-to-date synopsis of current nomenclature and obsolete synonyms of medically relevant fungi, including the black yeasts, the reader is urged to access the excellent web site, Doctor Fungus (www.doctorfungus.com). Despite these difficulties, however, Sanche et al. (2003) presented a clear description of those factors that differentiate between the two groups of black yeasts previously defined by phylogenetic methods as well as the individual species comprising these groups. The reader is referred to this reference for details.

Within the scheme of Sanche et al. (2003), Group 1 consists of *Exophiala* species and *Wangiella dermatitidis*, both of which exhibit early growth as yeasts, but frequently convert to a mycelial phase in culture. There is a great deal of controversy regarding the correct taxonomy of *Wangiella dermatitidis* and its alternate binomial *Exophiala dermatitidis*. The issue basically comes down to two different interpretations on the mode of conidiogenesis in this fungus. Perhaps future genetic examination of the genomes of these putatively different fungi will settle the matter. Regardless of specific epithet, different species of these fungi are responsible for infections resulting in various forms of phaeohyphomycosis, eumycetoma, endocarditis, and chromoblastomycosis. However, it is primarily in phaeohyphomycosis that the yeast phase of these species is noted *in vivo*.

Group 2 of the black yeasts encompasses *Aureobasidium pullulans, Hormonema dematoides,* and *Phaeoannellomyces werneckii (= Hortaea werneckii)*. Cases of phaeohyphomycosis, peritonitis, onychomycosis, and keratitis have been attributed to *A. pullulans* and *H. dematoides*. Both of these fungi are characteristically found in soils, waters, and fruits. Again, the yeast phase is primarily observed in phaeohyphomycosis. Infection in all these pathologies usually occurs via traumatic implantation of the fungus. In contrast, *P. werneckii* is the etiological agent of a superficial type of phaeohyphomycosis designated tinea nigra. This pathology is characterized by darkened areas of the palm or sole of the foot, in which yeast-like cells can be observed. The condition is strictly cosmetic and infection presumably occurs via skin abrasion in the presence of a suitable environmental source of the fungus.

5.2. *Lacazia loboi*

Lobomycosis is a rare, chronic subcutaneous infection of the skin. The infection is marked by the formation of keloidal, ulcerated, or verrucose lesions that contain the etiological agent, *Lacazia loboi* (Fonseca 2007, Talhari and Pradinaud 2005). The disease is confined to parts of Central and South America and also appears to be associated with seawater off the coasts of these areas. It is there and in other offshore tropical waters that infected dolphins have been documented (Haubold et al. 2000). However, the exact source of the organism is unknown, particularly since *L. loboi* has never been cultured from nature. Some evidence exists that the organism has been cultured in experimental animals using infected tissue (Talhari and Pradinaud 2005).

Diagnosis of infection is made by the histopathological observation of *L. loboi* in tissue. This fungus is present in large numbers mainly as chains of yeast cells connected by a small isthmus. Solitary yeast cells are also present, but hyphae have never been noted.

Despite the absence of an *in vitro* culture system for *L. loboi*, advances have been made to phylogenetically assess the lineage of

this fungus. Using novel methods to extract DNA from infected lesions, various gene fragments were amplified, cloned, and sequenced (Haubold et al. 1998, Herr et al. 2001, Mendoza et al. 2005, Vilela et al. 2005). The resulting data clearly show that a close relationship exists between *L. loboi* and *Paracoccidioides brasiliensis*, thereby placing the former species within the ascomycetous order Onygenales.

5.3. *Pneumocystis*

Species of *Pneumocystis* are known pathogens of humans and animals. However, when first isolated in 1909, *Pneumocystis* was mistakenly identified as part of the life cycle of the protozoan parasite, *Trypanosoma cruzii*. This association relegated *Pneumocystis* to the protozoan realm, and virtual obscurity, until the 1950s when it was shown to be a cause of epidemic pneumonia. This prompted renewed interest in the pathogenicity of *Pneumocystis* as well as evoking studies directed towards its proper classification. Subsequent morphological and biochemical studies of this organism yielded some clues that suggested an affinity to the fungi, but these data were far from conclusive. Then, in 1988, Edman et al. (1988) demonstrated the relationship of *Pneumocystis* to the fungi based upon comparisons of ribosomal RNA gene sequences. Thereafter, a number of phylogenetic studies have been performed which include trees based upon SSU RNA gene sequences that infer a relationship with ascomyceteous yeasts (Gargas et al. 1995). For a more in-depth historical perspective of the taxonomy and phylogeny of *Pneumocystis*, the reader is referred to an excellent review by Cushion (2005), as well as Chapter 58 in this book.

A complete description of the biology of this fungus, its host range, pathogenicity, and diagnosis are beyond the scope of this work. Therefore, the reader is directed to several reviews that address these and other topics (Cushion 2005, Frenkel 1999, Hui and Kwok 2006, Morris et al. 2004a, Peterson and Cushion 2005, Redhead et al. 2006, Thomas and Limper 2007, Wazir and Ansari 2004). To summarize, however, there are currently four species of *Pneumocystis* recognized. *Pneumocystis jiroveci*, previously known as *P. carinii*, is a pathogen of humans, particularly those that are immunocompromised. Such conditions include HIV infection, leukemia, renal disease, co-infection by other viruses, and carcinoma. Moreover, *P. jiroveci* has been detected as a pathogen of neonates and pregnant women. Not all infections by *P. jiroveci* result in the pneumonia typically associated with HIV-infected patients. Extrapulmonary infections do occur in a variety of organ systems, though this is rare. The remaining species of *Pneumocystis* afflict other mammals, particularly rodents. Rats are infected by *P. carinii* and *P. wakefieldiae*, whereas mice are hosts for *P. murina*. Diagnosis of infection by culture is not possible given the absence of a continuous *in vitro* system for *Pneumocystis*. Instead, diagnosis relies on microscopic observations of stained specimens, serological tests, and molecular methods involving DNA amplification techniques.

6. SUMMARY

The medically significant yeasts comprise more genera than the traditionally held pathogens in the genera *Candida* and *Cryptococcus*. Clinically important yeast forms can also be found among the endemic dimorphic fungi, the dematiaceous molds, and even a noncultureable fungus. Collectively, these fungal pathogens exhibit either teleomorphs of the Ascomycota or Basidiomycota, or their anamorphic forms express morphological and genetic features consistent with one of these taxa. They comprise a diverse spectrum of fungi that have found the means, primarily by exploiting a host organism's weakened immune system, to become noteworthy mycotic agents. Furthermore, they portend the potential for the spectrum of fungal pathogens to become wider and deeper in the number of etiological agents derived from normally benign species. Vigilance by the general as well as the medical mycologist must be maintained so as to better understand how to address the future challenges likely to be posed to public health by fungi, particularly the yeasts.

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Chapter 3

Yeast Biotechnology

Eric A. Johnson and Carlos Echavarri-Erasun

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The following genus abbreviations are used in this chapter: *Bla., Blastobotrys; C., Candida; Crypt., Cryptococcus; D., Debaryomyces; E., Eremothecium; Geo., Geotrichum; K., Kluyveromyces; Kom., Komagataella; O., Ogataea; Ph., Phaffia; P., Pichia; Pseud., Pseudozyma; Rhspor., Rhodosporidium; Rh., Rhodotorula; S. Saccharomyces; Scopsis, Saccharomycopsis; Schef., Scheffersomyces; Schiz., Schizosaccharomyces; Schwan., Schwanniomyces; Tor., Torulaspora; Tr., Trichosporon; X., Xanthophyllomyces; Y., Yarrowia; Z., Zygosaccharomyces.*

1. INTRODUCTION

Yeasts have benefitted humankind for millenia. They have wide-ranging fundamental and industrial importance in scientific, food, medical, and agricultural disciplines (Fig. 3.1). Traditional industrial attributes of yeasts include their primary roles in many food fermentations such as beers, cider, wines, sake, distilled spirits, bakery products, cheese, sausages, and other fermented foods (Table 3.1). Other long-standing industrial processes that involve yeasts are the production of fuel ethanol, single cell protein (SCP), feeds and fodder, industrial enzymes, and small molecular weight metabolites. More recently, *Komagataella* (*Pichia) pastoris*, *Saccharomyces cerevisiae*, *Ogataea* (*Hansenula) polymorpha*, and certain other yeast species have been developed as industrial organisms for the heterologous production of enzymes and proteins, including protein pharmaceuticals. Yeasts, especially *S. cerevisiae*, are increasingly being used as hosts for expression of protein biocatalysts and multi-enzyme pathways for the synthesis of fine chemicals and small molecular weight compounds of medicinal and nutritional importance. Yeasts have important roles in agriculture as agents of biocontrol, bioremediation, and as indicators of environmental quality. Several of these processes and products have reached commercial utility, while others are in development. Owing to advances in functional genomics and systems biology, *S. cerevisiae* is presently the primary model organism for study of eukaryotic biology and human disease. The objective of this chapter is to describe yeast processes currently used by industry and those in developmental stages and close to commercialization. Emphasis will be given to new developments and opportunities in industrial applications of yeasts since traditional processes have been thoroughly described in the existing literature.

2. HISTORICAL HIGHLIGHTS

Since ancient times, fermented beverages and foods produced through the activities of yeasts have contributed prominently to the worldwide advancement and sustainability of human societies (Legras et al. 2007, Ulber and Soyez 2004). The domestication of *Saccharomyces cerevisiae* can be considered a pivotal event in human history. Archaeologists found evidence that alcoholic fermented beverages produced by yeasts were consumed in Neolithic times (8500–4000 BC) in China, Iran and Egypt, and other areas of the world (Cavalieri et al. 2003, McGovern 2003, McGovern et al. 1997, 2004, Ulber and Soyez 2004). Babylonian stone tablets more than 6,000 years old illustrated beer and wine recipes (Legras et al. 2007, Ulber and Soyez 2004). Many other fermented foods also originated in Neolithic times, such as African kafir and sorghum beer, pulque in Mexico, leavened breads in various regions, and several fermented foods and beverages from soy, rice, and vegetables (Aidoo et al. 2006, Beuchat 1995, Boekhout and Robert 2003, Dirar 1994,

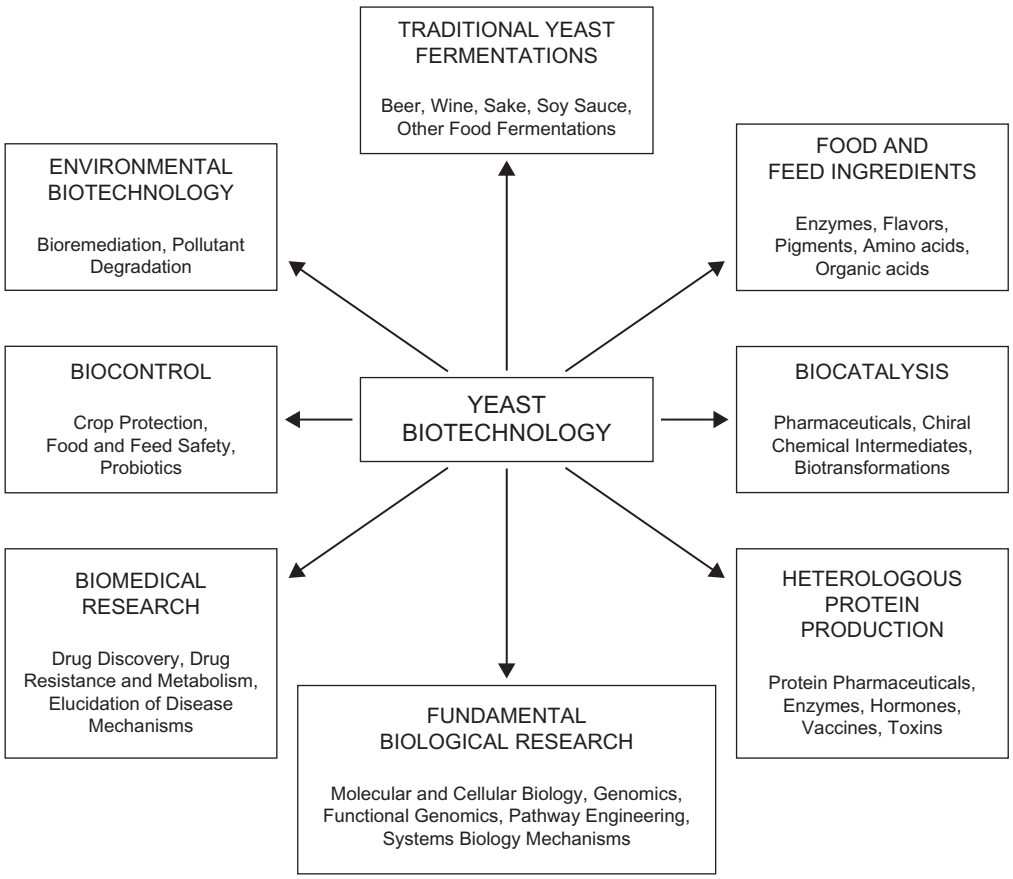


FIGURE 3.1 Various disciplines in yeast biotechnology (adapted and expanded from Walker 1998).

TABLE 3.1 Representative Yeast Genera and Species Associated with Fermented Foods and Feeds

Food	Yeast Species Involved
Beers and ales	*Saccharomyces cerevisiae*
	Saccharomyces bayanus
	Saccharomyces pastorianus (=*S. carlsbergensis*)
	Saccharomyces bayanus var. *uvarum*
Breads and bakery products	*Saccharomyces cerevisiae*
	Torulaspora delbrueckii
	Candida krusei (sourdough)
	Candida milleri (sourdough)
	Kazachstania exigua (sourdough)
	Zygosaccharomyces rouxii
Cachaça	*Saccharomyces cerevisiae*
	Schizosaccharomyces pombe
Cheeses	*Debaryomyces hansenii*
	Candida spp.
	Kluyveromyces marxianus
	Kluyveromyces lactis
	Yarrowia lipolytica
	Geotrichum candidum
	Other *Geotrichum* spp.
	Rhodotorula spp.
	Trichosporon spp.
	Saccharomyces cerevisiae
Other dairy products (e.g., kefir; yoghurt, fermented milk)	*Kluyveromyces lactis*
	Kluvyveromyces marxianus
	Candida kefyr
	Candida famata
	Candida krusei
	Debaryomyces hansenii
	Geotrichum candidum
	Yarrowia lipolytica
	Saccharomyces cerevisiae
Ciders	*Saccharomyces cerevisiae*
	Saccharomyces bayanus
Cocoa	*Saccharomyces cerevisiae*
	Hanseniaspora uvarum
	Kloeckera apiculata
	Kluyveromyces marxianus
	Pichia fermentans
Coffee	*Kluyveromyces marxianus*
	Saccharomyces bayanus
	Schizosaccharomyces spp.
	Candida boidinii
Fermented meats and sausages	*Debaryomyces hansenii*
	Candida spp.
	Cryptococcus spp.
	Rhodotorula spp.
	Saccharomyces cerevisiae
	Yarrowia lipolytica
Fermented milks	*Kluyveromyces* spp.
	Candida parapsilosis
	Candida krusei
	Candida valida
	Saccharomyces bayanus
	Yarrowia lipolytica
Fermented olives and cucumbers	*Debaryomyces* spp.
	Candida spp.
	Kluyveromyces marxianus
	Lachancea cidri
	Pichia spp.
	Rhodotorula spp.
	Saccharomyces spp.
Kenkey (African fermented maize)	*Candida* spp.
	Debaryomyces spp.
	Kluyveromyces spp.
	Saccharomyces spp.
	Trichosporon spp.
Kimchi	*Candida* spp.
	Cryptococcus spp.
	Debaryomyces spp.
	Saccharomycopsis spp.
	Kluyveromyces spp.
	Pichia spp.
	Rhodotorula spp.
	Saccharomyces spp.
Lao Chao	*Saccharomycopsis fibuligera*
	Saccharomycopsis malanga
Soy paste (Chiang; Miso)	*Zygosaccharomyces* spp.
	Candida spp.
Soy sauce (Jiang yu; Shoyu)	*Zygosaccharomyces rouxii*
	Candida famata
	Candida etchellsii
	Candida versatilis
	Debaryomyces spp.
	Other *Candida* spp.
Tea fungus	Zygosaccharomyces *Kombuchaensis*
	Candida spp.
Wines	*Saccharomyces cerevisiae*
	Saccharomyces bayanus
	Saccharomyces bayanus var. *uvarum*
	Saccharomyces kudriavezii
	"Saccharomyces sake"
	Other *Saccharomyces* spp.
	Hanseniaspora uvarum
	Kloeckera apiculata
Silage	*Candida* spp.
	Cryptococcus spp.
	Pichia spp.
	Saccharomyces spp.
	Trichosporon spp.
Probiotics	*"Saccharomyces boulardii"*
	Saccharomyces cerevisiae
	Kluyveromyces marxianus
	Candida spp.

Primary sources: Bekatorou et al. 2006, Hesseltine and Wang 1986, Hui et al. 2004, Zeikus and Johnson 1991; also see individual sections in this chapter. Where several species within a genus are involved or the species have not been determined, only the genus is listed.

Hui et al. 2004, Steinkraus 2004). The production of fermented beverages and foods occurred in parallel with the onset of agriculture, and provided nutrition and sustenance to humans (Legras et al. 2007, Ulber and Soyez 2004). Historical evidence indicates that the availability of fermented beverages and foods was a motivation for humans to settle in geographic areas and to become agriculturists (Katz and Voight 1989). Settlement was a successful strategy to provide a reliable and secure food supply compared to nomadic life, and provided social, economic, and health attributes for human nourishment and development (McGovern et al. 2004).

The technologies and know-how used in food and alcoholic fermentations have been continuously refined over millenia, comprising the earliest developed biotechnology applications. The practical skills required for efficient yeast fermentation processes were transferred from generation to generation without detailed knowledge of the scientific principles governing the processes. In 1864, it was reported that alcoholic fermentation was carried out by a substance made by *S. cerevisiae*, which contained nitrogen, could be precipitated by ethanol, and transformed sugar into alcohol in yeast extracts free of cells (Straathof and Adlercreutz 2000). This led to the discovery of enzymes, literally meaning "in yeast". The scientific and technological understanding of fermentations was elucidated primarily from the investigations of Louis Pasteur (1822–1895). In his studies of wine and beer fermentations, he reported in 1876 that microorganisms were responsible for alcohol formation from sugars (Barnett 1998, 2000, 2003, Cuny 1966, Dubos 1960). Pasteur also introduced the concept of aseptic conditions and pure cultures to help resolve problems of "bad" fermentations, and he recognized the distinction between alcoholic fermentation and aerobic growth of yeasts. Pasteur also proposed that wine yeasts occurred on the surface of grapes, which provided an inherent source for inoculation of grape juice (Mortimer and Polsinelli 1999).

Pure cultures of *S. cerevisiae* and other yeasts were further established in 1888 by Emil Christian Hansen from the Carlsberg brewery in Copenhagen, and in 1890 by Müller-Thurgau in Geisenheim, Germany (Dequin 2001, Verstrepen et al. 2006). Emil Fischer and Eduard Büchner and their contemporaries began to unravel the cell-free basis of yeast metabolism in the late 1800s, which led to detailed studies of yeast biochemistry and metabolism and fundamental discoveries in biochemistry and cell biology. Yeast technologists, notably those of the Delft school, including Beijerinck, van Niel, Kluyver and Phaff (Bennett and Phaff 1995, Lachance 2003, Robertson 2003, van Niel 1949), advanced the understanding of yeast ecology, diversity, physiology and technological value, which ushered in the modern era of yeast biotechnology.

An important contemporary attribute of *S. cerevisiae* is its general acceptance as the prominent model organism for the investigation of fundamental biological processes in eukaryotes, including humans (Dolinski and Botstein 2005, Glaever et al. 2002, Mustacchi et al. 2006, Nielsen and Jewett 2007, Oliver 2006, 2007, Suter et al. 2006). The facile genetic manipulation and the availability of defined strain collections are being utilized in a number of scientific disciplines. The importance of *S. cerevisiae* as a model organism derived in part from the landmark achievement of the complete genome sequence of strain S288C during 1992–1996 through the cooperation and unity among yeast biologists (Dolinski and Botstein 2005, Goffeau et al. 1996, Hohmann 2005, Oliver 2007). The genome of *S. cerevisiae* was the first eukaryotic genome sequenced, and remains today the most thoroughly characterized and exploited (Dolinski and Botstein 2005, Fisk et al. 2006). Post-modern yeast biotechnology elaborated during the past two decades has incorporated new disciplines of functional genomics, including metabolomics, metabolic engineering, and systems biology (Mustacchi et al. 2006, Nielsen and Jewett 2007, Oliver 2007). The availability of complete genome sequences of other species (see section 18) has also presented the opportunity for detailed studies of properties of yeasts, including species of existing and potential industrial relevance.

3. OVERVIEW OF THE INDUSTRIAL IMPORTANCE OF YEASTS

Saccharomyces cerevisiae and certain other yeast species are arguably the most important group of biotechnological organisms. Yeasts are the major producer of biotechnology products worldwide, exceeding production, in capacity and economic revenues, of any other group of industrial microorganisms. The annual world production of *S. cerevisiae* is more than 1 million tons (Hansen 2004, Verstrepen et al. 2006), a level that exceeds the combined production of other industrial microorganisms by about two orders of magnitude (Hansen 2004). The economic values of fermented beverages and foods involving yeasts are enormous. Beer had an estimated annual production of >60 million tons with a total revenue of $294.5 billion in 2006 (Verstrepen et al. 2006). This reflects only sales and does not include other aspects including employment, business services, construction, tourism, and taxes generated. More than 30 million tons of wine are produced annually (Verstrepen et al. 2006). In the USA, the economic impact of wine and grape products on the American economy was >$162 billion (MKF Research 2007). An estimated 600,000 tons of baker's yeast and 800,000 tons of single cell yeast protein are produced each year (Hui 2004, Verstrepen et al. 2006). Due to diminishing resources, environmental factors, and the need for sources of sustainable energy, yeasts have attracted renewed interest in recent years for the production of fuel alcohol and other industrial products from biomass (Antoni et al. 2007, Lynd et al. 2002). Yeasts are an important source of enzymes for traditional markets including food, feed, and agriculture, as well as specific biocatalysts, which are increasingly used in pharmaceutical and fine chemical synthesis, an industry long dominated by total chemical syntheses (Blaser et al. 2005, Faber 2004). The market size of industrial enzymes and biocatalysts was about $1.5 billion in 2002, and is expected to grow to more than $8 billion by 2011 (Cherry and Fidanstef 2003). Enhanced utilization of yeasts as sources of native and heterologous enzymes in the pharmaceutical and chemical industries is leading to new products such as chiral intermediates for the production of pharmaceuticals and fine chemicals (Faber 2004, Schmidt 2004, Walsh 2005, 2006). Global pharmaceutical sales were ca. $600 billion in 2003–2006 (Melmer 2005).

The following sections describe industrial yeasts and their importance in various industries. Emphasis will be given to new developments and opportunities in these disciplines. The unit operations in traditional and well-studied yeast processes such as food and beverage production are not reviewed since several excellent treatises cover the production of wines, beer, distilled spirits, bakery, fuel alcohol, food and fodder yeasts, as well as other yeast technological processes (Boekhout and Robert 2003, Hui et al. 2004, Hutkins, 2006, Oliver, 1991, Prescott and Dunn 1940 and subsequent editions, Rehm and Reed 1995, Rose and Harrison 1993). Similarly, various aspects of the ecology, physiology, structure, classification, phylogeny, genetics, and other properties of yeasts related to industrial activities have been expertly reviewed and the reader is referred to excellent reference works (Boekhout and Kurtzman 1996, Boekhout and Robert 2003, de Winde 2003, Kurtzman and Fell 1998, Phaff et al. 1978). Expert treatises of methods for isolation, culturing, identification, characterization, cell biology, and genetic manipulation of yeasts are available (Amberg et al. 2005, de Winde 2003, Kurtzman and Fell 1998, Phaff 1990, Phaff et al. 1978, Rosa and Péter 2006, Sherman 1998) as well as a large body of descriptions in the journal literature and on the Internet that is too voluminous to cite.

4. PRINCIPAL YEAST SPECIES OF INDUSTRIAL IMPORTANCE

Several yeast genera and species are used industrially or have potential in biotechnology. The main yeasts are described in this section and are summarized in Table 3.2.

TABLE 3.2 Principal Yeast Species of Importance in Biotechnology[a]

Yeast Species
Saccharomyces cerevisiae
Schizosaccharomyces pombe
Kluyveromyces lactis
Kluyveromyces marxianus
Schwanniomyces occidentalis
Lipomyces spp.
Saccharomycopsis spp.
Debaryomyces hansenii
Ogataea polymorpha
Komagataella pastoris
Scheffersomyces stipitis
Pichia spp.
Rhodotorula spp.
Rhodosporidium spp.
Yarrowia lipolytica
Candida spp.
Trichosporon spp.
Blastobotrys adeninivorans
Xanthophyllomyces dendrorhous

[a]*These yeasts were chosen on the basis of the potential and realized importance in industrial fermentations and biotechnological processes. The list does not encompass the large number of yeast species involved in food spoilage and defects (Boekhout 2003, Chapter 5), or in human and animal disease (Chapter 2).*

4.1. *Saccharomyces cerevisiae*

Saccharomyces cerevisiae is the principal yeast utilized in biotechnology worldwide, due largely to its unique physiology and associated key roles in many food fermentations and other industrial processes (Phaff et al. 1978, Rose and Harrison 1993, Walker 1998). It is also the principal model eukaryotic organism utilized for fundamental research (Mustacchi et al. 2006, Oliver 2007). The Saccharomycetales comprise a diverse group of ascomycetous yeasts (Kurtzman 2003, Kurtzman and Robnett 2003, Suh et al. 2006b, Vaughan-Martini and Martini 1998), and studies of classification, phylogeny, physiology, and ecology have provided valuable insights and opportunities of this group of yeasts for industrial applications and as model organisms (Martini 2003, Middelhoven and Kurtzman 2003, Pizarro et al. 2007, Vaughan-Martini and Martini 1998, Vaughan-Martini 2003). Ironically, despite the tremendous importance of *S. cerevisiae*, relatively little is known about its origins and natural lifestyle (Fay and Benavides 2005, Martini 1993, 2003, Mortimer and Polsinelli 1999, Vaughan-Martini and Martini 1995, 1998). Industrial "domesticated" strains generally differ from laboratory strains, as well as from "wild" strains, in genetic and physiological properties (Bakalinsky and Snow 1990, Fay and Benavides 2005, Mortimer and Polinelli 1999, Porro et al. 2005, Schuller et al. 2007). Robert Mortimer (1927–2007), a pioneer in yeast genetics, carried out research in the later years of his career to study the origins and ecology of wine yeasts (Cavalieri et al. 2003, Mortimer and Polsinelli 1999), and his conclusions complement those from other laboratories, which conclude that industrial *S. cerevisiae* strains used in industrial processes have primarily evolved within the industrial environment.

While laboratory strains of *S. cerevisiae* can be grown stably under haploid or diploid states, industrial strains are usually diploid or aneuploid and often sporulate poorly (Bakalinsky and Snow 1990, Barre et al. 1993). This creates difficulties in performing classic mating procedures and other genetic manipulations (Benitez et al. 1996, Hashimoto et al. 2006, Lindegren and Lindegren 1943). The genome sequences and genetic architecture can also differ within *S. cerevisiae*, as recently shown for an opportunistically pathogenic strain of *S. cerevisiae* (Wei et al. 2007). Laboratory strains (e.g., the strain S288C for which the genome has been analyzed) also differ from industrial strains in several phenotypic responses to environmental changes, nutrient limitations, dessication and cold stresses, and other properties of considerable importance to successful industry performance (Gibson et al. 2007, Pizarro et al., 2007, Pretorius 2000). Industrial strains of *S. cerevisiae* express phenotypes important in commercial processes, such as rapid and complete sugar fermentation, increased alcohol production and tolerance, formation of desired flavors and aromas, enhanced flocculation, ability to utilize disaccharides and trisaccharides, low foaming propensity, and other traits (Benitez et al. 1996, Bisson 2004, Dequin 2001). The genetic and phenotypic diversity of commercial *S. cerevisiae* strains likely represent adaptations within industrial environments, such as breweries, wineries, and bakeries, as well as repeated use in industrial processes (Fay and Benavides 2005, Mortimer and Polsinelli 1999, Vaughan-Martini and Martini 1995, 1998).

Due to its desirable physiological properties and established methods for genetic manipulation, *S. cerevisiae* will undoubtedly continue to be the desired organism for many industrial applications including those extending beyond the "classical" yeast biotechnology of food, beverage, and feed processes (Fig. 3.1). Due to its long history of safe use and consumption, and lack of production of toxins, most strains of *S. cerevisiae* have generally been considered as Generally Recognized as Safe (GRAS) for use in foods and as a production organism of native and recombinant products.

4.2. *Schizosaccharomyces pombe*

Schizosaccharomyces pombe does not have the industrial utility of *S. cerevisiae*, but it has been elegantly utilized for fundamental studies of eukaryotic biology (Hayles and Nurse 2001) and for production and uses of heterologous proteins (Giga-Hama and Kumugai 1998). *S. cerevisiae* and *Schiz. pombe* are among the most widely exploited model eukaryotic systems for studies in basic biology, and these studies have extended to biotechnology. The 2001 Nobel Prize in Medicine was awarded to Lee Hartwell and Paul Nurse for their studies of the genetics and molecular biology of *S. cerevisiae* and *Schiz. pombe*, respectively. These two yeasts share more than 200 genes homologous to the human genes involved in disease, including 23 genes involved in human cancer (Botstein 2003, Hartwell 2002). These yeasts will continue to be utilized for the elucidation of fundamental problems in eukaryotic biology and for understanding of human biology and disease.

Although *S. cerevisiae* is the pre-eminent organism of biotechnology, several other yeast species are of considerable industrial and agricultural importance (Phaff et al. 1978, Spencer et al. 2002, de Winde et al. 2003, Wolf 1996) (Table 3.2). These yeast species have commonly been referred to as "non-conventional" yeasts in biotechnology (Porro et al. 2005, Spencer et al. 2002, Wolf 1996). This list of non-conventional yeasts is slightly expanded in this chapter to include additional species currently being investigated and developed for biotechnological applications.

4.3. *Schwanniomyces* (*Debaryomyces*) *occidentalis*

Schwanniomyces occidentalis is a member of the Saccharomycetales, and is closely related to certain species of *Debaryomyces* and *Candida*

(Kurtzman 2003, Kurtzman and Robnett 2003, Suh et al. 2006b). *Schwan. occidentalis* is of biotechnological interest primarily because of its production of hydrolytic enzymes, especially its active amylolytic system (Ingledew 1987, Wang et al. 1999). The amylolytic system is capable of degrading complex sources of starch from a variety of sources, including potato, barley, corn, wheat, and others. The amylase system is primarily comprised of endo-enzymes that hydrolyze starch to maltose, maltotriose, and higher oligosaccharides, with release of comparatively small quantities of glucose. *Schwan. occidentalis* has been used in small-scale industrial processes, such as food fermentations performed in developing countries. The efficient production of sugars and sugar syrups by *Schwan. occidentalis* has also been exploited for low volume production of ethanol, and single-cell protein (SCP). For large-scale processes, the more potent and thermostable amylase systems from *Bacillus* sp. and filamentous fungi including species of *Aspergillus* and *Trichoderma* are mainly used industrially (Aehle 2004, Pandey et al. 2006). *Schwan. occidentalis* has been considered for production of heterologous proteins, and certain other products (Wang et al. 1999).

Schwanniomyces occidentalis is also capable of degrading glycogen and utilizes a variety of carbon sources including glucose, fructose, xylose, raffinose, lactose (some strains), cellobiose, ethanol, and alkanes. *Schwan. occidentalis* can form up to about 6% ethanol (v/v) by fermentation (Jamal et al. 2007), and higher concentrations have been achieved in co-culture with *S. cerevisiae*. Several of its starch-degrading enzymes have been cloned and expressed in *S. cerevisiae* at three– to six–fold higher levels than achieved in *Schwan. occidentalis* (Ghang et al. 2007, Kang et al. 2003). Other amylolytic yeasts of potential biotechnological value include *Lipomyces kononenkoae* and *Saccharomycopsis fibuligera* (Know et al. 2004).

Schwanniomyces occidentalis produces phytase activity, which is a valuable enzyme for the utilization of phytates as a sole source of phosphate (Kaur et al. 2007). Phytases have considerable commercial and environmental importance, since they catalyze the release of phosphate from phytate, which is the major form in which organic phosphorous is stored in plant seeds and grains (Kaur et al. 2007). Currently, most commercial phytases are produced by filamentous fungi (Aehle 2004, Pandey et al. 2006). *Schwan. occidentalis* also produces killer proteins and antifungal substances, and the yeast has been considered for biocontrol of undesirable fungi (Chen et al. 2000).

4.4. *Debaryomyces hansenii*

Debaryomyces spp., particularly *D. hansenii*, have biotechnological potential in a diversity of areas (Breuer and Harms 2006). *Debaryomyces* spp. belong to the lipid-accumulating or "oleaginous" yeasts. Some of these yeasts can accumulate 20–70% of their biomass as lipids (Cohen and Ratledge 2005, Ratledge 2002). In addition to *D. hansenii*, other oleaginous yeasts include species of *Candida*, *Cryptococcus*, *Pichia* (*Hansenula)*, *Lipomyces*, *Pseudozyma*, *Rhodosporidium*, *Rhodotorula*, *Trichosporon*, *Trigonopsis*, *Yarrowia*, *Saccharomycopsis*, and potentially *Phaffia rhodozyma* and *Xanthophyllomyces dendrorhous*. The ability of oleaginous yeasts to accumulate high quantities of lipids offers the commercial potential for production of lipids or "single cell oils" (Fickers et al. 2005, Papanikolaou et al. 2002), biodiesel generation (Dai et al. 2007) and accumulation of lipid-soluble fine chemicals of high value, such as carotenoids, surfactants, and flavorants (see section 13).

Debaryomyces spp. are remarkably osmotolerant, being able to grow in media and foods containing up to 4 M NaCl (~ 10% w/w) and 5% glucose. In contrast, the most osmotolerant strains of *S. cerevisiae* are restricted in growth to media containing less than 1.7 M NaCl (Onishi 1963). Consequently, *Debaryomyces* spp. are frequently found in salted, sugared, and fermented foods of high osmolarity. Osmotolerance of *Debaryomyces* is desirable from a biotechnological perspective as the yeast can be grown in media that are resistant to contamination, thus reducing costs of the fermentation (Breuer and Harms 2006). It is intriguing that *Debaryomyces hansenii* also has high resistance to chlorine dioxide (ClO_2) (Ramirez-Orozco et al. 2001), a property that could also be exploited to maintain asepsis in fermentations. *D. hansenii* produces killer toxins active against various yeast species, which may be of value in maintaining aseptic conditions in industrial fermentations and for potential control of yeast infections (Buzzini and Martini 2001b). The ability of *D. hansenii* to tolerate extreme stresses could be highly advantageous in the implementation of low-cost fermentation processes (Breuer and Harms 2006).

Debaryomyces hansenii efficiently produces xylitol from D-xylose in wood hydrolysates, generating high xylitol:ethanol ratios (Breuer and Harms 2006). This capability is of potential importance in biomass conversion since a major bottleneck in this process is the bioconversion of pentoses to ethanol (Hahn-Hägerdahl et al. 2007, Jeffries 2006, Saha 2003). *D. hansenii* also produces other sugar alcohols from pentoses, including arabinose (Breuer and Harms 2006). *D. hansenii* synthesizes several exo-enzymes including β-glucosidases, esterases, and inulinases, an enzyme system of increasing industrial importance (Ricca et al. 2007, Sandhya and Pandey 2006).

4.5. *Kluyveromyces lactis* and *Kluyveromyces marxianus*

The genetics and systematics of *Kluyveromyces* spp. have been extensively studied, particularly by two prominent yeast biologists (Lachance 1993a, 2007, van der Walt 1970). *Kluyveromyces* is an ascomycetous yeast that readily forms asci. Several genetic techniques have been developed for manipulation of *K. lactis* for basic studies and industrial development (Spencer et al. 2002, van Ooyen et al. 2006). The availability of genetic and molecular tools and genomic data for *K. lactis* and *K. marxianus* (Dujon 2006, Dujon et al. 2004) has facilitated the development of the yeast for heterologous protein production and potentially other industrial applications (van Ooyen et al. 2006).

Species of *Kluyveromyces* produce β-galactosidase (lactase) that enables the utilization of lactose (Rubio-Texeira 2006), an attribute of particular importance for the dairy industry. *Kluyveromyces* spp. can be grown on inexpensive substrates and waste streams containing lactose such as cheese whey (Siso 1996). This yeast genus also has industrial potential for production of single-celled protein, exopolysaccharides, and fine chemicals (Antoni et al. 2003, van Ooyen et al. 2006).

Kluyveromyces lactis has been investigated for production of heterologous proteins, and has the capability for efficient expression and secretion of a variety of peptides and high molecular weight proteins in good yields (Fleer 1992, Romanos et al. 1992, van Ooyen et al. 2006). High cell densities have been obtained in fermentations, achieving approximately 100 g dry cell weight per liter with secretion of recombinant human serum albumin in several grams per liter (Fleer 1992, Romanos et al. 1992). A drawback to the use of *K. lactis* for the production of heterologous proteins is that the glycosylation of proteins does not conform to the human pattern. It may be possible to adapt a "humanized" glycosylation system to *K. lactis*, such as those developed for *Komagataella* (*Pichia*) *pastoris* and *S. cerevisiae* (Hamilton and Gerngross 2007, Li et al. 2007, Wildt and Gerngross 2005) (see section 17). *K. lactis* forms the killer toxin zymocin that is active against certain ascomycetous yeasts (Jablonowski and Schaffrath 2007). Since *K. lactis* is present in many dairy products that are consumed by humans, it is considered to be GRAS and the yeast can be utilized for production of food ingredients and as a dietary supplement (van Ooyen et al. 2006).

4.6. Methanol Utilizing Yeasts – *Komagataella* (*Pichia*) *pastoris,* Certain Other *Komagataella* spp., *Ogataea* (*Hansenula*) *polymorpha, Ogataea minuta,* and Certain *Candida* spp.

The methylotrophic yeasts were initially isolated in the late 1960s and early 1970s (Kato et al. 1974, Ogata et al. 1969). These yeasts have the intriguing property of being able to efficiently use methanol as a sole source of carbon and energy. Methanol utilization is associated with the robust expression of the enzyme methanol oxidase (Mox) (also referred to as alcohol oxidase), and the *mox* promoter governing the expression of the gene has been exploited for high-level expression of native and heterologous genes (Boettner et al. 2007, Cregg 2007, Gellissen et al. 2005, Houard et al. 2002, Porro et al. 2005). The heterologous proteins accumulate in peroxisomes, and at high levels of expression, peroxisomes can occupy as much as 80% of the cell volume, imparting a striking cellular morphology (Gellisen 2002, Tanaka and Ueda, 1993, Veenhuis et al. 1983).

Initially, the methylotrophic yeasts were considered for the production of biomass and single-cell protein from an inexpensive source of carbon (methanol). Industrial development of the yeast was performed at Phillips Petroleum Company for the production of single-cell protein for feeds (Sreekrishna and Kropp 1996, Wegner 1983). High levels of biomass (ca. 130 g dry cell weight (DCW) per liter) and high yeast productivity (>10 g DCW/l-h) was achieved with a specialized fermentation system including injection of pure oxygen and high mass transfer conditions. A similar process was developed by ICI using *Methylophilus methylotrophus* for the production of Pruteen (Macauley-Patrick et al. 2005). Despite these achievements, the economics of protein production became unfavorable compared to proteins from soybean and other sources, and efforts were turned to the development of *Kom. pastoris* and *O. polymorpha* for heterologous protein production (Macauley-Patrick et al. 2005, Romanos et al. 1992, Wegner 1990).

Of the methylotrophic yeasts, *Kom. pastoris* and *O. polymorpha* have been most intensely investigated for heterologous protein production (Cregg 2007, Jahic et al. 2006, http://faculty.kgi.edu/cregg). In *O. polymorpha*, several heterologous proteins including membrane-bound and labile enzymes have been efficiently produced (Cregg 2007, Gellisen 2002, 2005). The yield of heterologous proteins in *Kom. pastoris* and *O. polymorpha* is often higher than other yeasts, including *S. cerevisiae*, and grams per liter can be obtained for certain proteins. Secretion is generally more efficient and protein degradation diminished in these yeasts compared to *S. cerevisiae*. The expression systems, fermentation conditions, downstream processing, and limitations of heterologous protein production in *Kom. pastoris* and *O. polymorpha* have been extensively reviewed (Boettner et al. 2007, Cregg 2007, Daly and Hearn 2005, Gellisen 2002, Gellissen et al. 2005, Macauley et al. 2005). Heterologous protein production in *Kom. pastoris*, particularly optimization of glycosylation, is discussed more thoroughly in section 12.

4.7. *Yarrowia (Candida) lipolytica*

Yarrowia lipolytica is an ascomycetous yeast that is the teleomorph of *Candida lipolytica*. Industrial interest in *Y. lipolytica* derived initially from its unique physiological capabilities to utilize polyalcohols, organic acids, and long-chain hydrocarbons as substrates (Fickers et al. 2005, Gellissen et al. 2005). *Y. lipolytica* also produces high levels of lipolytic enzymes several of which have industrial utility. The yeast has been evaluated as a source of single-cell protein (SCP) from lipid substrates, such as crude oils and hydrocarbons (Cohen and Ratledge 2005, Ratledge 2005). The yeast also produces relatively large quantities of organic acids (e.g., pyruvate, citric acid and isocitrate) from various carbon sources (see section 11). *Y. lipolytica* produces higher value compounds as well, including lactones as flavorants (Garcia et al. 2007, Waché et al. 2006) (see section 13). Enzymes including cytochrome P450s and lipases with commercial uses in biotransformations of steroids, synthesis of pharmaceutical intermediates, and production of fine chemicals by *Y. lipolytica* (Fickers et al. 2005). The availability of the genome sequence of this yeast (Dujon 2006) should lead to advances in its genetic manipulation and utilization.

4.8. *Candida* spp.

Candida is an extremely heterogenous genus (see Chapter 90) that comprises a wide diversity of yeasts of ascomycetous affinity that lack known sexual states. The commercial utility and potential of *Candida* spp. includes synthesis of cytochrome P450 monooxygenases for biocatalysis, production of SCP from a variety of substrates including hydrocarbons, formation of D-amino acids from racemic mixtures, production of hydrophobic intermediates of the alkane oxidation pathway such as fatty alcohols, fatty acids, and especially dicarboxylic acids of commercial interest, reduction of xylose to xylitol, and reclamation of chemicals, such as solvents (Guo et al. 2006, Klein and Favreau 1995, Spencer et al. 2002, Wolf 1996). Several *Candida* spp. grow on a diversity of substrates including n-alkanes, fatty acids, xylose and many carbohydrates (Tanaka and Ueda 1993, Klein and Favreau, 1995, Wolf 1996.

Candida species that have been developed for industrial processes include alkane and phenol utilizing species, particularly *C. maltosa* and *C. tropicalis* (Klein and Favreau 1995). *C. maltosa* is able to utilize aromatic and certain other amino acids as the sole nitrogen source, and has been utilized for the resolution of D- and L-racemic mixtures of amino acids by metabolism of the undesired isomer. The utilization of *n*-alkanes and certain other lipid compounds requires cytochrome P450 (P450, CYP) enzymes, which are increasingly being investigated and developed as industrial biocatalysts (Faber 2004, Panke et al. 2004, Patel 2007, Straathof and Aldercreutz 2000, Straathof et al. 2002). Two species that have yielded valuable industrial biocatalysts and are extensively described in the chemical literature are *Pseudozyma antarctica* and *Candida cylindracea*. Other species investigated for their (*Candida*) P450 systems include *C. tropicalis*, *C. maltosa*, and *C. rugosa. C. tropicalis* and *C. utilis* have been used industrially for the synthesis of single-cell protein (SCP) (Klein and Favreau 1995). These organisms grow and produce biomass on a variety of substrates and waste streams including oils, plant hydrolysates, apple pomace, sulfite waste liquor, and many others (Halász and Lásztity 1991, Klein and Faveau 1995, Bekatorou 2006).

4.9. *Trichosporon* spp.

Trichosporon spp. are anamorphic basidomycetous yeasts that are widespread in nature and have been isolated from soils, sediments, waste waters, sludge, wood pulp, and clincal specimens (see Chapter 161). Industrial interest has focused on the ability of the species to utilize a range of substrates, particularly aromatic compounds, aliphatic lipids, amines, and complex nitrogenous compounds as sole sources of carbon and energy, including uric acid, ethylamine, hydroxyproline, tyramine, and L-phenylamine (Middelhoven et al. 2004). There has been industrial interest in the use of *Trichsporon* cells or enzyme systems to metabolize pollutants and xenobiotics in bioreredіation processes (Bergauer et al. 2005, Gdjevargova 2003, Middelhoven 1993). Safety evaluation of *Trichosporon* species for industrial uses is important, since certain species have been

associated with infections in humans, particularly in patients with underlying immunodeficiencies (Antachalopoulos et al. 2007).

4.10. *Blastobotrys* (*Arxula*) *adeninivorans*

Blastobotrys (*Arxula)* spp. are anamorphic ascomycetous yeasts (Middelhoven et al. 1984, van der Walt et al. 1990). These yeasts have the ability to assimilate purine compounds (uric acid and adenine) as well as various alkyl-amines as sources of carbon and energy (Böer et al. 2005, Middelhoven and Kurtzman 2003, Wolf 1996). This genus has been investigated for biotechnological applications, particularly as a source of hydrolytic enzymes and for production of heterologous proteins (Böer et al. 2005). *Bla. adeninivorans* has also attracted industrial attention as an expression platform for native and heterologous proteins, production of SCP, and formation of polyhydroxyalkanoates (Terentiev et al. 2004a). Although a sexual cycle remains to be identified, haploid strains of the species are amenable to certain genetic manipulations, including transformation and expression of heterologous protein genes (Gellissen 2005). Strains have also been developed that are able to sensitively detect estrogens and other compounds in the environment related to human health (Baronian 2004, Hahn-Hägerdahl et al. 2006).

4.11. *Scheffersomyces* (*Pichia*) *stipitis*

Scheffersomyces (*Pichia) stipitis* is an ascomycetous yeast that has been extensively investigated for the fermentation of xylose to ethanol, L-lactic acid and other products from hemicellulose, the second abundant component of cellulosic biomass (Hahn-Hägerdal et al. 2007, Ilmén et al. 2007, Jeffries 2006). Laboratory strains of *Schef. stipitis*, which are amenable to genetic and physiological manipulation, have been developed by metabolic engineering for xylose utilization (Hahn-Hägerdahl et al. 2007, Jeffries 2006, Jeffries et al. 2007). The genome sequence was recently obtained for this yeast and will provide a valuable resource for enhancement of xylose utilization and other industrial attributes by *Schef. stipitis* (Jeffries et al. 2007). Genes from *Schef. stipitis* have also been introduced into *S. cerevisiae* to enable fermentation of pentoses (Hahn-Hägerdahl et al. 2007, Jeffries 2006, Jeffries et al. 2007).

4.12. *Xanthophyllomyces dendrorhous* (Anamorph *Phaffia rhodozyma*)

Xanthophyllomyces dendrorhous (anamorph *Phaffia rhodozyma*) is a basidiomycetous yeast that produces the high-value carotenoid astaxanthin (Johnson and An 1991, Johnson and Schroeder 1995, Lukács et al. 2006, Visser et al. 2003). Astaxanthin is one of most common carotenoids in the biosphere, particularly in marine environments, and is produced by a few species of bacteria, microalgae, thraustochytrids, and fungi (Aki et al. 2007, Bhosale and Bernstein 2005, Dufosse 2006, Higuera-Ciapara et al. 2006, Johnson and Schroeder 1995). These organisms serve as the base of a food chain for various macro-creatures that leads to attractive pigmentation of birds, such as the flamingo and scarlet ibis, marine crustacea, including shrimp and lobsters, and fish, including salmonids (Johnson 2003, Johnson and Schroeder 1995, Rajasingh et al. 2007). Since these animals cannot biosynthesize astaxanthin, this pigment or appropriate precursors must be included in the animals' diets to obtain their characteristic pigmentation and associated metabolic functions. Astaxanthin also has beneficial health attributes for humans, and has been deemed beneficial for the prevention of degenerative syndromes such as cancer and cardivascular disease (Higuera-Ciapara et al. 2006).

Wild strains of *X. dendrorhous* and *Ph. rhodozyma* produce low quantities of astaxanthin (200–500 μg per g dry yeast), while industrial strains and processes have been developed for *X. dendrorhous* that yield values of 6,000 to 15,000 μg per g. *X. dendrorhous* also can reach very high cell densities of 100–130 g dry cell weight per liter in submerged fermentations with sufficient mass transfer and oxygenation. Although astaxanthin, like many other fine chemicals discussed in this chapter, has traditionally been produced by chemical synthesis, consumer demands for natural food and feed ingredients have led to a currently small niche market for *X. dendrorhous* in the feed industry (Bjerkeng et al. 2007, Dufosse 2006, Johnson and Schroeder 1995). The physiology and biotechological properties of *X. dendrorhous* and *Ph. rhodozyma* and the comparison to other natural sources of astaxanthin have been described in Chapters 134 and 152 as well as in several reviews (Dominguez-Bocanegra et al. 2007, Johnson 2003, Johnson and An 1991, Johnson and Schroeder 1995, Lukács et al. 2006, Visser et al. 2003). The genetic engineering of yeasts including *X. dendrorhous* for the recombinant production of isoprenoids, including carotenoids, is described in section 13.

4.13. *Pseudozyma* (*Candida*) *antarctica*

Pseudozyma (*Candida*) *antarctica* is an anamorphic yeast of basidiomycetous affinity (Chapter 153). The yeast has attracted industrial attention, primarily as a source of lipase enzymes used in a number of industrial processes (Faber 2004, Gotor-Fernández 2006, Liese et al. 2000, Patel 2004, Roberts 2001) and for biodiesel production (Narasimharao et al. 2007). *Pseudozyma* has also been considered for production of native surfactant proteins (Cameotra et al. 2004, Morita et al. 2007), antimycotics (Avis and Belanger 2001), itaconic acid (Levinson et al. 2006), degradation of plastic wastes (Seo et al. 2007), and heterologous proteins (Avis et al. 2005).

5. TRADITIONAL FOOD FERMENTATIONS

Yeasts have been involved since ancient times in a wide array of food fermentations (Table 3.1). Since these processes have been thoroughly described in the literature (reviewed in Bamforth 2005, Hui et al. 2004, Hutkins 2006, Prescott and Dunn 1940, Querol and Fleet 2006, Rose and Harrison 1993, as well as other definitive texts and treatises), the emphasis of this section is on new developments and opportunities in these traditional yeast applications.

5.1. Wines

Wine manufacture predates recorded history (Bisson et al. 2002, Legras et al. 2007). Wine is an integral component of many societies and it is produced on all six arable continents by affluent as well as less-prosperous nations. The uniqueness of wine as a worldwide valuable economic commodity and pleasing beverage is well known (Bisson et al. 2002).

The advent of the scientific understanding of winemaking is mainly attributed to Louis Pasteur, who demonstrated that wines were the product of an alcoholic fermentation of sugars (mostly glucose and fructose) in grape juice by yeast with the formation of ethanol and carbon dioxide (Amerine 1980). *S. cerevisiae* is the dominant organism in wine fermentation, primarily due to its ability to produce and tolerate high levels of alcohol (Bisson 1991, 2004). Several other yeast species are commonly present during wine fermentations, but their roles in wine quality are largely unknown (Bisson 1991, Pretorious 2000). Several excellent treatises describing wine

production and quality evaluation have been published, including two by legendary experts (Amerine 1980, Ribéreau-Gayon 2006).

Several properties of wine yeasts have been targeted for improvements in wine technology (Bisson 2004, Borneman et al. 2007, Dequin 2001, Pretorius 2000, Pretorius et al. 2003, Schuller and Casal 2005). Advances have been made in yeast fermentation vigor and complete utilization of sugars, wine processing, including clarification, and enhanced formation of desired flavors and decrease of off-flavors to enhance the organoleptic qualities of finished wines (Bisson 2004, Borneman et al. 2007, Pretorius et al. 2003, Schuller and Casal 2005). Additional developments in industrial wine yeasts include methods for genotypic and genetic differentiation of *S. cerevisiae* strains, and improvement of stress properties including osmotolerance and ethanol resistance. Stuck and sluggish fermentations continue to be a challenge in wine production (Bisson 1999), and studies of yeast traits to overcome this limitation are an active area of research (Bisson 2004).

The elimination of ethyl carbamate, a potential carcinogen (Coulon et al. 2006, Hasnip et al. 2007), from wines and other fermented foods has also been targeted to eliminate toxic risks. The development of strains that convert malic acid to lactic acid instead of relying on the malo-lactic fermentation by lactic acid bacteria have been strived for, as well as strains that produce higher levels of lactic acid and glycerol for enhancement of the balance of sweetness and acidity (Dequin 2001, Husnik et al. 2006). Decreases in levels of undesirable volatile acids, particularly acetic acid, have been investigated. Strains and processes for improved polysaccharide degradation offer advantages to winemakers including better juice yields, and liberation of desirable compounds from grape skins, particularly color components to enhance the brightness and color of the wine (Bisson 2004, van Rensburg et al. 2007). Addition of exogenous enzyme preparations is a common practice to increase yields and promote clarification but it adds cost in winemaking, and yeast strains that produce polysaccharide-degrading enzymes, including pectinases, xylanases, and glucanases, would be beneficial to the industry (Moreno-Arribas and Polo 2005, van Rensburg et al. 2007). Strains possessing antifungal and antibacterial capabilities potentially could be utilized to control fermentation contaminants. Recently, the consumption of resveratrol derived from grapes in red wines appears to have desirable health benefits (Baur and Sinclair 2006, Halls and Yu 2008).

Despite the availability of methods for genetic manipulation of industrial wine strains of *S. cerevisiae* (Dequin 2001, Pretorius 2000, Pretorius and Bauer 2002, Schuller and Casal 2005), genetically engineered yeasts have not been generally adapted by the wine industry due to consumer and regulatory concerns (Bisson 2004, Cebollero et al. 2007, Pretorius and Bauer 2002, Plahutaa and Raspor 2007, Schuller and Casal 2005). The acceptance of genetically-engineered (GMO) strains in food industries is expected to increase as their safety is more thoroughly understood (Lehrer et al. 1996, Pariza and Johnson 2001, Plahuta and Raspor 2007, Pretorius and Bauer 2002).

A complex and particularly important aspect of wine quality is flavor and aroma. The physiology and neurobiology of human olfaction and assessment of the desired sensory properties greatly impacts the desirability and economics of wine (Bisson et al. 2002). Yeast strains that produce fruity notes from compounds such as monoterpenols, linalool, geraniol, sweetness and viscosity from glycerol, as well as other desired organoleptic traits have the potential to greatly improve the organoleptic properties, desirability and appreciation of wines and other fermented foods. The human genome project and advances in neurobiology of smell and taste have led to an enhanced appreciation of the complexity of the organoleptic properties of wines and other foods. In 2004, the Nobel Prize in Physiology and Medicine was awarded to Richard Axel and Linda Buck for their discoveries of odorant receptors and the organization of the human olfactory system (Axel 1995, Buck 2006, Buck and Axel 1991). They discovered a large family of more than 1,000 genes (~3% of human genes) that give rise to olfactory receptor cells, which are capable of sensing more than 10,000 different odors. This information is relayed to various parts of the brain, forming a complex pattern or mosaic of olfactory recognition (Buck 2006, Zou et al. 2005). This enhanced understanding of olfactory perception provides a fundamental basis for understanding the complexities of fermented food preferences and for enhancing quality.

5.2. Beers

During the past several decades, technological factors have been targeted for improvement of brewer's yeast and the brewing process (Bamforth 2000, Dequin 2001, Linko et al. 1998). Many of these modifications have been introduced into laboratory strains of the closely related yeasts *S. pastorianus* (used for lager) and *S. cerevisiae* (used for ale and cider), but have not been introduced into commercial brewing processes as they await regulatory and consumer approval (Dequin 2001). Targeted properties include high fermentation performance in normal and high-gravity worts, and optimal formation of acids, esters, fusel oils, glycerol and other compounds for quality, as well as enhanced flocculation towards the end of the primary fermentation for removal of yeast and clarity of the product (Dequin 2001, Linko et al. 1998). Attempts to develop fungicidal and bactericidal brewer's yeast strains have been strived for to eliminate undesired contaminants. A strong emphasis has also been devoted to brewer's yeast strains that can utilize dextrins ($\geq$ four sugar units), since typical dextrins comprise about 25% of malt wort sugars and have a high caloric impact on beer with decreased alcohol yields. Exogenous glucoamylases, generally from *Aspergillus* spp., are used in the brewing process to produce light beers with lesser quantities of carbohydrates, but with added cost. The construction of strains that secrete β-glucanases would decrease viscosity, promote more efficient filtration, and potentially eliminate the need for addition of exogenous bacterial and fungal enzyme preparations. The use of strains that degrade proteins and other components that cause haze would be of considerable value. As with many fermented beverages, excess formation of diacetyl and other vicinal ketones can be detrimental to the savory properties of beers. Yeasts producing α-acetolactate decarboxylase for enhanced formation of acetoin and decreased diacetyl formation from α-acetolactate have been cloned from bacteria and expressed in brewer's yeast (Linko et al. 1998). Vicinal diketone reduction by alcohol dehydrogenases results in lower levels of the offensive compounds on a laboratory scale (Bamforth and Kanauchi 2004). Even low concentrations of hydrogen sulfide and dimethyl sulfide can be offensive, and yeast strains altered in sulfur metabolism have been developed. Alleviation of other flavor defects such as staling, formation of cardboard flavor attributed to (*E*)-2-nonenal, and elimination of offensive odors derived from lipid oxidation can affect the quality of beer (Vanderhaegen et al. 2006). Strains that produce enhanced levels of sulfite with enhanced antioxidant and antibacterial properties have been developed. Fermentation performance and desired flavor profiles continue to be challenging in high-gravity worts and in light beers (Blieck et al. 2007). Continuous brewing using immobilized yeast cells or maturation using immobilized cells has long been a goal of the brewing industry, and continues to attract research interest (Blieck et al. 2007, Linko et al. 1998, Verbelen et al. 2006, Willaert and Nedovic 2006).

5.3. Ciders

Cider is produced by yeast fermentation of the apple (*Malus pumila*) (Beech 1993, Valles et al. 2007). The fermentation involves a mixed microbiota predominated by yeasts, particularly *S. cerevisiae* and *S. bayanus*, but species of the genera *Dekkera*, *Lachancea*, *Ogataea,*

Pichia, *Candida*, *Hanseniaspora*, *Rhodotorula*, and *Trichosporon* have also been isolated from fermented ciders (Beech 1993, Boekhout and Robert 2003, Coton et al. 2006, Valles et al. 2007). Flow cytometry was used to demonstrate the presence of different cohorts of yeasts during cider fermentations (Herrero et al. 2006). Important physiological properties of yeasts for production of quality cider are rapid onset of fermentation and vigor, resistance to sulfite, creation and tolerance of acidic (low pH) conditions, ethanol tolerance, minimal foaming and gushing, and a desirable organoleptic profile, especially minimal formation of reduced sulfide components and optimal concentrations of glycerol, organic acids, higher alcohols, and esters (Beech 1993, Herrero et al. 2003, Xu et al. 2006). Other desirable traits are starter cultures (yeast and bacteria) that produce polygalacturonase and perform a malolactic fermentation on an industrial scale yielding a product of high stability and sensual quality (Beech 1993, Herrero et al. 2005).

5.4. Fortified Wines and Distilled Spirits

Targeted yeast traits for enhancing the quality of fruit wines, rice wine (sake), fortified wines, and distilled liquors are relatively undetermined compared to wines and beers, but are probably mostly similar. These include strong fermentation vigor, invertase formation, ethanol tolerance, osmotolerance, sulfite resistance, minimal formation of urea and ethyl carbamate, copper resistance, and desired flavor profiles (de Araújo et al. 2006, Fiore et al. 2005, Lilly et al. 2006, Schehl et al. 2007, Schwan et al. 2001, Steger and Lambrechts 2000). Analysis of gene expression during sake brewing has been accomplished, providing an enhanced understanding at the cellular and molecular level of the sake brewing process (Wu et al. 2006).

5.5. Bakery Products

The history and technology of the baking industry and baker's yeast have been expertly reviewed (Rose and Harrison 1993, Trivedi 1986), and new developments and opportunities are described here. Bakery foodstuffs present several challenges for improvement of yeast properties to enhance the processes and products. Among the most critical phenotypes for improvement are *S. cerevisiae* strains that tolerate high-levels of sucrose, endure freeze-thawing stress, rapidly utilize maltose, and produce high levels of carbon dioxide. Baking procedures subject yeasts to several stresses. Doughs can contain up to 30% sucrose per weight of flour, which exerts severe osmotic stress on *S. cerevisiae* and other component organisms (Verstrepen et al. 2006). Baker's yeast strains must efficiently utilize maltose, which is derived from flour in low-sugar doughs. *S. cerevisiae* strains that have high sucrose tolerance and also rapidly use maltose have been genetically developed and are used commercially (Higgins et al. 2001). Analysis of gene expression of sucrose-tolerant and maltose-utilizing yeasts indicated that the expression profiles differed between the two yeasts (Tanaka-Tsuno et al. 2007). Using a functional genomics approach with microarrays, the expression of genes involved in accumulation and metabolism of glycerol and trehalose, which are involved in resistance to osmotic stress, were higher in sucrose-tolerant yeasts. Strains showing enhanced growth rates also had deletions in genes involved in central carbon and nitrogen metabolism. This study indicates how functional genomics can be used for analysis of industrial yeast strains and improvement of fermentation processes.

A preferred trait for baker's yeast is the development of strains that utilize the disaccharide melibiose. Raffinose, a promiment component of molasses, is hydrolyzed by yeast invertase to fructose and melibiose (Dequin 2001). Baker's yeast does not have the ability to utilize melibiose as it lacks α-galactosidase. This enzyme is present in bottom-fermenting brewer's yeast strains, and the gene encoding the MEL1 enzyme from strains has been introduced into laboratory baker's yeast strains. The derived strains give increased biomass without alteration of growth rate in model bakery fermentations (Dequin 2001). One of the most desired properties of baker's yeast strains is a rapid fermentation rate. Free sugars in dough comprise mainly sucrose, glucose, fructose and maltose, which are sequentially consumed due to transport and catabolite repression regulatory mechanisms. Amylases in the dough release maltose from starch, but many strains of baker's yeast utilize maltose poorly, primarily due to repression of maltose utilization by other sugars through catabolite repression. Overcoming this bottleneck has long been a desired trait to enhance baking productivity (Rose and Harrison 1993, Trivedi 1986).

The popularity of frozen doughs, particularly sweet frozen doughs, has increased markedly in popularity in recent years (Rosell and Gomez 2007). Enhancing the freeze-tolerance and freeze-thawing survival of yeasts is an attribute that would benefit the production and quality of these bakery products, and cryoresistant baker's yeast strains have have been developed (Randez-Gil et al. 1999, Tanghe et al. 2003). *Torulaspora delbrueckii* is highly tolerant to freezing and freeze-thawing, and this yeast has been considered as a primary yeast or adjunct in frozen-dough products (Hernández-López et al. 2007).

5.6. Asian Fermented Foods

Yeasts are integral to the successful production of many indigenous fermented foods, many of which are prepared in the home (Blandino 2003, Hui 2004, Steinkraus 2004). Most indigenous fermented foods involve complex mixtures and successions of microorganisms during the processes (Aidoo et al. 2006, Hesseltine and Wang 1986, Hui et al. 2004, Steinkraus 2004). In some soy-fermented beverages and foods, such as soy sauce and miso, the organisms and fermentation patterns have been defined (Aidoo et al. 2006, Hui et al. 2004), while many others often involve a complex mixture and successions of organisms that remain to be defined. In these products, enhanced fermentation productivity and desired flavor profiles, particularly in newer products such as low-salt soy sauce, are preferred properties to enhance consistency and quality (Aidoo et al. 2006, Hauck et al. 2003, Hui et al. 2004, Kijima and Suzuki 2007, Ohata et al. 2007, Steinhaus and Schieberle 2007, Suezawa and Suzuki 2007).

5.7. Miscellaneous Fermented Foods

Yeasts have important activities in many other fermented foods. The preparation of cocoa involves pectinolytic and fermentative yeasts including *S. cerevisiae* (Table 3.1) (Boekhout and Samson 2005, Schwan 1998). Similarly, coffee fermentation involves pectinolytic yeasts that digest the pulp surrounding the bean (Boekhout and Samson 2005).

The microbial populations in some fermented foods including fermented meats, vegetables, and cereals are dominated initially by lactic acid bacteria, and yeasts often play a secondary role in ripening and flavor development (Hui et al. 2004, Steinkraus 2004). Yeast genera commonly isolated in these complex fermented foods are *Candida*, *Ogataea, Pichia*, *Rhodotorula*, *Saccharomyces*, and *Saccharomycopsis* (Blandino et al. 2003, Hesseltine and Wang 1986, Steinkraus 2004). An important potential defect that has been targeted for elimination in several multispecies fermented beverages and foods is the formation of toxicants such as ethyl carbamate, histamine, and mycotoxins (Kung et al. 2007, Park et al. 2007, Schollenberger et al. 2007, Shetty et al. 2007). Robust and rapid fermentations with lowering of pH and production of antagonistic compounds can prevent the growth and survival of pathogens such as Salmonella spp., *Staphylococcus* spp., and *Clostridium botulinum* (Holzapfel 2002, Johnson 1991, Motarjemi

2002). Rapid fermentation also preserves and enhances nutritional quality (Schwan et al. 2007), and is highly desired in most indigenous food fermentations.

5.8. Genetically Modified and Recombinant Yeasts for Use in Foods

Because of its long history of safe use and consumption, *S. cerevisiae* was among the first organisms to be designated "generally recognized as safe" (GRAS), and the first genetically modified organism (GMO) used for recombinant production of food and feed additives. In 1990, a genetically modified strain of *S. cerevisiae* reportedly became one of the first GMOs to be approved for food-use in the UK (Aldhous 2000). It is used in bakery products for enhanced production of carbon dioxide. Many genes encoding desirable traits mentioned above have been cloned in *S. cerevisiae*, *S. pastorianus*, and *S. bayanus* with primary roles in food fermentations (Bisson 2004, Pretorius 2003, Schuller and Casal 2005). However, most of these strains have not been used commercially because of regulatory and public perception hurdles.

Concerns have been raised that certain yeast species and strains may be opportunistically pathogenic or toxigenic to immunocompromised humans (Fenn 2007, Klein and Favreau 1995, Lin and Heitman 2006). Select strains of *S. cerevisiae*, *Candida*, *Trichosporon* and *Cryptococcus* have shown pathogenic potential (Murphy and Kavanagh 1999, Wei et al. 2007), and careful assessment of safety is needed for applications in food and biotechnology uses (Flamm 1991, Olemska-Beer et al. 2006, Pariza and Johnson 2001, Spok 2006). Allergenicity has been a major concern regarding yeasts in human diets (Airola et al. 2006, Lehrer 1996, Smith 1996).

The advent of functional genomics (sections 17 and 19) has created opportunities for in-depth understanding, analysis, and improvement of yeasts in foods and other industrial applications. Scientific, public, and regulatory concerns with GMOs, such as spread of antibiotic resistance genes, insecticide or other resistance genes, can be obviated with modern genetic manipulations (Lehrer et al. 1996, Pariza and Johnson 2001, Plahuta and Raspor 2007, Pretorius and Bauer 2002). *S. cerevisiae* is also used for the production of insulin, hepatitis B vaccine, and other products for human treatment, and it is of utmost importance that these strains and their by-products do not pose a risk for human health.

6. FOOD AND FEED YEASTS

Yeasts have long been cultivated as rich sources of protein, minerals, vitamins (particularly B vitamins), and other nutrients for humans and animals (Anupama and Ravindra 2000, Bekatorou et al. 2006, Boze et al. 1995). Several yeast species have been used for biomass production, including *C. utilis*, other non-methylotrophic *Candida* spp., *Saccharomycopsis* (*Endomycopsis*) *fibuligera*, *Kluyveromyces* spp., and *S. cerevisiae*. Methylotrophic, ethanol-utilizing, and fat- and hydrocarbon-utilizing yeasts including species of *Candida*, *Ogataea*, *Pichia*, and *Trichosporon* have also been used for biomass production (Bekatoruou et al. 2006, Boze et al. 1995). Production of yeast SCP has certain advantages compared to plant, animal, and other microbial sources of SCP including rapid growth and accumulation of biomass, high protein content (up to $\sim$50%), high contents of vitamins and minerals, and ability to grow on a wide variety of substrates, including various industrial waste streams (Halász and Lásztity 1991, Klein and Favreau 1995). The production of value-added SCP from inexpensive substrates could help to alleviate world shortages in the food supply, particularly in developing countries (Anupama and Ravindra 2000). Substrates utilized have included molasses, starch, cassava, Jerusalem artichoke, whey products, sulfite waste liquor, potato wastes, brewery wastes, and other waste streams from agricultural processes, food processing, and industrial processes (Boze et al. 2006, Halász and Lásztity 1991, Klein and Favreau 1995, Ozyurt and Deveci 2004). Due to the relatively large cell size and flocculation abilities of yeasts, they can be more easily harvested than bacteria from the fermentation liquor. Compared to bacteria, many yeasts contain low quantities of nucleic acids, which can have detrimental nutritional effects (Ravindra 2000). Certain yeasts used as food supplements have been suspected of causing various health problems such as allergies, vaginitis, irritable bowel syndrome, immunodeficiency, and other maladies (Airola et al 2006, Lehrer et al. 1996, Smith 1996). It has been hypothesized that causes of certain ill-effects are due to the presence of yeast (fungal) antigens, or to high levels of chromium and salicylates, and possibly contaminants within the processes (Airola et al. 2006, Breitenbach 2008, Chou et al. 2005, Smith 1996). The nutritional value and safety of SCP has received some evaluation (Halász and Lásztity 1991, Scrimshaw and Murray 1995).

7. BIOETHANOL AND BIODIESEL

Rapid global population growth is taking place concurrently with increased demands for food, fuel and energy (Goldemberg et al. 2007, Nass et al. 2007, Ragauskas et al. 2006). World oil production will not keep pace with increase in demand for petrochemical fuels (Kerr 2007). Limited oil reserves, pollution concerns, global warming, and political instability and disagreements have renewed interest and led to financial support for the generation of environmentally compatible and sustainable sources of energy (Agrawal et al. 2007, Antoni et al. 2007, Farell et al. 2006, Hill et al. 2006, Ragauskas et al. 2006). Due to the outstanding capacity of *S. cerevisiae* and certain other yeasts to produce ethanol and other organic products, yeasts will continue to be developed as producers of ethanol and other fuels.

Biofuels including bioethanol and biodiesel rely on the conversion of renewable feedstocks to fuels, with current emphasis mainly on digestion of biomass and lignocellulose sources such as crop residues, perennial grasses, and other abundant materials. These materials are plentiful in many terrestrial environments, and it has been estimated that more than 1.3 billion tons of biomass could be produced annually in the United States on a sustainable basis (Himmel et al. 2007). Recently, the US government set forth the Biofuel Initiative, which has the goal of replacing 75% of the current fossil fuel resources with biofuel by 2025 (Herrero 2006). Although additional types of biofuels are being investigated, such as methane, hydrogen, and others, bioethanol fermentation is by far the largest scale microbial process, with a strong history of productivity in several countries (Antoni et al. 2007).

As a result of the oil crises in 1973 and 1979, Brazil developed industrial bioethanol technology based on yeast fermentation of sugars (Dorfler et al. 2007, Goldemberg 2007, Laluce 1991). Currently, approximately 55% of harvested sugarcane in Brazil is used for ethanol fermentation, and biomass provides about 30% of the country's energy requirements. This successful program in Brazil supports the potential of other countries to develop similar sustainable energy programs. However, the availability of inexpensive sources of fermentable sugar is limited in most areas of the world, and the efficient conversion of cellulosic biomass or other inexpensive substrate sources to usable fuels will be required.

A primary limitation in biomass fermentations is that yeasts cannot directly convert cellulose, hemicellulose, and associated components inherent in biomass to ethanol (Hahn-Hägerdahl 2006, Jeffries 2006, Jeffries et al. 2007, Lynd et al. 2002). The lignin component in terrestrial biomass is exceptionally recalcitrant to digestion and conversion to bioproducts by most microorganisms, except for white rot fungi, but degradation by these fungi is slow and inefficient. Cellulose and hemicellulose require digestion to fermentable sugars before they can

be utilized by yeasts (Hahn-Hägerdahl 2006, Jeffries 2006, Jeffries et al. 2007, Lynd et al. 2002). The current rate of enzymatic cellulosic biomass conversion to sugars is about two orders of magnitude slower than the average fermentation rate with yeast (Antoni et al. 2007). In addition, xylose and most other pentoses, which constitute about 25% of biomass, are not efficiently fermented to ethanol by *S. cerevisiae* and other yeasts, such as *Schef. stipitis*, which only slowly use xylose and other pentoses resulting in low biomass and ethanol productivity (Gray et al. 2006, Hahn-Hägerdahl et al. 2007, Jeffries 2006, Lynd et al. 2002, Saha 2003). Two primary strategies are being pursued for fermentation of cellulosic biomass by yeast: (a) enhance and optimize xylose and other pentose utilization by *Schef. stipitis* or other pentose-fermenting yeasts; or (b) introduction of the pathways for fermentation of xylose and other pentoses into *S. cerevisiae* to be exploited by its well-known strong fermentation capacity and high ethanol tolerance (Chu and Lee 2007, Jeffries 2006, Lynd et al. 2002, Ostergaard et al. 2000, Saha 2003, van Maris et al. 2006). Metabolic engineering and modeling of the metabolic pathways involved in the fermentation of pentoses and other carbon sources is being exploited to enhance fermentation productivity, as well as other limiting factors such as ethanol resistance (Alper et al. 2006, Flores et al. 2000, Ostergaard et al. 2000, Stephanopolous, 2007). The availability of the genome sequences from *Schef. stipitis* (Jeffries et al. 2007) and other yeasts has provided important resources for improvement of biomass utilization. Marked improvements have been made in fermentation of cellulosic hydrolysates by yeasts, yet the processes have not reached the stage of economic viability and industrialization.

Although emphasis has been on terrestrial sources of biomass, freshwater and marine sources of biomass are abundant in oceans and coastal waters, and preliminary studies indicated that these resources harbor numerous yeasts (Fell 1976, Johnson et al. 1977a). Marine biomass sources such as kelp are composed of non-cellulosic carbohydrates and may be more amenable to enzymatic digestion and fermentation compared to cellulosic biomass. Marine biomass may be a potential source of non-cellulosic and non-lignified resource for enzymatic digestion and ethanolic fermentation by yeasts, as well as substrates for high-value products.

Biodiesel fuels consist of monalkyl esters of fatty acids that are mainly produced from waste streams of vegetable oils. The principal current method is chemical transesterification with petrochemically derived methanol (Antoni et al. 2006). Microalgae and selected plant species with high productivity and lipid content are being investigated as sources of single-cell oils (Cohen and Ratledge 2005). Since several yeast species are oleaginous and accumulate high concentrations of lipids (Cohen and Ratledge 2005), they warrant evaluation as components for industrial production of oils and biodiesel (Cohen and Ratledge 2005, Dai et al. 2007, Matsumoto et al. 2001, Ratledge 2002). As opposed to culture in terrestrial water bodies, production of single-cell oils could be done in fermentors or in specialized solar reactors, which would be more ecologically sound than certain other technologies. A by-product of biodiesel is glycerol that can accumulate in substantial quantities. *Y. lipolytica* and other yeasts have been evaluated for the fermentation of glycerol to higher-value products such as the bulk chemical citric acid (Fickers et al. 2005, Levinson et al. 2007).

8. FOOD AND AGRICULTURAL YEAST ENZYMES

8.1. Overview

The term "enzyme" (literally "in yeast") was coined by Kühne in 1876 (Aehle 2004). In 1907, Eduard Büchner (1860–1917) received the Nobel Prize in Chemistry for his discovery of "cell-free fermentation" using baker's yeast cell-free extracts (http://www.nobelprize.org). Enzyme technology utilizing cell-free enzymes and whole-cell biocatalysts is integral to several large-scale chemical, pharmaceutical, and agricultural bioprocesses (Aehle 2004, Pandey et al. 2006, Panke et al. 2004). The economic value of the industrial enzyme market in 2005 was approximately $3 billion, and is expected to reach more than $8 billion by 2009 (Porro et al. 2005). The enzyme market is generally categorized into four utility classes (Cherry and Fidanstef 2003): (a) technical enzymes, which comprise about 65% of the market, including enzymes used in the detergent, starch, textile, leather, pulp and paper, and personal care industries; (b) food enzymes, about 25% of the market, including enzymes used in brewing, dairy, wine and juice, fats and oils, and baking industries; (c) feed enzymes, about 10% of the market, used in animal feeds; and (d) diagnostic enzymes, comprising a small portion of the overall enzyme market. The six classes of enzymes used commercially are classified functionally as specified by the Enzyme Nomenclature Committee (IUBMB 1992): (a) oxidoreductases; (b) transferases; (c) hydrolases; (d) lyases; (e) isomerases; and (f) ligases.

In recent years, growth of the bulk enzyme industry has been particularly robust in the baking and animal feed sectors, in industrial organic syntheses for fine chemicals and pharmaceuticals, and to a lesser degree for paper and pulp processing, production of biofuels, and for personal care (Aehle 2004, Kirk et al. 2002). The food industry is the largest user of bulk enzymes, accounting for about 45% of total use (Pandey et al. 2006). The bulk enzyme market is dominated by enzymes produced by bacteria and filamentous fungi cultivated in submerged culture, particularly *Bacillus* and *Aspergillus* species (Aehle 2004, Pandey et al. 2006). The genes encoding enzymes from extreme environments such as hot springs and acid-mines have also been cloned and expressed in heterologous hosts for industrial uses (Ferrer et al. 2007a, b). Only a limited number of yeast enzymes are currently used as bulk enzymes in commodity processes (Table 3.3). However, several yeast enzymes have found

TABLE 3.3 Industrial Enzymes from Yeasts

Enzyme	Yeast	Industry
Chymosin	*Kluyveromyces* spp. *Saccharomyces cerevisiae*	Food processing
α-Galactosidase	*Saccharomyces* spp.	Feed applications
L-Glutaminase	*Zygosaccharomyces rouxii*	Therapeutic Analytical
Inulinases	*Candida* spp. *Kluyveromyces marxianus*	Food applications
Invertase	*Saccharomyces cerevisiae*	Food applications
Lactase	*Candida pseudotropicalis* *Kluyveromyces* spp.	Food processing
Lipase	*Candida rugosa* *Pseudozyma antarctica* A, B *Geotrichum candidum* *Trichosporon fermentum* *Yarrowia lipolytica*	Food processing Flavors Wastewater Degreasing Bioremediation Therapeutic Detergent
L-Phenylalanine ammonialyase	*Rhodotorula* spp. *Rhodosporidium* spp.	Pharmaceutical
Phenylalanine dehydrogenase	*Candida boidinii*	Pharmaceutical
Phytase	*Ogataea polymorpha*	Feed Nutrition

Sources: Aehle 2004, Hasan et al. 2006, Liese et al. 2006, Pandey et al. 2006, Vakhlu and Klur 2006. Also see text for additional references.

application in the production of high-value specialized fine chemicals and for biotransformation of pharmaceutical intermediates (see section 13).

Currently, about 90% of industrial enzymes are produced as heterologous proteins by recombinant methods (Cherry and Fidanstef 2003). Examples of industrially-relevant recombinant enzymes produced in yeasts are presented in Table 3.4. Certain yeasts, especially *Kom. pastoris* and *S. cerevisiae*, are increasingly being utilized for heterologous production of enzymes and a variety of other proteins (Aehle 2004, Cregg 2007, van Beilen and Li 2002). *Bla. adeninivorans*, *O. polymorpha*, *K. lactis*, *Schiz. pombe*, *Y. lipolytica*, *Pseudozyma* spp., and other yeast species have also been developed for the production of heterologous proteins (Avis et al. 2005, Buckholz and Gleeson 1991, Gellissen 2005, Gellissen et al. 2005, Madzak et al. 2004, van Ooyen et al. 2006). Industrial recombinant enzymes and those close to commercialization produced by yeasts are presented in Table 3.4. Yeasts are desirable hosts of enzymes for food uses because of their lack of production of toxic secondary metabolites (Olempska-Beer et al. 2006). *K. lactis* is currently approved by the FDA for production of recombinant enyzmes (chymosin) for uses in foods. Whole cells used as biocatalysts for high-value pharmaceuticals and fine chemicals is a rapidly growing sector of the enzyme industry (Table 3.5).

8.2. Bulk Yeast Enzymes

Select yeast enzymes used industrially or with significant industrial potential (Table 3.3) are highlighted in this section.

TABLE 3.4 Examples of Industrial Recombinant Enzymes Produced in Yeasts

Enzyme	Recombinant Yeast Host
Chymosin	*Kluyveromyces lactis*
Glycolate oxidase	*Komagataella pastoris*
Phytase	*Komagataella pastoris*

Sources: Cowan 1996, Cregg 2007.

8.2.1. Inulinases

Inulinases release fructose and oligo fructose polymers from inulin, a β-(2-1) linked polymer that serves as a storage polymer in several plants of the Asteraceae, including the Jerusalem artichoke (*Helianthus*), and chicory (Ricca et al. 2007, Sandhya and Pandey 2006). The enzymatic digestion of inulin (fructans) yields fructose syrups, which have been reported to have beneficial health applications in humans (Kaur and Gupta 2002, Warrand 2006). While commercial inulinases are mainly obtained by submerged culture from filamentous fungi, particularly *Aspergillus* spp. (Sandyha and Pandey 2006), several yeasts including *D. hansenii*, *Y. lipolytica*, *K. lactis*, and some species of *Candida*, *Cryptococcus*, and *Pichia* are also sources of inulinases (Sandhya and Pandy 2006). In particular, the inulinase from *K. marxianus* is produced at levels approaching commercial utility (Sandhya and Pandey 2006). The inulinase gene from *Aspergillus niger* has been cloned in *Kom. pastoris* and is expressed at 11−times the level of that in the native fungus (L.H. Zhang et al. 2003). This example illustrates increasing trend of utilizing yeasts for the industrial production of heterologous enzymes and other proteins.

8.2.2. β-Galactosidase

Kluyveromyces lactis is a well-recognized source of β-galactosidase (lactase), an enzyme that hydrolyzes lactose to sugars which can be fermented by various yeasts (van Ooyen et al. 2006). Lactases are also used for dietary relief of lactose intolerance in humans, and this application is increasing in importance with globalization of cow's milk as a food (Wiley 2007). It has been estimated that up to two-thirds of the world's population cannot readily digest lactose (Wiley 2007). Lactase is used for the production of lactose-free dairy products and provides nutritious foods that can be consumed by lactose-intolerant populations. *K. lactis* is also an industrial source of recombinant bovine chymosin for cheese-making (van Ooyen et al. 2006). Owing to the safety history, dried and inactivated *K. lactis* was used as a protein supplement in food in the 1960s (van Ooyen et al. 2006) and as a baby food supplement during the Biafra war

TABLE 3.5 Yeast Enzymes/Whole Cells Used in Biocatalytic Processes

Enzyme Class	Enzyme	Yeast Source
I. Oxidoreductases EC 1	Dehydrogenase	*Zygosaccharomyes rouxii*
	Dehydrogenase	*Geotrichum candidum*
	Dehydrogenase	*Candida sorbophila*
	Reductase	*Ogataea methanolica*
	Reductase	*Aureobasidium pullulans*
	Reductase	*Saccharomyces cerevisiae*
	D-Amino acid oxidase	*Trigonopsis variabilis*
	β-Galactosidase	*Kluyveromyces lactis*
	Formate dehydrogenase	*Candida boidinii*
Transferases EC 2	Lipase	*Candida cylindracea*
	Lipase	*Candida antarctica* A, B = *Pseudozyma antarctica*
Hydrolases EC 3	β-Galactosidase	*Kluyveromyces lactis*
	Lactamase/racemase	*Cryptococcus laurentii*
Lyases EC 4	Pyruvate carboxylase	*Saccharomyces cerevisiae*
	Enoyl-CoA hydratase	*Candida rugosa*
	L-Phenylalanine ammonia lyase	*Rhodotorula rubra*
Isomerases EC 5		No significant commercial sources from yeasts
Ligases EC 6		No significant commercial sources from yeasts

(adapted from Liese et al. 2006)

(Bonekamp and Oosterom 1994). These uses attest to its potential as a safe food supplement in additional applications.

8.2.3. Lipases and Esterases

Lipases, phospholipases, and esterases comprise an important and versatile group of enzyme biocatalysts that are used for modification and degradation of oils, for generation of aromas and flavors in foods, stereospecific modification of pharmaceuticals, pesticides, and cosmetics, and in detergents (Houde et al. 2004, Jaeger and Eggert 2002, Pandey et al. 1999). Lipases catalyze the hydrolysis of water-insoluble esters such as triglycerides (Kazlauskas and Bornscheuer 1998). Lipases currently comprise approximately 5% of the industrial enzyme market. Yeasts are a source of lipases and phospholipases used for traditional applications (Aehle 2004, Faber 2004). Lipases are also being increasingly used for the synthesis of high-value fine chemicals and pharmaceuticals (Aehle 2004, Akoh and Shaw 2004, De Maria et al. 2007, Faber 2004, Hasan et al. 2006, Straathof and Adlercreutz 2000). Although commercial lipases are mainly derived from animal and plant sources (Koul et al. 2005), certain yeast species are sources of industrial lipases, including *Pseud. antarctica, C. cylindracea, C. rugosa, Geo. candidum, Sporidiobolus* spp., *Tr. beigeli*, *Tr. fermentans*, and *Y. lipolytica* (Breuer et al. 2004, Kirk and Christensen 2002, Koul et al. 2005, Straathof et al. 2002, Vakhlu and Kour 2006). Most of these yeasts grow on alkanes, which require lipid-catalyzing enzymes including lipases and oxygenases. Several lipases have enantio-selectivity for their substrates, which is an important property in the synthesis of chiral fine chemicals and pharmaceuticals (Jaeger and Eggert 2002). Certain yeast lipases are also stable in organic solvents and in supercritical CO_2 (Romero et al. 2005).

In addition to the hydrolysis of glycerides, yeast esterases are exploited for the synthesis of esters, fatty acids, and related compounds, which are mostly used as flavorants in the food industry (Aguedo et al. 2004, Schrader et al. 2004, 2006, Vandamme and Soetaert 2002, Waché et al. 2006). Esterases currently also have applications in various food and oil modification processes (De Maria et al. 2007), and growing applications in fine chemical and pharmaceutical syntheses (Faber 2004, Liese et al. 2000).

8.2.4. Cytochrome P-450 Monooxygenases (P450s; CYPs)

Cytochrome P450 monoxygenases (P450s; CYPs) comprise a large family of enzymes that function as versatile and diverse enzyme catalysts. P450s are involved in the synthesis of sterols, steroids, lipids, vitamins and other essential cellular components, biotransformation of drugs, xenobiotics and carcinogens, and biosynthesis of a myriad of natural products (Bernhardt 2006, Chefson and Auclair 2006, Johnson 2002, Lewis 2001). P450s have the remarkable ability to insert molecular oxygen in non-activated C-H bonds, a property that has attracted the interest of chemists for decades (Chefson and Auclair 2006). Recently, there has been an emphasis in the development of P450 biocatalysts for industrial products, especially for the synthesis of fine chemicals and pharmaceuticals (Bernhardt 2006, Peters et al. 2007, Urlacher and Eiben 2006).

Many yeast species possess a diverse array of P450s, including members of enzyme families that are found in mammalian and human cells. Yeast species that utilize alkanes, aromatic compounds, and other lipids as substrates, or produce secondary metabolites such as carotenoids, possess P450s that catalyze reactions with current and potential uses for industrial biotransformations. The principal yeasts investigated have included *Candida* spp., *O. polymorpha*, *Rhodotorula* spp., *Y. lipolytica, X. dendrorhous*, and others (Bernhardt 2006, He and Chen 2005, Ullrich and Hofrichte 2007, van den Brink et al. 1998). An interesting example of a P450 that performs a complex reaction is the β-carotene 3-hydroxylase/4-ketolase that converts β-carotene to astaxanthin. Our laboratory (Johnson and coworkers) first proposed that a P450 system was involved in astaxanthin biosynthesis (An et al. 1989). Hoshino et al. (2000) and Echavarri-Erasun (2005) subsequently discovered this enzyme's activity in β-carotene conversion in *X. dendrorhous* using a β-carotene mutant (Yan-1) isolated in our laboratory. Echavarri-Erasun also showed that the defect in β-carotene conversion in Yan-1 was due to incorrect mRNA splicing during P450 expression (Echavarri-Erasun 2005). Subsequently, the gene encoding the enzyme was partly characterized and specified as belonging to the human 3A1 family, and the defective splicing reactions were confirmed (Álvarez et al. 2006, Ojima et al. 2006). Despite these advances, much remains to be elucidated about the substrate specificity, mechanisms of activity, and regulation of the P450 system(s) in *X. dendrorhous.*

In contrast to *E. coli*, *S. cerevisiae* can functionally express most animal and plant P450s involved in biosynthetic pathways, including those of secondary metabolites (Pompon et al. 1996). This discovery stimulated the cloning and expression of numerous P450s in *S. cerevisiae* and other yeasts from a wide variety of eukaryotic organisms, as well as development of strains and vectors specifically designed for this process (Hamann and Møller 2007). At present, many plant and animal P450s are produced as heterologous proteins in *Kom. pastoris*, *O. polymorpha*, *S. cerevisiae*, *Schiz. pombe*, *Y. lipolytica*, *K. lactis*, and other yeasts, and these are being pursued by industry (Bernhardt 2007, Cregg, 2007, Fickers et al. 2005, Hamann and Møller 2007, Schuler and Werck-Reichart 2003). See section 13 for further description of fine chemical and pharmaceutical syntheses using yeasts expressing heterologous P450s.

8.2.5. Feed Enzymes from Yeasts

The primary enzymes used in animal feed are xylanases, β-glucanases, and phytases (Aehle 2004, Kirk et al. 2002, Pandey et al. 2006). Xylanases and β-glucanases assist in digestion of polysaccharides in monogastric animals, which, in contrast to ruminants, have limited ability to fully digest plant-based feeds containing high quantities of cellulose and hemicellulose. Most commercial feed enzymes are produced by bacteria and filamentous fungi (Aehle 2004, Kaur et al. 2007, Pandey et al. 2006). However, feed enzymes are increasingly being produced heterologously in yeasts with the advent of highly efficient expression systems (Aehle 2004, Cregg 2007).

Phytases have emerged as prominent feed enzymes to enhance the utilization of phosphate, which is 85–90% bound in phytic acid. Phytases also diminish the release of phosphate as a pollutant into the environment. Since the recognition of bovine spongiform encephalopathy (BSE), certain countries have banned the use of bone meals in feeds, which was a traditional source of phosphorous, and this policy has enhanced the use of phytases. Phytases have also been found to increase the uptake of other nutrients, especially essential metals (Kirk et al. 2002). In 1999, the annual sales of phytases as an animal feed supplement was estimated to be US $500 million (Kaur et al. 2007). Phytases are also finding uses in non-traditional agricultural industries such as aquaculture (Kaur et al. 2007), in which feed components cost up to 70% of overall fish production costs. Phytases have attracted interest for improvement of human nutrition, especially to counteract zinc and iron deficiencies (Kaur et al. 2007). Several yeast species, including *Bla. adeninivorans*, *Candida* spp., *Cryptococcus* spp., *K. lactis*, *Wickerhamomyces anomalus*, *Rh. gracilis*, *Saccharomyces* spp., *Schwanniomyces* spp., and *Tor. delbrueckii*, produce phytases, but few of the enzymes have been extensively studied (Kaur et al. 2007).

9. BIOCATALYSTS FOR PHARMACEUTICAL AND FINE CHEMICAL PRODUCTION

Catalysis in the chemical and pharmaceutical industries has traditionally been dominated by chemical syntheses using non-biological catalysts (Bernhardt 2006, Blaser 2003, Blaser et al. 2005, Bonrath and Netscher 2005). However, several disadvantages are inherent to certain industrial chemical synthetic processes, including relatively low catalytic efficiency for many reactions, lack of enantiomeric specificity for chiral syntheses, the need for reaction conditions of high temperature, low pH and high pressure requirements, as well as the extensive use of organic solvents with consequent formation of organic waste and pollutants. These concerns and drawbacks have stimulated keen interest in biocatalytic processes using enzymes (Bonrath and Netscher 2005, Rozzell 1999). Advantages of enzymes for chemical processes include mild reaction conditions, i.e., operation at temperatures from 20 to 80°C, neutral or slightly acidic pHs, and atmospheric conditions (Koeller and Wong 2001, Rozell 1999). In contrast to organic catalysts, enzymes typically catalyze reactions without substrate functional-group protection and many enzymes have a long half-life, typically several days to months. Other beneficial properties are the stereoselectivity of enzymes for their substrates that yields stereo- and regiochemically defined reaction products, and the enormous rate acceleration of 10^5 to 10^8 (Aehle 2004, Koeller and Wong 2001, Rozell 1999). They also catalyze reactions on unnatural substrates, leading to enormous compound diversity. Another property of enzymes as industrial catalysts is that they can be genetically selected and chemically modified to enhance stability, substrate specificity, and specific activity (Aehle 2004, Koeller and Wong 2001, Rozell 1999). Several enzymes are active in organic solvents, supercritical fluids, high pressures, and ionic solvents ("Green solvents") (Klibanov 2001, Rezaei et al. 2007, Yang and Pan 2005). Hydrophobic environments and ionic solvents are optimal for some hydrophobic reactions using biocatalysts, such as those catalyzed by lipases (Yang and Pan 2005).

Immobilized enzyme processes can have advantages over enzymes in solution, including stability, process duration, and catalytic efficiency (Sheldon 2007). A drawback to certain enzyme syntheses is that they require cofactors, but this problem can be minimized by various approaches, including cofactor recycling (Straathof and Aldercreutz 2000) and the use of whole cells, such as engineered *S. cerevisiae* (Faber 2004).

Although a large number of studies and a voluminous literature have been devoted to the production of fine chemicals using enantioselective catalysis by enzymes, relatively few enzymatic processes are currently used on an industrial scale (Blaser 2003, Bonrath and Netscher 2005, De Mot and Verachtert 1982). It has been estimated that about 150 industrial syntheses currently utilize enzymes or microbial whole cell catalysts (Straathof et al. 2002, Woodley 2006, Yazbeck et al. 2004). Several yeasts produce enzymes and bioacatalysts of realized and potential value in the traditional enzyme industry and as chiral-specific biocatalysts for the fine chemical and pharmaceutical industries (Tables 3.5 and 3.6) (Aehle 2004, Liese et al. 2000, Pandey et al. 2006, Patel 2004, 2007, Straathof and Adlercreutz 2000). Useful case studies of commercial enzymatic and microbial biotransformations, including several involving yeasts, have been described (Table 3.5) (Cheetham 2000). Lipases and esterases, commonly produced by yeasts, are the most frequently used biocatalysts in industrial organic syntheses (Chenevert et al. 2006).

Despite the advantages of biocatalysts, they are still an underutilized technology (Bernhardt 2006, Rozzell 1999). Recently, the discovery of enzymes and metabolites for use in industrial biotechnology has been vitalized through metagenomics (Ferrer et al. 2007, Lorenz and Eck 2005). This approach has led to the discovery of enzymes, antimicrobials, and other compounds of industrial potential (Ferrer et al. 2007, Lorenz and Eck 2005, Podar and Reysenbach 2006). However, most metagenomic studies have been directed towards understanding bacterial diversity, and not yeasts, filamentous fungi, and other eukaryotes (Lorenz and Eck 2005). It is anticipated that more studies will be devoted to fungi because of their enormous biodiversity and ability to produce a multitude of secondary metabolites. About 74,000 species of fungi including yeasts have been described, while estimates of the total number of fungal species has been estimated to be as high as 1,500,000 (Hawksworth 2004), compared to 270,000 and 1,000,000 estimated numbers of species of plants and bacteria, respectively (Boekhout and Samson 2005). Thus, fungi are among the richest kingdoms on earth with respect to biodiversity, but much work is needed to understand their potential to provide valuable industrial resources.

The paucity of metagenomic studies conducted in yeasts, filamentous fungi, and other eukaryotes, such as protozoa, is primarily due to the comparatively large size of genomes in fungi compared to bacteria and viruses, and the relatively large nucleotide sequencing efforts required to obtain a representation of species diversity (Hall 2007). With advances in sequencing capacities and transcriptomics, metagenomic approaches offer a promising approach for identification of novel yeasts and fungi as potential resources in industrial biotechnology and for understanding their ecology (Bailly et al. 2007, Borneman and Hartin 2000, Hall 2007). Other areas of enhanced interest and utility in enzyme biotechnology are directed evolution (Bloom et al. 2005, Boersman et al. 2007, Haseltine and Arnold 2007, Yuan et al. 2005), systems biology (Bloom et al. 2006), and synthetic biology approaches (Alcade et al. 2006, Leisola and Turunen 2007, Yeh and Lim 2007).

10. YEAST METABOLITES AND BULK CHEMICALS

Several yeast species produce commodity chemicals in levels at or approaching commerical utility. The uses of yeasts in "White Biotechnology" applications, or production of low-cost, high-volume products is accelerating. *S. cerevisiae*, *K. lactis*, and *Schef. stipitis* have been developed for the production of L-lactic acid (Chotani et al. 2000, Ilmén et al. 2007, Saito et al. 2004). The availability of lactic acid from yeasts and other organisms has led to expanded uses such as its polymerization to polylactic acid. Polylactic acid and related polymers are under development for a variety of products including biodegradable plastics and textile fibers (Aristidou and Pentilä 2000, Ilmén et al. 2007, Porro et al. 1999).

Saccharomyces cerevisiae and *Rh. glutinis* have been used for medium-scale production of amino acids including lysine, methionine, phenylalanine, and proline (El-Batal 2002, Odunfa et al. 2001, Stepanova et al. 2001, Takagi et al. 2007). Yeasts have also been used for the production of alcohols used in bulk processes. *C. magnoliae*, *C. peltata*, and a *Candida* sp. produce erythritol in 41 to 56% yields from glucose or xylose in an approximately 3-day fermentation (Saha 2003). Mannitol, widely used in the food, pharmaceutical and chemical industries, is produced by various yeast species from glycerol (Baha 2003).

Glycerol is a commodity chemical that is used in a number of industrial products (Chotani et al. 2000). It has been traditionally produced by chemical synthesis from propylene, and is also recovered following hydrolysis of fats, but the latter process is laborious and inefficient (Chotani et al. 2000). *C. glycerinogenes* produces glycerol (144 g/l) from glucose in a 72-hour batch fermentation (Saha 2003). *S. cerevisiae* produces glycerol during ethanol formation, and synthesis is increased by osmotic stress (Attfield 1997). In the early

TABLE 3.6 Examples of Yeast Enzymes Used in Biotransformation/Biocatalytic Processes in the Pharmaceutical and Fine Chemicals Industries

Yeast Enzyme or Whole Cell	Product	Reference
Lipase[1]	Taxol	Koeller and Wong 2001
Monoxygenase (*Saccharomyces cerevisiae*)	Cyclic lactones	Stewart et al. 1998
Nucleoside phosphorylase[1]	Antiviral ribavarin	Koeller and Wong 2001
Zygosaccharomyces rouxii (dehydrogenase)	Benzodiazepine	Rozell 1999 Liese et al. 2006
Dehydrogenases[1]	Optically active alcohols	Breuer et al. 2004
Dehydrogenases[1]	Ephedrine	Breuer et al. 2004
Esterase[1]	Racemic alcohols	Koul et al. 2005
Reductase[1]	Ataxanavir (HIV protease inhibitor)	Patel 2004
Lipase (*Candida cylindracea*)	Lobucavir (antiviral)	Patel 2004, 2007
Lipase (*Candida cylindracea*)	Hepatitis B antiviral	Patel 2004, 2007
Lipase (*Pseudozyma antarctica*)	Ribavarin (antiviral)	Patel 2004
Reductase (*Pichia* spp.,)	Pacliataxel (anticancer drug)	Patel 2004, 2007
Reductase (*Aureobasidium pullulans, Candida* spp.)	Retinoid receptor antagonists	Patel 2004
Lipase (*Candida cylindracea*)	Pharmaceutical intermediate	Patel 2004
Reductase (*Candida* spp.) *Pichia* spp., *Rhodotorula* spp., *Saccharomyces* spp.)	Pharmaceutical intermediate	Patel 2004
Epoxide hydrolase (*Rhodotorula glutinis*)	Melantonin receptor antagonist	Patel 2004
Whole cell racemate resolution (*Candida boidinii, Ogataea methanolica, Ogataea polymorpha*)	Pharmaceutical intermediate	Patel 2004, 2007
Reductase (*Geotrichum candidum*)	Hydroxy methyl glutaryl CoA inhibitors (cholesterol lowering agents)	Patel 2004
Lipase (*Pseudozyma antarctica*), *Hyphozyma* sp., *Cryptococcus tsukubaensis*	Tachykinin receptor antagonists)	Patel 2004
(S)-2-pentanol, *(S)*-2-heptanol	Anti-Alzheimer drugs	Patel 2007
(R) - *(S)* oxidase (*Ogataea polymorpha*) (*Candida boidinii, Ogataea methanolica, O. polymorpha*)	Mixed racemate resolution	Patel 2007
Lipase, reductase (*Pseudozyma antarctica, S. cerevisiae*)	Beta-blockers	Zelaszcyk and Kiec-Kononowicz 2007

[1]*Yeast species not referenced.*

1900s, Carl Neuberg found that glycerol production in *S. cerevisiae* was enhanced by chemical diversion of central metabolic pathways (Prescott and Dunn 1944). To increase the cellular availability of more reducing equivalents (NADH/NADPH) for glycerol production, agents such as sulfite or alkali were added to the fermentations to inhibit the conversion of acetaldehyde to ethanol, and to shuttle carbon flow to glycerol (Chotani et al. 2000). The use of sulfites may have utility in other fermentations, such as in the fermentaion of xylose, in which availability of reducing equivalents appears to limit production of high yields of ethanol (Jeffries 2006) and in astaxanthin formation by *X. dendrorhous* in which biosynthesis requires high quantities of reducing equivalents (Johnson and Schroeder 1995). Genomic and metabolic modeling approaches are also being pursued to increase production of commodity chemicals in *S. cerevisiae* and other yeasts (Aristidou and Pentilä 2000, Cordier et al. 2007, Ishida et al. 2006, Kern et al. 2007, Nielsen and Jewett 2007).

Yarrowia lipolytica has been used for the industrial production of organic acids including α-ketoglutaric, pyruvic, citric and isocitric acids, which are used in food products (Finogenova et al. 2005, Föster et al. 2007, Kamzolova et al. 2007). Citric acid is a high-volume commodity fermentation product, second only to ethanol (Levinson et al. 2007). The ability of *Y. lipolytica* and certain *Candida* spp. to form high quantities of organic acids from various substrates, such as sucrose and glycerol, has seen renewed interest (Fickers et al. 2005, Förster et al. 2007, Levinson et al. 2007, Peters 2007, Soccol et al. 2006). The production of citric acid from *Y. lipolytica* depends critically on the carbon source. Citric acid has been produced from sucrose by a recombinant strain of *Y. lipolytica* containing the invertase gene of *S. cerevisiae* at concentrations up to 140 g/l and a yield of 0.82 g/g from sucrose after 191 h in a fed-batch fermentation, at 41 g/l from glucose, and 21.6 g/l from glycerol (Förster et al. 2007, Levinson et al. 2007). Gluconic acid is produced by the yeast-like fungus *Aureobasidum pullulans* at 74% yield from glucose in a 26-hour continuous fermentation, and 2-phenylethanol is produced by *P. fermentans* in 45% yield from L-phenylalanine in a 16-hour fermentation (Baha 2003). Other yeast species, including *C. glabrata*, have been used industrially for the production of pyruvic acid (Liu et al. 2007). Several yeasts have attracted industrial interest for production of primary chemicals such as itaconic, malic, gluconic, brassylic, sebacic, and fumaric acids (Hui and Khachatourians 1995, Walker 1998), but several of the processes are presently non-competitive with other commercial chemical or fermentation processes.

Yeasts have been used for production of vitamins. *Meyerozyma* (*Pichia*) *guilliermondii* overproduces riboflavin from xylose and ribitol in response to iron deprivation in the medium (Leathers and Gupta 1997), but the quantities of riboflavin produced are substantially less than those produced by commercial strains of *E. ashbyii*, *E. gossypii*, or *Bacillus subtilis* (Survase et al. 2006). *Pichia* spp. have been investigated for the production of pyridoxine (Halász and Lásztity 1991, Walker 1998).

Several yeast species produce glycolipids and surfactants that are of industrial interest. Basidiomycetous yeasts often colonize the

phylloplane, where they commonly secrete copious quantities of glycolipid biosurfactants that could have applications in the oil, food, cosmetic, and pharmaceutical industries (Banat et al. 2000, Cameotra and Makkar 2004). Various structures of glycolipids are produced in high quantities by species of *Pseudozyma* (Konishi et al. 2007, Mimee et al. 2005, Morita et al. 2007), *Candida* (Ogawa and Ota 2000), and *Kurtzmanomyces* (Kakugawa et al. 2002, Rehm and Reed 1995).

Yeasts are well-recognized as sources of food flavor enhancers for foods including nucleotides and yeast extracts and autolysates (Rose and Harrison 1993, Walker 1998). Nucleotide taste enhancers are also produced by the enzymatic hydrolysis of yeast RNA into nucleotide phosphates (Cheetham 2004, Halász and Lásztity 1991, Hui and Khachatourians 1995).

11. HETEROLOGOUS PROTEIN PRODUCTION IN YEASTS

Since the early 1980s, yeasts have been utilized for heterologous production of a variety of proteins (Cregg 2007, Gellissen 2005, Gellissen et al. 2005, Hitzeman et al. 1981, Romanos et al. 1992, Smith et al. 1985). The production of heterologous proteins in yeasts holds enormous potential for biotechnological processes. A major breakthrough in heterologous protein expression in yeast was the cloning, expression, processing, and secretion of human proinsulin in *S. cerevisiae* in the 1980s (Cousens et al. 1987, Hadfield et al. 1993, Ladisch and Kohlmann 1992, Thim et al. 1986). Insulin from *S. cerevisiae* had increased pharmacological efficacy and reduced side effects compared to porcine insulin. Subsequent studies showed that *S. cerevisiae* effectively synthesized and secreted many mammalian and human proteins, including α-interferon, epidermal growth factor, human serum albumin, hepatitis B surface antigen, epidermal growth factor, β-endorphin, and prochymosin. Several of these proteins have been developed and commercialized as high-value human pharmaceuticals or enzymes (Gellissen 2002, Gellissen et al. 2005, Hadfield et al. 1993, Romanos et al. 1992, Smith et al. 1985). Yeasts have several advantages as hosts for native and heterologous production, including ease and rapidity of growth; facile methods of genetic manipulation; high expression in optimized yeast systems; the ability to perform eukaryotic post-translational modifications, including intron splicing, proteolytic processing, folding, formation of disulfide linkages, glycosylation; and maintenance of quality suitable for biochemical and structural analyses (Gellissen 2005, Gellissen et al. 2005).

Several yeast species have been investigated for heterologous protein production, primarily the non-methylotrophs *S. cerevisiae*, *Schiz. pombe*, *K. lactis*, *Y. lipolytica*, *Z. rouxii*, *Z. bailii*, and *Bla. adeninivorans* (Böer et al. 2007, Gellissen 2005, Gellissen et al. 2005, Madzak et al. 2004, Porro et al. 2005, van Ooyen et al. 2006), and the methylotrophs *Kom. pastoris*, *O. polymorpha*, *C. boidinii*, *O. methanolica*, and *Schwan. occidentalis* (Böer et al. 2007, Gellissen 2002, Houard et al. 2002, Jahic et al. 2006, Labuschagne and Albertyn 2007). Of these yeasts, *S. cerevisiae* and *Kom. pastoris* have been most extensively developed for heterologous protein production. More than 500 heterologous proteins have been producted in *Kom. pastoris*, including plant, animal, and human proteins, as well as membrane-associated proteins which are often difficult to functionally express in many other systems (Cregg 2007, Labarre et al. 2007, Macauley-Patrick et al. 2005, Porro et al. 2005, http://faculty.kgi.edu/cregg). *Kom. pastoris* has the exceptional ability to produce high quantities of proteins, glycosylate them in patterns similar to that of humans, efficiently secrete them into the medium, and avoid aggregation and proteolysis during recovery for many proteins. Proteins can be expressed in sufficient quantity and quality for applications in protein engineering and structural analyses (Daly and Hearn 2005).

TABLE 3.7 Advantages and Disadvantages of Yeasts for Recombinant Protein Production

Advantages
High surface to volume ratio of the yeast cell enabling fast growth rate and efficient production of proteins and other metabolites.
Presence of a thick cell wall that protects from physical damage during fermentations.
Certain species have well-characterized genetic systems facilitating cloning and expression of recombinant proteins.
Certain species have GRAS (generally regarded as safe) status and are considered safe organisms for production of enzymes for the food industry (Pariza and Johnson 2001) and biopharmaceuticals.
Fermentation technology is, for some species, well-developed for large-scale fermentations.
As eukaryotes, they have the ability to perform post-translational modifications of proteins
Disadvantages
Glycosylation patterns may vary from that in the mammalian host
Expression levels of recombinant proteins can be 5% or less of total protein

(Adapted and Expanded from Walsh 2001).

Despite these advantages, several challenges are encountered in therapeutic protein production in yeasts. Limitations have been encountered in the use of *Kom. pastoris* processes including catabolite repression of the AOX1 promoter, proteolysis, and aggregation of some secreted proteins, and cell death in high density bioreactor conditions (Jahic et al. 2006). A systematic analysis of the expression of 79 heterologous human genes (cDNAs) in *Kom. pastoris* showed that elevated expression was associated with low abundance of AT-rich regions of the expressed gene, the isoelectric point, size, and structure of the protein, which can alter fidelity of synthesis and secretion (Boettner et al. 2007, Gellissen 2005). One of the most critical challenges is achieving the human-equivalent glycosylation profile of the heterologous protein (Gellissen 2005, Sethuraman and Stadheim 2006, Wildt and Gerngross 2005). A summary of the advantages and drawbacks to heterologous production of proteins in yeasts is presented in Table 3.7.

Despite certain advantages of *Kom. pastoris* compared to *S. cerevisiae*, including higher expression, secretion of larger proteins, and reduced proteolysis, *S. cerevisae* has been primarily utilized for the production of protein pharmaceuticals and vaccines (Crommelin et al. 2008, Liljeqvist and Stahl 1999, Walsh 2003). This is mainly due to the more extensive understanding of the physiology of *S. cerevisiae*, availability of genetic systems for cloning and expression, and the long history of safe use in a variety of processes. As the field of yeast heterologous protein production advances, *Kom. pastoris*, and possibly *O. polymorpha* or other yeasts described above, may become the primary production yeasts of heterologous proteins as human pharmaceuticals and other industrial processes.

12. SECONDARY METABOLITES, NON-PROTEIN PHARMACEUTICALS, AND FINE CHEMICALS FROM YEASTS

12.1. Secondary Metabolites and High-Value Primary Metabolites

In this section, bioconversions by yeasts for production of high-value fine chemicals and pharmaceuticals as well as recombinant processes for the formation of secondary metabolites are described. The

fermentative production of bulk chemicals was described in section 11. Overall, high-value fine chemical and small-molecule pharmaceuticals are principally produced by synthetic chemistry using inorganic catalysts (Faber 2004, Panke et al. 2004, Rozzell 1999, Straathof and Adlercreutz 2000). Yeasts are also not generally employed for production of secondary metabolites, which involve complex biosynthetic pathways, and are produced in submerged fermentation by actinomycetes, bacilli, and filamentous fungi, as well as being derived from plants (Demain and Davies, 1999, Kleinkauf and von Döhren, 1997, Osiewacz 2002).

Yeasts appear to lack the ability to synthesize many classes of secondary metabolites, and presumably do not contain the genes encoding the enzymes involved in synthesis of various classes of secondary metabolites, including polyketides through the acetate pathway, phenylpropanoids through the shikimate pathway, alkaloids from amino acid and nicotinic and purine precursors, aminoglycosides, modified peptides such as penicillins and β-lactams, and peptide and protein toxins. Certain filamentous fungi that grow as a yeast-like stage as part of their life cycle produce antibiotic compounds, e.g., aureobasidin (Zhong et al., 2000), but these fungi are generally considered not to be true yeasts. However, with the increasing availability of genome sequences, it will be useful to search for genes involved in these secondary metabolite pathways as they occur in filamentous fungi, and remnants of the active pathways in yeasts may be evident by genome analysis but the complete and active pathways were partially lost during evolution. The ecological selective factors obviating synthesis of antibiotics and certain other secondary metabolites in yeast metabolites is not known, but is likely related to their ecophysiology, especially their ability to colonize habitats in the absence of a need for production of antibiotics and related secondary metabolites for antagonism against competing organisms (Rosa and Péter 2006).

Some yeasts produce classes of primary and secondary metabolites utilized industrially, including isoprenoids, ergosterol, vitamins, adenosine triphosphate, coenzyme A, and other compounds (Demain and Davies 1999, Rehm and Reed 1996, Rehm et al. 1996, Roehr 1996, Vandamme 1989). Yeasts are also used in the combinatorial and recombinant synthesis of plant secondary metabolites, such as alkaloids, flavonoids, and polyketides (Julsing et al. 2006). Yeast enzyme systems are able to catabolize and degrade various natural toxins, xenobiotics, and pollutants, which is described in section 15.

The generation of natural flavors and colors involving yeast biotransformations and fermentations is an area of commercial value (Hagedorn and Kaphammer 1994, Vandamme and Soetaert 2002). The concept of "natural" has been defined by the regulatory agencies in the USA and in Europe (Vandamme and Soetaert 2002), and has been shown to be important in general public assessment and acceptance of food ingredients. Genetically engineered *S. cerevisiae* strains have been developed for industrial production of methyl-benzoate, a food industry flavor with fruity properties that also has applications in perfumery (Farhi et al. 2006). Dihydrocoumarin for the perfume industry has also been derived from metabolism of coumarin by *S. cerevisiae* (Haser et al. 2006). Phenethyl alcohol, which imparts floral odors in certain foods and perfumes, is formed from metabolism of phenylalanine by *S. cerevisiae* (Stark et al. 2002). Basidiomycetous yeasts have been developed as sources of organic sulfur compounds (VOSCs) when fed L-methionine, and they produce an array of higher alcohols and esters including 3-(methylthio)-1-propanol, methanethiol, S-methyl thioacetate, dimethyl disulfide, dimethyl trisulfide, allyl methyl sulphide and 4,5-dihydro-3(2H)-thiophenone (Buzzini et al. 2005a). Yeasts are also used for flavor encapsulation of important metabolites including limonene (Normand et al. 2005).

Enzymes or whole cells of yeasts are utilized as efficient biocatalysts for the production of lipid-derived flavors and fragrances (Hagedorn and Kaphammer 1994, Waché et al. 2006). The enzyme activities integral to these biotransformations and syntheses include hydrolysis, esterification, oxidation, and lyase reactions (Hagedorn and Kaphammer 1994, Waché et al. 2006). Yeasts have considerable biodiversity in their capabilities to perform these reactions. Lipid-derived flavors include γ-decalactone with fruity notes, which has mainly been derived from ricinoleic acid in low-priced castor oil (*Ricinus communis*).

Isoprenoids comprise a large group of natural products that have several industrial applications. They are used as food flavorants (e.g., apritone, neroloidol), colorants (e.g., astaxanthin, zeaxanthin, β-carotene), disinfectants (e.g., camphor, pinene), medicines (taxol), and nutrients (e.g., vitamins A, E, K). In nature, they also have prominent roles as signaling molecules, antioxidants, pollination attractants, antibacterials and antifungals, and other functions (Dewick 1997). Evidence is also accumulating that certain isoprenoids have preventative functions in cancer, cardiovascular disease, and other degenerative diseases (Bertram and Vine 2005, Hussein et al. 2006, Lockwood et al. 2006). Although most isoprenoids are prepared by chemical synthesis or by extraction of plant materials (Teisseire 1994), there has been considerable research devoted to microbial syntheses, including by yeasts, of 10–30 carbon isoprenoids including essential oils and other compounds (Chemler et al. 2006, Maury et al. 2005, Oswald et al. 2007, Takahashi et al. 2007, Withers and Keasling 2007). However, most small-molecular, non-enantiomeric isoprenoids are much less expensive to synthesize by chemical synthesis, and are not yet produced on a commercial scale by fermentation or biocatalysis.

12.2. Fine Chemicals and Pharmaceuticals by Pathway Expression

The expression of cloned genes into *S. cerevisiae* and certain other yeast species (Table 3.8) has created new opportunities in industrial yeast biotechnology. With the advances in genetic systems and functional genomics in yeasts, particularly in *S. cerevisiae*, yeasts are increasingly being utilized as hosts for the incorporation of entire or partial multi-enzyme biosynthetic pathways for various products. This is a trend in yeast industrial microbiology that is expected to advance in scope and activity.

Microbial recombinant biosynthesis of natural products, particularly fine chemicals and pharmaceuticals of high economic value, has certain advantages over chemical synthesis methods or extraction of

TABLE 3.8 Examples of Industrial Fine Chemicals and Small Molecular Weight Pharmaceuticals Produced in Yeasts: Introduction of Multiple Heterologous Genes

Yeast	Compound	Reference
Saccharomyces cerevisiae	Polyketides	Mutka et al. 2006, Wattanachaisaereekul et al. 2007
	Artemisinic acid	Ro et al. 2006
	Nicotianamine	Wada et al. 2006
	Taxoids (Taxol®)	Dejong et al. 2006
	Terpenoid indole alkaloids	Geerlings et al. 2001
	Flavonoids	Chemler et al. 2006
	β-Carotene	Verwaal et al. 2007
Schizosaccharomyces pombe	Hydrocortisone	Bureik et al. 2002, Dragan et al. 2005, Szcebara et al. 2003

compounds from plant biomass (Chemler et al. 2006). Advantages include lower energy requirements and emissions, less toxic waste such as solvents and catalysts, and the utilization of renewable feed stocks as substrates (Chemler et al. 2006). Also, biosynthesis enzymes catalyze stereospecific and chiral reactions that result in the synthesis of the physiologically active isoform compared to chiral mixtures obtained in many chemical syntheses.

Owing to the advanced technology in metabolic engineering and functional genomics there have been major advances in the expression in *S. cerevisiae* of single or multiple genes encoding partial or entire biosynthetic pathways for primary metabolites, and especially fine chemicals, secondary metabolites, and pharmaceuticals (Table 3.8) (Branduardi et al. 2008, Chartrain et al. 2000, Chemler et al. 2006, Chotani et al. 2000, Kern et al. 2007, Ostergaard et al. 2000). *S. cerevisiae* is the primary model eukaryotic organism for studying fundamental properties of eukaryotic biology, and the yeast has many features that make it useful for industrial applications.

Carotenoids are 40-carbon isoprenoids that display a wide range of colors. Carotenoids are used industrially as pigments mainly in feeds, and more recently as nutraceuticals. Carotenoids are generally separated into carotenes (hydrocarbons, e.g. β-carotene), and xanthophylls (oxygenated carotenoids, e.g., astaxanthin) (Bhosale and Bernstein 2005, Johnson and Schroeder 1996). Carotenoids have traditionally been used for pigmentation in the aquaculture and poultry industries, and the global market was estimated to be nearly $1 billion in 2005 (BCC Research 2005, http://www.bccresearch.com). The feed market is the largest application segment and it was estimated at approximately $530 million in 1999 (BCC Research 2005). The carotenoid demand in the pharmaceutical sector is increasing with an estimated annual growth rate of 7%. Important carotenoids include astaxanthin and β-carotene, which comprised approximately 28% of total sales (ca. $261 million in sales in 2005) (BCC Research 2005). The third largest carotenoid in value is canthaxanthin (19% of total). Globally, Europe accounts for 45% of the worldwide market, which is used mainly for sociocultural preferences for pigmentation and enhancing the appeal of many foods. The US market is smaller (19%), with an increasing focus on the use of carotenoids as natural antioxidants and prevention of human disease, and carotenoids are increasingly marketed as neutraceuticals. Although the industrial importance of microbial carotenoids (and other isoprenoids) is currently small, it appears to be growing.

Even though the production of carotenoids is still dominated by chemical synthesis, substantial efforts have been undertaken to produce carotenoids from microbial sources, for example by cloning and expression of genes in *E. coli* and in *Zymomonas mobilis* (Das et al. 2007), as well as in yeasts, particularly *C. utilis* and *S. cerevisiae* (Miura et al. 1998, Verwaal et al. 2007). In early studies with yeasts, *C. utilis* was used for the heterologous production of carotenoids (Sandmann and Misawa 2002). However, productivity was low, and synthesis by yeast could not compete with carotenoids produced by chemical synthesis, particularly carotenes and xanthophylls possessing relatively simple structures. In more recent studies, genes from *X. dendrorhous* were transformed to *S. cerevisiae*, and relatively high yields of β-carotene (~5.9 mg per g DCW) were obtained (Verwaal et al. 2007). However, this productivity is still not comparable to that of synthetic β-carotene, and its industrial utility will rely on niche markets for "natural" products. Astaxanthin is among the most important component of salmonid feeds and appears to be increasing in importance as a nutraceutical. The natural fermentation involving *X. dendrorhous* was described in section 8.2.4. and in Chapter 134.

Saccharomyces cerevisiae strains have been developed that produce polyketides, which are an important group of industrial secondary metabolites, including antibiotics, immunosuppressive agents, cholesterol lowering drugs, and other biological activities. Polyketide-producing *S. cerevisiae* strains have been constructed by introduction of polyketide biosynthetic genes and metabolic engineering (Kealy et al. 1998, Mutka et al. 2006, Rokem et al. 2007, Wattanachaisaereekul et al. 2007).

Recombinant *S. cerevisiae* and *Schiz. pombe* strains have also been developed that produce hydrocortisone, the main steroid of mammals, and an important intermediate in the synthesis of a number of drugs with various pharmacological activities (Bureik et al. 2002, Dragan et al. 2005, Szcebara et al. 2002). In an extraordinary series of experiments, *S. cerevisiae* strains that expressed 11 recombinant genes were demonstrated to perform the conversion of 11-deoxycortisol to hydrocortisone. As with expression of several other fine chemicals and pharmaceuticals, an adequate supply of NADH/NADPH as reducing power and a balanced redox environment was needed for maximum expression.

The antimalarial drug precursor, artemisinic acid, and its direct precursor amorpha-4-11-diene, have successfully been produced in *S. cerevisiae* (Lindahl et al 2006, Ro et al. 2006). Artemisinic acid was produced at titers of ~100 mg/l and at a sufficiently high productivity to augment or potentially replace the compound extracted from plants (Ro et al. 2006). The production strain was metabolically engineered in its mevalonate pathway, and was also tailored by introduction of a P450 gene from the plant *Artemisia annua* (Ro et al. 2006). The same strategy of combining genes from different organisms in *S. cerevisiae* strains was used to develop novel strains that produce paclitaxel (Taxol®) (Dejong et al. 2006, Julsing et al. 2006). In this example, eight taxoid biosynthetic genes were functionally expressed in *S. cerevisiae* from episomal vectors containing gene cassettes (Dejong et al. 2006). A bottleneck in production was encountered in the accumulation of the first P450 product, and means of overcoming this limitation were described.

In another intriguing example of metabolic engineering in yeasts, a strain of *S. cerevisiae* was genetically engineered for the expression of heterologous genes from plant, bovine, and human sources for the synthesis of the important steroids pregnenolone and progesterone at levels of about 60 mg/l from endogenous sterols in the yeast cells (Duport et al. 1998). Until this development (Chartrain et al. 2000), the synthesis of these steroids required a combination of chemical and biotransformation steps, using cholesterol or phytosterols as the starting materials.

Metabolic engineering of *S. cerevisiae* has been performed for the production of nicotianamine (NA), a plant-derived metal chelator with potential medicinal application as a non-peptidyl angiotensin I-converting (ACE) enzyme for control of blood pressure (Wada et al. 2006). A yeast strain was developed that accumulated up to 100 times the wild-type quantity of S-adenosylmethionine (SAM), the primary precursor of NA. The maximum concentration of NA that accumulated in *S. cerevisiae* was approximately 766 μg/g (wet weight). Like certain other metabolites, it accumulated intracellularly in vacuoles, which would potentially limit its production due to the inability to secrete the compound. The intracellular accumulation as opposed to extracellular secretion is also a major limitation in the fermentative production of other lipophilic compounds such as carotenoids.

Plants are a rich source of alkaloids, and are known to produce more than 12,000 compounds within this class of secondary metabolites. Several alkaloids are used medicinally, and the world market exceeds $4 billion (Julsing et al. 2006). The cloning and expression of alkaloid biosynthetic genes in yeast has recently been investigated (Julsing et al. 2006). The overexpression of biosynthetic enzymes from the Vinac group of alkaloids and feeding of the precursors tryptamine and secologanin led to the production of modest quantities of strictosidine (Geerlings et al. 2001). *S. cerevisiae* is also being investigated for biotransformation of alkaloids by single enzymatic steps (Rathbone and Bruce 2002).

Flavonoids are found exclusively in plants, produced by the phenylpropanoid pathway. Phenylpropanoids have a myriad of biological

attributes and function as pigments, antioxidants, estrogen promotion, antivirals, antibacterials, and anti-cancer agents (Birt et al. 2001, Chemler et al. 2006, Forkman and Martens 2001). Biosynthesis begins by the deamination of phenylanine or tyrosine by phenylanine ammonia lyase (PAL) to yield cinnamic acid. The 15-carbon phenylpropanoid core is formed, which is modified by rearrangement, alkylation, oxidation, and glycosylation (Chemler et al. 2006, Dewick 1997). *Rh. glutinis*, *Rhspor. toruloides*, and certain other yeast species possess active PALs, which have been the principal commercial sources of this enzyme (Wall et al. 2008). PALs from other sources have also been cloned and expressed in *S. cerevisiae* and *Kom. pastoris* (Chemler et al. 2006, Jiang et al. 2005, Vannelli et al. 2007). Recently, the gene encoding pathways for various flavones and flavonoids have been expressed in *S. cerevisiae* and biosynthesis enhanced by metabolic engineering (Jiang et al. 2005, Leonard et al. 2005, Ro and Douglas 2004, Vannelli et al., 2007). Expression of the PAL gene from *Rh. glutinis* was employed for the production of p-hydroxycinammic acid and p-hydroxysterene from glucose, with the potential for production of this and other fine chemicals from renewable resources (Sariasiani 2007). These results illustrate the promise of yeasts as heterologous hosts for industrial synthesis of flavonoids and related secondary metabolites from plants.

Several species of yeasts produce higher-value lipid-related products such as sophorolipids with potential industrial utility as surfactants, antimicrobials, surface-enhanced soil remediation and for mitigation of algal blooms (Felse et al. 2007, Kim et al. 2002, Mulligan et al. 2001, Shete et al. 2006). Novel families of glycolipids from basidomycetous yeasts have also been characterized (Heise et al. 2002, Morita et al. 2007).

12.3. Protein Pharmaceuticals from Yeasts

Proteins currently constitute about 25% of new approved drugs in the USA, with the majority being monoclonal antibodies (Gellissen, 2005, Sethuraman and Stadheim 2006, Walsh 2005, 2006). As of 2006, more than 165 protein biopharmaceuticals have been approved by European and US regulatory agencies, and more than 500 product candidates are in preclinical and clinical development (Walsh 2006). In 2004, the global market for recombinant protein therapeutics and nucleic acid-based products was more than than $33 billion and is expected to reach $60–70 billion by 2010 (Evans and Das 2005, Pavlou and Reichert 2004, 2005, Schmidt 2004, Walsh 2006).

Although mammalian cells (e.g., CHO cells), and to a lesser extent *E. coli*, remain the primary organisms used for biopharmaceutical protein production, both sources have significant drawbacks. Mammalian cell culture is technically complex, slow, expensive, yields are typically low, and there exists potential for viral and prion contamination (Walsh 2006). The majority of protein pharmaceuticals are glycoproteins (Sethuran and Stadheim 2006), and *E. coli* does not perform necessary glycosyl modifications, and current commercial protein products from *E. coli* are limited primarily to small molecular weight relatively simple proteins such as insulin. Furthermore, yields, purification, therapeutic activity, and the potential for the presence of endotoxin in the product are of concern when using *E. coli* as an expression host for protein pharmaceuticals.

Yeasts are intensively being developed as protein expression systems, which in comparison to mammalian cell lines have higher productivity, higher cell yields, shorter fermentation cycles, and can be cultured in defined media under relatively inexpensive conditions. In addition, yeasts can efficiently secrete proteins, they possess post-translational modification pathways that can mimic those of humans, and are nonpathogenic and nonpyrogenic (Schmidt 2004). Advantages and disadvantages of yeasts for recombinant protein production are summarized in Table 3.7. The primary yeast species being developed for protein pharmaceutical and enzyme production are *S. cerevisiae*, *Kom. pastoris*, *O. polymorpha*, *Bla. adeninivorans*, *Y. lipolytica*, and *K. lactis* (Schmidt 2004). Certain peptide and protein therapeutics produced in *S. cerevisiae* and more recently *O. polymorpha* and *Kom. pastoris* have been commercialized (Table 3.9) (Gerngross 2004, Walsh 2003).

One disadvantage to the synthesis of protein biopharmaceuticals in certain yeast species is that the resulting products often have a non-human glycosylation pattern (Gemmill and Trimble 1999, Gerngross 2004, Schmidt 2004, van Ooyen et al. 2006) (Table 3.7). Non-human glycosylation of therapeutic proteins can affect various biological properties, including half-life, tissue distribution,

TABLE 3.9 Representative Commercial Recombinant Protein Pharmaceuticals and Vaccines Produced in Yeasts

Product	Use	Yeast Host
Short-acting recombinant insulin	Diabetes mellitus	*Saccharomyces cerevisiae*
Granulocyte macrophage colony Stimulating factor (GM-CSF)	Bone marrow transplantation Regulation of hematopoiesis Acute myologenous leukemia	*S. cerevisiae*
Hirudin/lepuridin	Anticoagulant	*S. cerevisiae*
Urate oxidase	Hyperuricemia	*S. cerevisiae*
Platelet-derived growth factor	Diabetic ulcers	*S. cerevisiae*
Human serum albumin	Excipient, shock, cirrhosis, other uses	*S. cerevisiae*
Erythropoietin	Renal disease	*S. cerevisiae*
Glucagon	Hypoglycemia	*S. cerevisiae*
Human growth hormone	Dwarfism, tissue repair	*S. cerevisiae*
Platelet derived growth factor	Anemia	*S. cerevisiae*
Insulin	Diabetes	*S. cerevisiae*
Hepatitis A vaccine	Hepatitis A	*S. cerevisiae*
Hepatitis B vaccine	Hepatitis B	*S. cerevisiae, Ogataea polymorpha, Komagataella pastoris*
Diphtheria, tetanus, pertussis	Hepatitis B	*S. cerevisiae*
Haemophilus influenzae type B	Combination vaccines and polio	*S. cerevisiae*
Human papilloma virus (HPV) antigen	Human papillomavirus	*Kom. pastoris*

(Adapted and Expanded from Crommelin et al. 2008, Melmer 2005, Schmidt 2004, Walsh 2003).

pharmacokinetics, and immunogenicity (Hamilton and Gerngross 2007). Most yeast species have the propensity to glycosylate proteins with high mannose-containing N-glycans (Gemmill and Trimble 1999). To resolve the problem of glycosylation, yeasts are being developed for "humanization" of post-translational modifications (Li et al. 2007, Wildt and Gerngross 2005). Emphasis in this area has been with *Kom. pastoris*, which is being optimized by "glycoengineering" through gene alterations to eliminate undesirable protein modifications (Gerngross 2004, Hamilton and Gerngross 2007). After knockout of four genes to eliminate glycosylation patterns typical of *Kom. pastoris*, and the introduction of 14 heterologous genes allowing the mimicking of human cell glycosylation, strains were derived that produced glycoproteins with greater than 90% desired sialyation. Such glycoengineered yeast strains have been used for the expression of functional erythropoietin and are being evaluated for production of several glycosylated human proteins (Hamilton and Gerngross 2007). Although the primary yeast studied for humanization of glycosylation is *Kom. pastoris*, the transfer of such genes to *S. cerevisiae* would have potential advantages considering the advanced genomic and systems analysis of this yeast (Nielsen and Jewett 2007). Advances in the humanization of glycosylation patterns in yeasts offer promise that they will be increasingly used as sources of protein biopharmaceuticals and enzymes due to their desirable properties (Table 3.7).

Yeasts are currently commercially used or are close to commercialization for the production of a variety of heterologous protein pharmaceuticals (Table 3.9). High-level expression of human interferons (Chang 2006, Cousens et al. 1987), tetanus fragment C (Clare et al. 1998), HIV-1 envelope glycoprotein gp120 (Jordan and Gibbins 2006), and others have been achieved in *S. cerevisiae*, *K. pastoris*, and other yeast species (Hadfield et al. 1993).

The use of monoclonal antibodies (mAbs) as human biologics was initially made possible by the pioneering studies of Köhler and Milstein (Köhler and Milstein, 1975). mAbs are the most prevalent and high-value class of protein drugs (Gasser and Mattanovich 2007, Maggon 2007, Pavlou and Reichert 2005), and presently have an estimated global market of $10 billion, which is expected to increase to $17 billion in 2008, and to $30 billion in 2010 (Evans and Das 2005, Gasser and Mattanovich 2007). mAbs have traditionally been produced in mammalian cell lines, mostly recombinant CHO cells and other lines, but this process is slow and expensive (Farrid 2006). The production of antibodies in yeasts and other fungi is also being actively pursued, but it has been challenging to develop antibody producing systems in yeasts (Gasser and Mattanovich 2007). Yeasts primarily investigated for production of mAbs are *S. cerevisiae, O. polymorpha*, and *Kom. pastoris* (Sodoyer 2004).

13. PROBIOTICS AND PREBIOTICS

The beneficial impact of lactic acid bacteria on human health was described a century ago by Metchnikoff (Metchnikoff 1908). Certain yeast species have also been used as prebiotic and probiotic agents for preventing or treating various intestinal, nutritional, and toxicological disorders. In particular, "*S. boulardii*", originally isolated from fruit in Indochina, has been used for treatment of intestinal diseases in children and adults since 1950 (Buts and Bernasconi 2005, Edwards-Ingram et al. 2007). Recent studies have shown that it is conspecific with *S. cerevisiae*, but *S. boulardii* appears to have certain genotypic and phenotypic properties that may contribute to its probiotic properties (Edwards-Ingram et al. 2007). Controlled clinical trials have shown efficacy of *S. boulardii* for prevention or elimination of several intestinal disorders, including antibiotic-associated infection by *Clostridium difficile* (Fric 2007). Yeasts have also been suggested to prevent other intestinal infections and disorders, including inflammatory bowel disease and Crohn's disease (Besirbellioglu et al. 2006, Buts and Bernasconi 2007, Dalmasso et al. 2006, Edwards-Ingram et al. 2007, Sougioultzis 2006, Villarruel et al. 2007). The mechanisms of probiotic activity have not been elucidated but may involve alteration of inflammatory and immune responses or destruction of toxic factors (Ozkan et al. 2007). Although *Saccharomyces* spp. and other yeasts may be promising therapeutic agents, they need to undergo controlled clinical trials to critically evaluate their efficacy.

Recently, the concept of a biodrug was introduced, which entails the oral administration of living recombinant microorganisms that express disease-fighting proteins (Blanquet et al. 2001). This strategy has been applied to yeasts (Blanquet et al. 2001, 2003, Garrait et al. 2007). *S. cerevisiae* expressing cytochrome P450 reductases has been evaluated in animal models for detoxification of compounds in the digestive environment. However, these studies have been evaluated only in animal systems, and their potential benefits in human health are presently unclear.

Preliminary evidence indicates that certain yeasts can produce prebiotics, which are compounds (generally oligosaccharides) that stimulate the growth of bifidobacteria and other beneficial bacteria in the gut of humans and animals, or oligopeptides that have beneficial health benefits by stimulation of immune response. Prebiotics are often sugar derivatives such as fructooligosaccharides (Maugeri and Hernalsteens 2007), which certain yeasts can catabolize due to their formation of inulinases. *K. lactis* was found to synthesize prebiotic oligosaccharides and immunostimulatory peptides from whey (Belem and Lee 1998). A survey of yeasts from fruits and flowers in Brazilian tropical forests showed that strains of *Candida*, *Rhodotorula*, and *Cryptococcus* produced substantial quantities of fructooligosaccharides (Maugeri and Hernalsteens 2007). The prebiotic trisaccharide, neokestose, was produced from sucrose in high yields by *X. dendrorhous* (Kritzinger et al. 2003). *X. dendrorhous* also converted maltose into prebiotic isomaltoligosaccharides by a novel α-glucosidase (Fernandez-Arrojo et al. 2007). As with probiotics, carefully controlled clinical trials will be necessary to show health benefits.

14. YEAST GLUCANS AND CELL WALL POLYSACCHARIDES

Yeast cell wall polysaccharides have been used as adjuncts for animal and fish feeds (Sauerwein et al. 2007). These polysaccharides have been proposed to promote animal growth and health by various mechanisms, including immunomodulation, oxidative status, binding of toxins and pathogens, and interactions with gut constituents.

Glucans and mannans have also been found to have a myriad of biological functions in animal models and potentially in humans, including modulation of histamine release (Holck et al. 2007), and antitumor activities (Ghoneum et al. 2007). Phagocytosis of *S. cerevisiae* induced apoptosis in human breast cancer cells *in vivo*, and glycans were involved in the apoptotic process (Ghoneum et al. 2007). Further studies are needed in this area to evaluate animal and human health promotion by yeast cell wall polysaccharides.

15. DEGRADATION OF POLLUTANTS, XENOBIOTICS, AND ROLES IN BIOREMEDIATION

Due to the ability of various yeast species to grow on a wide diversity of substrates, including aromatic molecules, alkanes, lipid compounds, amines and other recalcitrant compounds, they have the capacity for the transformation of deleterious compounds to innocuous derivatives. *Y. lipolytica* transformed 2, 4, 6-trinitrotoluene (TNT)

to derivative products (Jain et al. 2004, Neujahr 1990). Molecular oxygen and oxidative enzymes such as cytochrome P450s and oxygenases are often involved in the degradation pathways (Neujahr, 1990). Phenolic degradation is also carried out by several yeasts, particularly basidiomycetous genera such as *Cryptococcus*, *Rhodotorula*, and *Trichosporon* (Böer et al. 2005, Margesin 2007, Middelhoven 2006, Middelhoven et al. 1991, Sampaio 1999). Several species of *Candida* and *Trichosporon* spp. are recognized to efficiently transform halogenated aromatic compounds (Kurtz and Crow 1997). Polycyclic aromatic hydrocarbons from coastal sediments were degraded by species of *Candida*, *Cryptococcus*, *Rhodotorula*, and *Trichosporon* (MacGillivray and Shiaris 1993). Recombinant yeasts expressing a soybean cytochrome P450 enhanced the metabolism of phenylurea herbicides (Sminszky et al. 1999). It has been reported that *Pseud. jejuensis* is capable of degrading certain plastic wastes (Seo et al., 2007). Immobilized and cold-adapted yeast systems are being developed as industrial biodegradative systems (Krallish et al. 2006). Yeast systems have also been developed for the sensing and accumulation of various ecotoxicants such as heavy metals (Lettieri 2006, Park et al. 2007).

Xanthophyllomyces dendrorhous and *Ph. rhodozyma* have been reported to degrade ochratoxin, a potent mycotoxin (Péteri et al. 2007). *Trichosporon* spp. are capable of degrading ochratoxin A and zearalenone (Molnar et al. 2004) in laboratory cultures. *S. cerevisiae* strains have been reported to degrade patulin during cider fermenations (Moss and Long 2002). The ability of yeasts to degrade mycotoxins has important health implications, since these toxicants occur in commodities, such as feeds, foods, and beverages, and are considered as serious health hazards (Bryden 2007).

Genomic approaches in yeasts are increasingly being utilized to elucidate the mechanisms of xenobiotic, herbicide, and insecticide toxicity to eukaryotes, and mechanisms of resistance (Texeira et al. 2007). Advances in genomics and systems biology are fundamentally transforming the field of toxicology and the field of toxicogenomics is under development (Olden 2006, Simmons et al. 2002, Texeira et al. 2007, Waters and Fostel 2004). *S. cerevisiae* is a primary model organism employed in the study of ecotoxicology and toxicogenomics (Gatzidou et al. 2007, Lettieri 2006, Snell et al. 2003, Weiss et al. 2004a).

16. YEASTS FOR FUNCTIONAL TESTING OF HUMAN GENES AND DISEASE DISCOVERY

Saccharomyces cerevisiae has been developed as an extraordinarily valuable model organism to study fundamental aspects of mammalian cell biology and for discovery of disease mechanisms (Foury 1997, Mager and Winderickx 2005, Pache et al. 2008, Steinmetz et al. 2002) (Table 3.10). For example, yeast genetic systems have been used to study activation of human receptors by anti-estrogens, such as tamoxifen (Dudley et al. 2000). The use of *S. cerevisiae* was particularly valuable in this study since it lacks endogenous nuclear receptors and other receptor coregulatory proteins that are present in more complex mammalian cell lines. This strategy was also exploited to monitor endocrine disruptors and estrogenic activities in surface waters and animal feeds by a yeast recombinant assay (Beek et al. 2006, Bovee et al. 2006, Garcia-Reyero et al. 2001).

TABLE 3.10 Examples of Human Diseases Investigated using *Saccharomyces cerevisiae* as a Model Organism

Disease	Reference
Prion related diseases	Nakayashiki et al. 2005, Vishnevskaya et al. 2007
Alzheimer's/amyloid diseases	von der Haar et al. 2007,
Parkinson's disease	Doostzadeh et al 2007, Witt and Flower 2006
Cancer	Botstein 2003, Hartwell 2002
Channelopathies (e.g. migraine headaches)	Wolfe and Pearce 2006
Aging	Piper 2006

The primary attributes that make *S. cerevisiae* and *Schiz. pombe* attractive compared to other model eukaryotic systems for elucidation of disease mechanisms are their well-developed genetic systems, rapid growth, defined and simple culture conditions, and the finding that many of the basic cellular and molecular mechanisms in humans are present in yeasts (Hartwell 2002, Mager and Winderickx 2005, Suter et al. 2006). Comparison of *S. cerevisiae* and human genomes indicated that ca. 30% of human genes known to be involved in human disease have yeast orthologues (Foury 1997).

Valuable genetic approaches to understanding human gene function in *S. cerevisiae* and *Schiz. pombe* include gene disruption, gene marking, targeted mutations, gene-dosage effects, and genome-wide screening for alleles contributing to fundamental mammalian processes and human diseases (Foury 1997, Mager and Winderickx 2005, Oliver 2007, Steinmetz et al. 2002). In a pioneering study carried out in 1983, the protein targets of compactin and tunicamycin were identified by screening a genomic library for genes that conferred drug resistance when overexpressed. Lee and Nurse (1987) demonstrated that the human gene orthologue CDC2 could complement a *cdc2* mutant gene in *Schiz. pombe*. Several human proteins expressed in *Schiz. pombe* and *S. cerevisiae* have subsequently been demonstrated to successfully complement mutations in these yeasts. The ability to functionally complement *S. cerevisiae* with human proteins and to functionally express human proteins in yeast has enabled the development of sensitive cell-based screens for ligands and drugs (Armour and Lum 2005).

Strategies and methods for expression of human genes in yeasts have been reviewed (Waterham and Wanders 2007). Screens for functional interaction of proteins have been developed, particularly the yeast two-hybrid system (Fields and Song 1989), as well as refinements and improvement of this powerful technique (Izumchenko et al. 2007, Rajagopola et al. 2007). *S. cerevisiae* has been used to conduct whole genome analyses by various approaches (Eason et al. 2004, Glaver et al. 2002, Oliver 2007, Waterham and Wanders 2007). Strain collections consisting of single gene deletion mutants for all of the nearly 6000 genes in yeast now make it feasible to rapidly assess drug sensitivities and other phenotypes (Baetz et al. 2004, Chu and Davis, 2007). To facilitate whole genome analysis, each deletion has been tagged with a unique 20-mer DNA sequence, which functions as a molecular bar code and enables the identification of each deletion. The mixture of all the coded strains allows for the analysis of the entire genome with the manipulation of a single culture. When grown under various conditions, the loss of a tagged strain indicates the loss of a deletion from the yeast population. The level of each tag is determined by PCR amplication of the tags and hybridization to microarray chips that contains the complement to all of the DNA sequence tags. Other approaches for genome-wide screening processes have been developed in *S. cerevisiae* and several databases are accessible describing the yeast–human connection (Mager and Winderickx 2005). Another strategy using *S. cerevisiae* for studies of human acute and degenerative diseases is the generation of mutations altering the protein of interest (Chen and Contreras 2007, Waterham and Wanders 2007). *S. cerevisiae* has served as an extremely useful organism for study of cancer (Hartwell 1992, 2002), as a model for Parkinson's disease (Witt and Flower 2006), and as a model system for protein conformational diseases. The molecular bases of prion action, propagation, and inheritance have been studied in yeasts (Collinge and Clarke 2007, Wickner et al. 2007), as well as protein aggregation characteristic of diseases, including Alzheimer's,

Parkinson's, and Huntington's (Nakayashiki et al. 2005, Vishnevskaya et al. 2007, von der Haar et al. 2007). A summary of selected human diseases studied using *S. cerevisiae* is presented in Table 3.10.

Advanced genetic systems in *S. cerevisiae* have led to the development of new diagnostics and drugs for control of pathogenic yeasts, and understanding of the mechanisms of action of antifungal drugs (Armour and Lum 2005, Baetz et al. 2004, Nislow and Giaevery 2007, Tournu et al. 2005, Weig and Brown 2007). *S. cerevisiae* has had a prominent role in the development of anticancer therapies (Kaelin 2005). Genomic studies of yeasts have elucidated targets for food preservatives and crop protection (Kim et al. 2004a). The elucidation of fungal regulatory networks has revealed interactions of pathogens with hosts (Panepinto et al. 2005). The availability of the genome sequences for pathogenic yeasts including *Crypt. neoformans* and *C. albicans* has provided valuable information and led to new strategies in antifungal lead compound discovery (Anderson et al. 2003, Jiang et al. 2002). The future holds much potential for the use of yeasts as model eukaryotes for the study of basic human physiology, acute diseases, and degenerative processes, such as aging and dementia in humans (Bishop and Guarente 2007, Coughlan and Brodsky 2005, Doostzadeh et al. 2007, Kaeberlein et al. 2007, Piper 2006, Vishnevskaya et al. 2007).

17. GENOMES OF YEASTS AND THEIR INDUSTRIAL RELEVANCE

As emphasized in this chapter, the availability of the genome sequence of *S. cerevisiae* (Goffeau et al. 1996) has been of paramount importance in fundamental and applied microbiology. The availability and accessability of genomes of other yeast species is advancing rapidly, and will

TABLE 3.11 Completed and Ongoing Genome Sequencing Projects for Yeasts (March 2008)

Species	Strain	Center/Consortium
Candida albicans	1161	Sanger Institute
Candida albicans	SC5314	Standford University
Candida albicans	WO-1	Broad Institute
Candida glabrata	CBS 138	Genolevures
Candida tropicalis	CBS 94	Genolevures
Candida tropicalis	MYA-3404	Broad Institute
Clavispora lusitaniae	R265	Broad Institute
Cryptococcus neoformans	WM276	Genome Science Center
Cryptococcus neoformans var. *grubii*	H99	Broad Institute
Cryptococcus neoformans var. *neoformans*	B-3501A	Standford University
Cryptococcus neoformans var. *neoformans*	JEC21	TIGR
Debaryomyces hansenii	CBS 767	Genolevures
Kazachstania exigua	CBS 379	Genolevures
Kluyveromyces lactis	NRRL Y-1140	Genolevures
Kluyveromyces marxianus	CBS 712	Genolevures
Lachancea (*Kluyveromyces)* thermotolerans	CBS 6340	Genolevures
Lachancea (*Kluyveromyces) waltii*	NCYC 2644	Broad Institute
Lachancea (*Saccharomyces) kluyveri*	NRRL Y-12651	Washington University/Genolevures
Lodderomyces elongisporus	NRRL YB-4239	Broad Institute
Malassezia globosa	CBS 7966	Procter & Gamble
Malassezia restricta	CBS 7877	Procter & Gamble
Meyerozyma (*Pichia) guilliermondii*	ATCC 6260	Broad Institute
Millerozyma (*Pichia) farinosa*	CBS 7064	Genolevures
Naumovozyma (*Saccharomyces) castellii*	NRRL Y-12630	Washington University
Ogataea (*Pichia) angusta*	CBS 4732	Genolevures
Ogataea (*Pichia) angusta*	RB11	Qiagen
Pneumocystis carinii	—	University of Cincinnati
Pneumocystis jirovecii	—	Broad Institute
Pneumocystis murina	—	Broad Institute
Saccharomyces bayanus	623-6C	Washington University
Saccharomyces bayanus	MCYC 623	Broad Institute
Saccharomyces bayanus var. *uvarum*	CLIB 533	Genolevures
Saccharomyces cerevisiae	S288c	Sanger Institute
Saccharomyces cerevisiae	RM11-1a	Broad Institute
Saccharomyces kudriavzevii	IFO 1802	Washington University
Saccharomyces mikatae	IFO 1815	Washington University
Saccharomyces paradoxus	NRRL Y-17217	Broad Institute
Scheffersomyces (*Pichia) stipitis*	CBS 6054	DOE Joint Genome Institute
Schizosaccharomyces japonicus	yFS275	Broad Institute
Schizosaccharomyces octosporus	yFS286	Broad Institute
Schizosaccharomyces pombe	972 h	*Schiz. pombe* European Sequence Consortium (EUPOM)
Vanderwaltozyma (*Kluyveromyces) polyspora*	DSM 70294	Trinity College Dublin
Yarrowia lipolytica	CLIB122	Genolevures
Zygosaccharomyces rouxii	CBS 732	Genolevures

Data tabulated from NCBI genome database (http://www.ncbi.nlm.nih.gov/Genomes/)

impact understanding of eukaryotic biology, human disease, as well as advance the development of yeasts for industrial purposes (Adrio and Demain 2003, Bennett and Arnold 2001, Steward, 2006). Currently, approximately 49 yeast genome projects have been completed or are in development (Table 3.11). This important focus in yeast genomics supports the high expectations of yeasts for their utility in biotechnology.

18. FUNCTIONAL GENOMICS, METABOLIC ENGINEERING, AND SYSTEMS BIOLOGY OF YEASTS

During the past decade, the fields of functional genomics and systems biology, primarily developed in *S. cerevisiae*, have opened new vistas for advances in industrial yeast processes. *S. cerevisiae* has been used as the premier model eukaryotic organism for the development of genomic methods and an understanding of organisms and processes at the level of systems biology (Mustacchi et al. 2006, Oliver 2006). Oliver (2006) eloquently points out that the "grand synthesis" is far from being achieved, and to reach this goal in systems biology will require international standards and reaching important benchmarks in a cooperative and collaborative manner among researchers in a wide variety of scientific disciplines. While functional genomics and systems biology approaches to industrial yeast biotechnology hold much potential, adapting these approaches to industrial organisms will present a considerable challenge.

19. SUMMARY AND PERSPECTIVES

Yeasts have a rich history and a bright future in biotechnology. Their involvement and importance in traditional food fermentations is unparalled by other organisms of biotechnological relevance. The utility of yeasts in biotechnological processes is accelerating due to a number of properties and developments. Most yeast species are nonpathogenic to humans and animals, and thus are anticipated to see more utility in a variety of disciplines of importance to human activities. It is likely that yeasts will be increasingly used as GMOs in traditional processes as their safety is more extensively established. *S. cerevisiae* and certain other species are being developed for the production of biofuels from cellulosic materials and potentially other substrates, and will have importance in the generation of new sources of energy. During the past decade, yeast systems have been developed for the production of heterologous proteins in high yields and with post-translational modifications equivalent or similar to modifications performed in humans. Yeasts are increasingly important as sources of biocatalysts for the production of high-value fine chemicals and and protein pharmaceuticals. Due to their metabolic capabilities, they have important roles in environmental bioremediation. *S. cerevisiae* has become the premier model eukaryotic organism for the understanding of human physiology, including disease processes, and will increase in importance for the understanding and treatment of disease. These advances provide important strategies and tools for enhancing the biotechnological importance of yeasts.

Chapter 4

Agriculturally Important Yeasts: Biological Control of Field and Postharvest Diseases Using Yeast Antagonists, and Yeasts as Pathogens of Plants

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INTRODUCTION

In this chapter, we discuss two important agricultural aspects of yeasts; control of plant diseases through application of yeasts as the control agent, and yeasts that are plant pathogens. Yeasts as biocontrol organisms is presented first, followed by a discussion of some of the more common plant pathogenic yeasts. Food and beverage spoilage, another aspect of impact of yeasts on agriculture, is discussed by Fleet in the chapter on spoilage (see Chapter 5).

In our discussion of biocontrol, it is convenient to divide biotic diseases of plants into those in which the pathogen predominantly gains entrance to the plant via its underground parts versus those that infect aerial tissues of the plant. The vast majority of research on the biological control of plant diseases in the field using yeasts or yeast-like fungi has concentrated on diseases of above ground parts of plants, but El-Tarabily and Sivasithamparam (2006) recently reviewed the potential of yeasts as biocontrol agents of soil-borne fungal plant pathogens.

Epiphytic yeasts are the predominant fungal colonists of aerial plant parts and comprise a significant proportion of their epiphytic microbiota. Some of the earliest work in documenting the potential of yeasts to suppress the development of diseases in aerial plant parts was conducted by Fokkema et al. (1976, 1979, 1987) who studied the colonization of monocot leaves with yeasts and their suppression of necrotrophic pathogens on those leaves. Williamson and Fokkema (1985) demonstrated that the common phyllosphere yeasts *Cryptococcus* (*Cr.*) *flavescens* and *Sporobolomyces* (*Sp.*) *roseus*, applied as a mixture onto maize plants 2–3 days before inoculation with *Colletotrichum graminicola*, reduced lesion density and necrosis by approximately 50%, apparently reducing the number of penetrations, but not the number of appressoria formed by the pathogen. Dik et al. (1991) determined that honeydew utilization by yeasts (predominantly *Sporobolomyces* spp. and *Cryptococcus* spp.) on wheat flag leaves dramatically reduced the level of the carbon source available for necrotrophic pathogens. The reviews of Blakeman and Fokkema (1982), Andrews (1992a), and Paulitz and Bélanger (2001) provide further insight on studies conducted prior to the year 2000 on the use of yeasts in the management of aerial plant diseases.

The use of yeasts to reduce decay on harvested commodities has also received considerable research attention. Application of yeasts for this purpose has been evaluated both as a pre- and as a postharvest treatment. Fruits are rich in easily utilizable carbon and are natural habitats for a variety of yeasts. Until recently, yeasts of grape and apple were studied most extensively because of their importance in vinification and making apple cider (Beech 1993, Cabranes et al. 1990, Davenport 1976). Only sporadic research has been conducted on other fruits such as tomato, strawberry (Buhagiar and Barnett 1971, Martini and Federici 1976), cherries (Stalarova 1982), citrus (Vacek et al. 1979), figs, and opuntia cacti (Miller and Phaff 1962, Starmer et al. 1987a). The finding that yeasts which naturally occur on apples can protect fruit against postharvest diseases (Janisiewicz 1987) spurred interest in the isolation of yeasts from various fruits in order to find new yeast antagonists against postharvest diseases.

1. REDUCTION OF SOIL-BORNE FUNGAL PLANT DISEASES USING YEASTS

El-Tarabily and Sivasithamparam (2006) mentioned three studies in which yeasts were implicated in reducing soil-borne pathogen disease. In the first of these studies, *Candida* (*C.*) *valida*, *Rhodotorula* (*Rh.*) *glutinis*, and *Trichosporon* (*Tr.*) *asahii*, isolated from the rhizosphere of sugar beet, individually were the most successful species to colonize the upper 4 cm of sugar beet roots in a sandy soil and, as a tri-inoculant, were more successful than other treatments in promoting plant growth and reducing root disease incited by *Rhizoctonia solani*. A variety of mechanisms of disease control were attributed to the yeasts, including the production of β-1,3-glucanase, inhibitory volatiles, and a diffusible antifungal metabolite by *C. valida*, *Rh. glutinis*, and *Tr. asahii*, respectively (El-Tarabily 2004). In the second study, El-Mehalawy (2004) reported that rhizosphere yeasts *Kazachstania* (*Saccharomyces*) *unispora* and *C. steatolytica* reduced wilt of beans caused by *Fusarium oxysporum* via the production of antifungal metabolites. In the third study, El-Mehalawy et al. (2004) concluded that several species of *Candida*, *Rhodotorula*, and *Trichosporon* applied individually or as mixtures reduced the incidence of late-wilt disease of maize caused by *Cephalosporium maydis*.

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TABLE 4.1 Examples of Yeast Antagonists of Various Diseases of Greenhouse and Field Crops

Yeast/Yeast-like Fungus	Disease	Assessment Utilized	Reference[1]
Aureobasidium pullulans	Brown rot blossom blight of cherries	Forced blossoms in mist chamber	Wittig et al. 1997
	Fireblight	Field tests on apples during flowering	Kunz 2006
Pseudozyma flocculosa	Powdery mildew	Cucumber, rose, wheat; greenhouse	Jarvis et al. 1989, Avis and Belanger 2002
Cryptococcus and *Candida* spp.	Late blight	Tomato plants; greenhouse	Júnior et al. 2006
Cryptococcus flavescens	Fusarium head blight	Wheat and durum; field	Schisler et al. 2002, Khan et al. 2004
Candida guilliermondii, C. oleophila	Gray mold	Tomato seedlings; growth chamber	Saligkarias et al. 2002a, 2002b
Rhodotorula glutinis		Geranium leaf disks	Buck 2002, Buck and Jeffers 2004
		Beans and tomatoes; growth room	Elad et al. 1994
		Tomatoes; greenhouse	Kalogiannis et al. 2006
Rhodosporidium diobovatum		Tomatoes; greenhouse	Utkhede and Mathur 2006, Utkhede et al. 2001
Aureobasidium pullulans		Stem segments, cucumber and tomato; greenhouse cucumber	Dik et al. 1999
Cryptococcus albidus		Beans and tomatoes; growth room	Elad et al. 1994
		Roses; greenhouse	Redmond et al. 1987
Cryptococcus albidus, Aureobasidium pullulans		Cucumber and tomato plants and fruit; greenhouse	Dik and Elad 1999
Exophiala jeanselmei		Roses; greenhouse	Redmond et al. 1987
Pichia membranifaciens		Grapevine plantlets	Masih and Paul 2002
Meyerozyma (*Pichia*) *guilliermondii*		Detached strawberry leaves; plants, fruits in greenhouse	Guetsky et al. 2001, 2002a, b
Metschnikowia fructicola		Strawberry plants, fruits; greenhouse, field	Karabulut et al. 2004
Candida sake, C. pulcherrima, and *Galactomyces geotrichum*		Kiwi fruit leaf disks; conidial liberation	Cook 2002a
Candida valida, Rhodotorula glutinis, and *Trichosporon asahii*	Rhizoctonia root disease	Sugar beet; laboratory and greenhouse assay	El-Tarabily 2004
Unidentified yeasts	Apple scab	Apple seedlings; greenhouse	Burr et al. 1996

[1]*Publications are grouped here, and are discussed in the text, according to the plant disease assessed for interactions with yeasts.*

1.1. Reduction of Diseases of Aerial Plant Tissues in Field and Greenhouse Environments Using Yeast Antagonists

A broad range of plant diseases of importance in field and greenhouse environments have been studied regarding their potential for being reduced by yeast antagonists (Table 4.1). Examples include the work of Burr and coauthors (1996), who determined that two unidentified yeasts reduced scab caused by *Venturia inaequalis* by an average of 33 to 50% in 4 of 8 experiments. Wittig et al. (1997) examined the antagonistic effects of *Aureobasidium* (*Aur.*) *pullulans*, a dimorphic filamentous ascomycete, on *Monilinia fructicola* infections on forced cherry blossoms grown in a mist chamber, as well as under field conditions, and determined that this yeast-like fungus reduced brown rot blossom blight by 54, 13, and 47%, respectively, in 3 years of field trials. Application of *Aur. pullulans* to blossoms also reduced latent infections on green cherries. In field trials, *Cr. albidus* was of modest utility in reducing *Sclerotinia sclerotiorum*, the causal agent of white mold of beans (Reeleder 2004). Studies by Júnior et al. (2006) showed that the severity of late blight incited by *Phytophthora infestans* on greenhouse-grown tomato plants was reduced by sprays containing cells of *Candida* sp. and *Cryptococcus* sp.

1.1.1. Powdery Mildews

The reduction of powdery mildew using yeast antagonists has been extensively studied. The use of the basidiomycetous yeast *Pseudozyma* (*Ps.*) *flocculosa* to reduce the severity of powdery mildew diseases, especially of greenhouse crops (rose, cucumber, and tomato), has been reviewed recently (Avis and Bélanger 2002, Paulitz and Bélanger 2001). Jarvis et al. (1989) were the first to report the efficacy of *Ps. flocculosa* and *Ps. rugulosa* against cucumber powdery mildew, and subsequent studies also identified significant activity for the species against rose and wheat powdery mildews (Hajlaoui and Bélanger 1991, 1993). This potential has attracted commercial interest in the development of *Ps. flocculosa* as a biofungicide and extensive greenhouse trials have been conducted on experimental formulations of the antagonist (Bélanger et al. 2002, Paulitz and Bélanger 2001). Sporodex®, a product that contains *Ps. flocculosa* as the active ingredient, has obtained approval for greenhouse use in Canada and the United States. Subject to approval for use in Europe, it is anticipated that the product could be commercially available within 2–3 years (Jarvis et al. 2007). The mode of action of this species is associated with the production of unusual fatty acids that naturally insert into powdery mildew cells and cause disorganization of cellular membranes and cell disintegration (Avis and Bélanger 2002). Kulakovskaya and co-workers (2005) presented evidence that an additional species, *Ps. fusiformata*, produces a cellobiose glycolipid that has antifungal activity against many species of yeasts, as well as yeast-like and filamentous fungi *in vitro*. In an effort to study the development and interactions of *Ps. flocculosa* with the plant and powdery mildew *in situ*, Neveu et al. (2007) genetically transformed *Ps. flocculosa* using green fluorescent protein. Growth of transformed strain *Ps. flocculosa* Act-4 was closely and almost exclusively associated with the colonies of the pathogen regardless of the powdery mildew species or the host

plant tested. Little growth of the yeast was seen in the absence of the pathogen, which offered correlative evidence that growth of *Ps. flocculosa* is dependent on the presence of powdery mildews. Working with various species of the yeast-like fungus *Tilletiopsis*, Urquhart and Punja (2002) found that a bioactive fatty acid ester and lytic enzymes such as chitinase and exo- and endo-β-1,3-glucanase were produced by these fungi, with the highest enzyme activity found in spent broths of *Tilletiopsis albescens* and *T. pallescens*. The fatty acid ester induced hyphal and conidiophore collapse on mildewed leaves when tested against a variety of mildew pathogens on whole plants in growth chamber tests. The recently described *Meira geulakonigii* (see Chapter 149) was found to reduce growth of the powdery mildew *Sphaerotheca fusca.* Cucumber leaf coverage with powdery mildew was only 43% when treated with *M. geulakonigii* if compared with a control, and considerably increased yields of cucumber (Szteijnberg et al. 2004).

1.1.2. Scab (Head Blight) of Wheat

The use of yeasts to reduce Fusarium head blight on wheat has received considerable research attention. Fusarium head blight is a devastating disease of wheat and barley in humid and semi-humid regions of the world. Originally isolated from wheat anthers, the yeast *Cr. flavescens* reduces Fusarium head blight, incited primarily by *Gibberella zeae*. Replicated field tests in winter wheat showed 45–60% reduction in disease severity (Khan et al. 2004) and similar reductions in severity on durum wheat in replicated field trials (Schisler et al. 2002). Subsequent studies on the strain by S. Zhang et al. (2005, 2006) have demonstrated enhanced survival and disease control by freeze- or air-dried cells after management of the C:N ratio and carbon loading of liquid production media, or forcing cells to adapt to lowering the temperature during cell production. Fluorescence anisotropy and atomic force microscopy were used to demonstrate that morphological changes occurred in the membranes of cells subjected to the cold adaptation period (Dunlap et al. 2007). Kolombet et al. (2005), working with the same strain of *Cr. flavescens*, found that combining a seed treatment of *Trichoderma asperella* with treatment of flowering heads with the yeast resulted in reduction of disease severity and decreased formation of the mycotoxin deoxynivalenol in harvested seed. In an alternative approach to biological control, Luongo et al. (2005b) showed that an isolate of *Aur. pullulans* was of modest use in reducing sporulation of *Fusarium graminearum* and *F. culmorum in vitro* via competition with the pathogen for colonization of crop debris. Yeasts have also been shown to be antagonists of other aerial plant diseases of wheat. Perello et al. (2002) conducted greenhouse studies in which isolates of the yeasts *Rh. rubra* and *Cryptococcus* sp. reduced spore germination and/or disease severity incited by *Bipolaris sorokiniana*, *Drechslera tritici-repentis*, and *Septoria tritici*.

1.1.3. Fire Blight

Fire blight is a major concern in the production of pome fruit worldwide. The disease is most often associated with epiphytic populations of *Erwinia amylovora* that develop in blossoms. Pusey (1999) noted that yeasts were more osmotolerant than bacterial strains isolated from flowers, when growth rates were tested on an artificial nectar medium containing 25% sugar, and therefore might outcompete bacterial pathogens. Seibold et al. (2004) determined that two strains of *Aur. pullulans* suppressed growth of *Erwinia amylovora* to a greater extent than other yeasts and yeast-like species when grown on an artificial nectar medium. In two field trials, the strains showed efficiencies 0–20% below Plantomycin (streptomycin). BlossomProtect is a product with a strain of *Aur. pullulans* as the active ingredient which, according to the website of Bio-Protect GmbH, the German company that sells the product, is commercially available for use against fire blight in Germany, Austria, and Switzerland. Kunz (2006) reported that the commercial product was successful in reducing fire blight severity by an average of 72% in field trials that were conducted over several years.

1.1.4. Gray Mold

The term "gray mold" is commonly used to refer to the sign of disease typical of plants infected with the fungal pathogen *Botrytis* (*B.*) *cinerea*. The majority of literature on the preharvest application of yeasts to reduce disease specifically deals with controlling gray mold on a variety of crops. Elmer and Regliniski (2006) reviewed the literature on biologically controlling *B. cinerea* in grapes, using a variety of biological agents including yeasts. Several of the studies dealt with applications of yeasts, or with bioassays conducted to simulate yeast and pathogen interactions on plant material taken from field or greenhouse environments. For instance, Masih et al. (2000, 2001) and Masih and Paul (2002) found that *Wickerhamomyces* (*Pichia*) *anomalus* and *Pichia membranifaciens* were antagonistic to *B. cinerea* when the yeasts and pathogen were cultured together on solid or liquid media. *P. membranifaciens* incited cytoplasmic leakage in hyphae of the pathogen which apparently resulted in reduction of disease on grapevine plantlets *in vitro*. The authors cited the secretion of β-1,3-glucanases by *P. membranifaciens* as one possible mechanism related to this antagonism (Masih and Paul 2002).

Several studies concentrated on the influence of yeasts on gray mold development on geraniums, in leaf or whole plant bioassays. *Rhodosporidium* (*Rhodosp.*) *toruloides* reduced lesion development after 96 hours on geranium leaf discs, and inhibited conidial development when co-inoculated at 1×10^6 or 1×10^7 cells/ml with *B. cinerea* conidia at 1×10^4 or 1×10^5 (Buck 2002). The author postulated that, under conditions of low nutrient availability and high antagonist to pathogen ratios, many phylloplane-inhabiting yeasts would antagonize *B. cinerea* colonization. When tested against 29 isolates of *B. cinerea* from greenhouse-grown ornamentals, *Rh. glutinis* reduced lesion development on leaf discs by 16 isolates of *B. cinerea* that varied considerably in aggressiveness on geranium leaf disc and seedling bioassays (Buck and Jeffers 2004). Low rates of the fungicide Vinclozolin reduced lesion development on seedlings, or improved biocontrol consistency compared to the yeast alone, versus fungicide sensitive or resistant isolates of *B. cinerea*, respectively. In addition to gray mold on geranium, the biological control of the disease on roses using yeasts has been studied by Redmond et al. (1987), who identified strains of *Exophiala jeanselmei* and *Cr. albidus* that reduced lesions on greenhouse grown roses by as much as 63%, a level of control statistically equivalent to the fungicide iprodione (74%).

In a study of disease on strawberry leaves and plants, Guetsky et al. (2002a) used scanning electron microscopy to reveal that significant inhibition of *B. cinerea* conidial germination was incited by the presence of *Meyerozyma* (*Pichia*) *guilliermondii. Mey. guilliermondii* competed with *B. cinerea* for glucose, sucrose, adenine, histidine, and folic acid, and also secreted a non-volatile inhibitory compound. The yeast reduced the number of diseased fruits by as much as 50% in greenhouse experiments that emulated commercial conditions (Guetsky et al. 2002b), and demonstrated improved consistency of control when combined with a bacterial antagonist on detached strawberry leaves (Guetsky et al. 2001). There is some concern over the use of *Mey. guilliermondii* and its anamorph *C. guilliermondii* for biocontrol because the species is an occasional clinical isolate (see Chapter 47, *Meyerozyma*). Karabulut et al. (2004) found the yeast *Metschnikowia* (*Metsch.*) *fructicola* to be as effective as the chemical fenhexamid in reducing gray mold of strawberries in two growing

seasons, and reduced rot incidence by more than 50% in greenhouses, open field culture, and in low plastic tunnels.

The concept of yeasts as biocontrol agents against gray mold on tomatoes, cucumbers, and beans, primarily in greenhouse growth environments, has also been considered. In 1994, Elad et al. reported that *Rhodosp. toruloides* and *Cr. albidus* reduced sporulation and severity of gray mold disease on beans and tomatoes. Yeasts reduced pod infection of beans by more than 75% compared to controls. Dik and Elad (1999) demonstrated that *Aur. pullulans* was the most consistent of the agents they tested, in reducing stem lesions and death of plants caused by *B. cinerea* in greenhouse grown cucumber and tomato. High temperature and vapor pressure deficit during the night reduced biocontrol efficacy (Dik et al. 1999). *Aur. pullulans* was the most successful of four yeasts and yeast-like species tested on tomato and cucumber stem segments against *B. cinerea*. The species reduced disease by more than 75% in all four experiments reported. Kalogiannis et al. (2006) used detached leaf assays to select yeasts isolated from greenhouse grown tomatoes and then tested selected yeasts on whole tomato plants. The authors concluded that their isolate Y-44, identified as *Rh. glutinis,* was a successful colonist of the plant surface and was as effective as two commercial fungicides in reducing gray mold. In an extended series of investigations, Utkhede and others (2001, 2004) studied the potential of *Rhodosp. diobovatum* to act against gray mold on tomatoes and gummy stem blight (causal agent, *Didymella bryoniae*) on cucumber plants. While the yeast was only occasionally effective in reducing gummy stem blight on hydroponically grown cucumbers (Utkhede and Koch 2004), on tomatoes in greenhouse trials it reduced lesion size and number of dead plants and increased total fruit number and yield when compared to controls with gray rot (Utkhede et al. 2001, Utkhede and Mathur 2002). The yeast also compared favorably with a variety of biological treatments including Plant Shield®, Prestop®, Quadra 136, RootShield® and a chemical treatment applied as preventative or curative sprays on greenhouse tomatoes grown in sawdust beds using near-commercial conditions (Utkhede and Mathur 2006). Saligkarias et al. (2002a, b) demonstrated that strains of *C. guilliermondii* (strains 101 and US 7) and *C. oleophila* (strain I-182) were effective in reducing gray mold on tomato seedlings, even though antagonism *in vitro* was not apparent in the case of *C. oleophila*. Nutrient amendments reduced the level of biocontrol in a stem bioassay suggesting that nutrient competition might partially explain the antagonism observed. *In vitro*, the yeasts secreted detectable amounts of β-1,3-exoglucanase and chitinase and were shown to adhere to the *B. cinerea* hyphae, while an inactive control strain did not adhere to hyphae of the pathogen.

1.2. Reduction of Postharvest Decays by Field Application of Yeast Antagonists

Preharvest application of yeast antagonists may be desirable when latent infections occur in the field, or postharvest treatment is undesirable. However, application of some microorganisms in the orchard during the growing season may have adverse effect on fruit quality, as in the case of *Rh. glutinis,* which caused extensive russet on "McIntosh" apple (Matteson-Heidenreich 1997). Preharvest application exposes yeasts to additional stresses of low nutrient availability on undamaged fruit surface, together with UV radiation, high temperature, and dry conditions, which can reduce the biocontrol efficacy of the yeast.

The reduction of gray mold and other postharvest decays of fruit has been the primary target of researchers that evaluated the feasibility of reducing disease via application of yeast antagonists prior to the harvest of a crop (Leibinger et al. 1997; Table 4.2). Strains of *Aur. pullulans* and *Rh. glutinis* were among antagonists applied to apple trees in the field late in the growing season (Leibinger et al. 1997). The yeasts reduced the size and number of lesions on wounded apples caused by the postharvest pathogens *Penicillium* (*Pen.*) *expansum*, *B. cinerea*, and *Pezicula malicorticis*. Population sizes of introduced antagonists on apple surfaces increased in the field and remained higher than controls after transfer of the fruit from the field into cold storage. A combination of two strains of *Aur. pullulans* and one strain of *Rh. glutinis* suppressed decay of the apples to the same extent as the commonly used fungicide Euparen. Working with preharvest applications of yeast on apples to control blue mold, Teixidó et al. (1998a) compared cells that were tolerant to low water activities (low δ_w-tolerant) and unmodified cells of *C. sake* CPA-1 for ability to control blue mold of apples caused by *Pen. expansum,* under commercial storage conditions. In the field, the population size of the unmodified treatment remained relatively unchanged, while the population size of the low δ_w-tolerant CPA-1 cells increased. When the harvested fruit was inoculated with the pathogen and placed in cold storage for 4 months, all yeast treatments reduced incidence and severity of decay by approximately 50−60%. In a subsequent study with unmodified cells of *C. sake*, Teixidó et al. (1999) found that preharvest application of the antagonistic yeast was less effective against *Penicillium* rot than postharvest treatment. No advantages in biocontrol were observed when apples received both a pre- and postharvest treatment.

Several different yeasts, which included *Cystofilobasidium* (*Cyst). infirmominiatum*, *Cr. laurentii*, and *Rh. glutinis*, maintained high populations on Bosc and d'Anjou pear fruit when applied in the field 3 weeks prior to harvest. *Cyst. infirmominiatum* provided the most consistent decay control in fruit treated 3 weeks before harvest (Benbow and Sugar 1999). *Cyst. infirmominiatum* and *Rh. glutinis* also provided significant postharvest decay control in Bosc fruit treated 1 day before harvest. Decay due to gray and blue mold and side rot decay were evaluated. However, in a later study that included 3 years of field data, *Cyst. infirmominiatum* was not shown to be effective in controlling postharvest decay of pear when the yeast was applied 1 week before harvest, despite maintaining high populations on fruit surfaces until treatment evaluation (Sugar et al. 2003).

Sweet cherries have also been studied to determine whether preharvest applications of antagonistic yeasts would reduce postharvest rot. Ippolito and coworkers (2005) applied *Aur. pullulans* strain L47 to sweet cherries 1 week prior to harvest and reduced the number of fruit infected by a variety of pathogens by about 50% after a regime of 15 days' cold storage followed by 7 days' storage at 20°C. Using isolates of *Tr. pullulans*, *Cr. laurentii* and *Rh. glutinis*, Tian et al. (2004) also applied yeasts to sweet cherry fruit in orchards prior to harvest, in an effort to reduce rot caused by the postharvest pathogens *Alternaria alternata*, *Monilinia fructicola*, *Pen. expansum*, and *B. cinerea*. Though all three yeasts colonized the surface of sweet cherry fruit, only *Cr. laurentii* and *Rh. glutinis* maintained populations at high and stable levels throughout the 4-day experiment period. *Cr. laurentii* was the most effective antagonist. It reduced incidence for all three storage temperatures tested for fruit harvested from two field treatment sites, though the extent of reduction varied widely depending on the level of disease incidence in the controls.

Helbig (2002), worked with *Cr. albidus*, a species shown to be effective against *B. cinerea* on beans and tomatoes (Elad et al. 1994), and determined that treatments with *Cr. albidus* during bloom of strawberries reduced the incidence of gray mold on ripe strawberry fruits after harvest by 33, 28 and 21% in 3 years of field trials. The effectiveness of the yeast was increased when formulation substances such as alginate, xanthan and cellulose were present.

Patiño-Vera and coworkers (2005) developed pilot-scale production methodologies for the yeast *Rh. minuta* and demonstrated that the application of freshly produced cells on mangos in orchards resulted, in two out of three tests, in less postharvest anthracnose

TABLE 4.2 Examples of Yeast Antagonists Applied Preharvest to Reduce Postharvest Pathogens

Yeast/Yeast-like Fungus	Disease	Assessment Utilized	Reference[1]
Aureobasidium pullulans	Various postharvest rots	Cherry fruit	Ippolito et al. 2005
Aureobasidium pullulans and *Rhodotorula glutinis*	Gray mold, blue mold, bull's eye rot	Apple fruit	Leibinger et al. 1997
Candida sake	Blue mold	Apple fruit	Teixidó et al. 1998, 1999
Cryptococcus albidus	Gray mold	Strawberry fruit	Helbig 2002
Cystofilobasidium infirmominatum, Cryptococcus laurentii, and *Rhodotorula glutinis*	Blue and gray mold, side rot	Pear fruit	Benbow and Sugar 1999, Sugar et al. 2003
Cryptococcus laurentii	Various postharvest rots	Cherry fruit	Tian et al. 2004
Metschnikowia fructicola	Gray mold, other postharvest rots	Table grape fruit	Karabulut et al. 2003
Rhodotorula minuta	Anthracnose	Mango fruit	Patiño-Vera et al. 2005

[1]*Publications are grouped here, and are discussed in the text, primarily according to the type of fruit affected with plant disease and the yeasts used in biological control studies.*

severity than found for the control, or for the treatment with the chemical benomyl. There was no treatment effect in the third test, where the level of anthracnose control was equal to or lower than that observed with a chemical fungicide.

Karabulut and coworkers (2003) applied the yeast *Metsch. fructicola*, ethanol, and sodium bicarbonate (SBC), alone or in combinations, to table grapes on vines 24 hours before harvest to control the incidence of postharvest diseases incited by *B. cinerea*, *Alternaria* spp., or *Aspergillus niger* after storage for 30 days at 1°C followed by 2 days at 20°C. All treatments reduced disease incidence by approximately 60% or more, though combination treatments did not improve the level of disease reduction. *Metsch. fructicola* populations persisted on berries during storage, when applied alone or after ethanol treatments, whereas SBC reduced its population significantly.

1.3. Reduction of Postharvest Diseases by Application of Yeasts to Harvested Plant Commodities

Following the initial work with biological control of blue mold on apple (Janisiewicz 1987), considerable effort was placed on the use of yeasts for control of postharvest decays of citrus fruit, mainly blue mold caused by *Pen. italicum* and gray mold caused by *Pen. digitatum* (Chalutz and Wilson 1990, Chalutz et al. 1998, McGuire 1994, Wilson and Chalutz 1989). This resulted in commercialization of the antagonistic yeast *C. oleophila* under the trade name Aspire (Ecogen, Inc., Langhore, PA) (Droby et al. 1993, 1998). More recently, two additional commercial products have appeared on the market, YieldPlus (Anchor Yeast, Cape Town), based on *Cr. albidus* (De Koch 1998) in South Africa, and Shemer (AgroGreen, Asgdod) based on *Metsch. fructicola* (Kurtzman and Droby 2001, Karabulut et al. 2002, 2003) in Israel, both registered in their respective countries for control of postharvest decays on several fruits including grapes, pome, stone, and citrus fruit. Some of the yeasts isolated from fruit, such as *Cr. laurentii* or *Sp. roseus,* had been shown to have strong biocontrol activity against pathogenic fungi in the phyllosphere (Fokkema and Van der Meulen 1976). Not surprisingly, *Cr. laurentii* reduced postharvest decays on many fruits, including blue mold (*Pen. expansum*) and gray mold (*B. cinerea*) of apple (Lima et al. 1998, Roberts 1990, Sugar 1999), gray mold of pear, strawberries, kiwifruit and table grapes (Chand-Goyal and Spotts 1997, Lima et al. 1998, H. Zhang et al. 2005), *Rhizopus* rot of strawberries and peach (Zhang et al. 2004, 2007), and *Pen. expansum* decay on jujube fruit (Qin and Tian 2004). Also, *Sp. roseus* reduced blue mold decay of apple (Janisiewicz et al. 1994).

Significant advances in biological control of postharvest diseases (BCPD) with yeasts have also been made with *C. sake* on pome and citrus fruits (Abadias et al. 2001a, b, c, Nunes et al. 2002a, b, Teixido et al. 1999, Usall et al. 2000), *C. saitoana* on citrus and pome fruits (El Ghaouth et al. 2000a, 2001a, b, 2003), *Metsch. pulcherrima* on pome fruits and grapes (De Curtis et al. 1996, Janisiewicz et al. 2001, Nigro 1999, Piano 1997, Sapardo et al. 2002), *Wick. anomalus* on pome fruits (Friel et al. 2007, Gravesse 1998, 2003, Jijakli et al. 1993, Jijakli and Lepoivre 1998), *Rh. glutinis* on various fruit (Clavente et al. 1999, Lima et al. 1998, Sansone 2005), *Cyst. infirmominiatum* on pome fruits (Chand-Goyal and Spotts 1996a, 1997, Sugar et al. 2003), *Mey. guilliermondii* on citrus and strawberries (Arras et al. 1998, Chalutz 1991, Droby et al. 1993, 1997, Wszelaki and Micham 2003), and *P. membranifaciens* on apple, stone fruits, and grapevine (Chan and Tian 2005, Fan and Tian 2000, Santos and Marquina 2004). In almost all of these systems, a quantitative relationship exists between concentrations of yeast cells, pathogen conidia, and resulting biocontrol. As the concentration of the pathogen propagules increases, the concentration of the antagonistic yeast must also be increased to maintain the original level of decay control (Janisiewicz 1987). This underscores the importance of maintaining good sanitation in packing houses to reduce the inoculum level in the treatment suspension. The yeasts can be applied to fruit after harvest in various ways, including drenching entire bins of fruit before placing them in storage, sprays or dips on packing lines, and they can also be applied in waxes. As indicated earlier, preharvest applications have not been studied extensively, however, they are generally less effective (see review by Ippolito and Nigro 2000).

Although most of the biocontrol work with yeasts has been done on harvested fruits, this approach has also been successful in other postharvest systems. For example, spoilage of wheat, rye, barley, and oats caused by *Pen. roqueforti* during airtight storage was effectively controlled by the application of *Wick. anomalus* (Druvefors et al. 2005, Passoth et al. 2006, Petersson and Schnurer 1998). Several strains of *Cr. laurentii* were modestly effective in reducing *Fusarium* dry rot incited on stored potato tubers by *Fusarium sambucinum* and *Fusarium solani* var. *coeruleum* (Schisler et al. 1995).

1.4. Yeasts in Integrated Control

Aspire, the first yeast biocontrol product on the market, alone could not provide control equivalent to fungicide treatment, but in combination with low doses of fungicides it provided adequate control (Brown and Chambers 1996, Droby et al. 1998). Because yeast application alone could not, in general, provide commercially acceptable protection

against various fruit decays, major efforts in biocontrol of postharvest diseases (BCPD) with yeasts have been devoted to combining yeast treatment with other, generally less effective treatments, or with nutrients that preferentially stimulate yeast populations in order to improve decay control. These combinations often resulted in an additive or even synergistic effect. The combination of yeasts with nutrients (Nunes et al. 2001), nutrient analogs (El-Ghaouth et al. 2000c, 2001a), low doses of fungicides (Chand-Goyal and Spotts 1996a, b, Qin and Tian 2004), various salts (Droby et al. 1997, McLaughlin et al. 1990, Wisniewski et al. 1995), and substances generally regarded as safe (GRAS) (El-Ghaouth et al. 2000a, b, Mari and Carati 1998, Nunes et al. 2002b, Porat et al. 2002, Qin et al. 2006, Wan et al. 2003, Wan and Tian 2005) improved control of the fruit decays to the level obtained with synthetic fungicides. Physical treatments such as UV irradiation (Wilson et al. 1994), microwave irradiation (Zhang et al. 2004) and hot air (4 days at 38°C) (Leverentz et al. 2000), or hot-water treatment (Porat et al. 2002, Zhang et al. 2007) combined with various antagonistic yeast treatments also improved control of fruit decays. Methyl jasmonate treatment, which can induce resistance in fruit against necrotrophic pathogens, combined with *Cr. laurentii* improved the control of postharvest decays of peach caused by *Monilinia fructicola* and *Pen. expansum* (Yao and Tian 2005). Growth regulators such as giberellic acid and indole-3-acetic acid (IAA) improved biocontrol of blue mold by *Cr. laurentii* on pears (Yu et al. 2006, Yu and Zheng 2007). Both growth regulators increased peroxidase and phenol oxidase activities, which indicated that stimulation of resistance in pear fruit may have been responsible for reduction in fruit decay. The combination of *C. saitoana* with lytic enzymes or chitosan salts improved control of postharvest decays on pome and citrus fruits (El Ghaouth et al. 2001b). A mixture of two yeasts, *Metsch. pulcherrima* and *Cr. laurentii* (Conway et al. 2007), or *Rh. glutinis* and *Cr. albidus* (Calvo et al. 2003), was much more effective than the individually applied yeasts in controlling blue mold, and blue and gray mold decay on apples, respectively. A mixture of *Metsch. pulcherrima* and *Cr. Laurentii*, in combination with sodium bicarbonate and controlled atmosphere storage, provided excellent control in laboratory and commercial scale tests (Conway et al. 2007, W. Janisiewicz, unpublished data). *Cyst. infirmominiatum* combined with *Cr. laurentii* was as effective as fungicide (TBZ) treatment in controlling the incidence of postharvest pear diseases (Chand-Goyal and Spotts 1997). Superior biocontrol of pome fruit decays was also achieved by combining yeasts with bacterial antagonists, e.g., *Sp. roseus* with *Pseudomonas syringae* (Janisiewicz and Bors 1995) and *C. sake* with *Pantoea agglomerans* (Nunes et al. 2002a). These examples indicate that yeasts are amenable to manipulation, and can provide the foundation for integrated control with various, partially effective treatments which can result in commercially acceptable control.

1.5. Mechanisms of Biocontrol

A variety of biocontrol mechanisms have been suggested for antagonistic yeasts effective in BCPD of fruits. Manipulation of the mechanism of biocontrol could improve the biocontrol potential of a yeast, but a complete explanation of the mechanisms involved has been elusive. This is because most antagonists probably operate by utilizing more than one mechanism, and the significance of each mechanism may change with changing conditions. Efficient colonization of fruit wounds is a prerequisite for any yeast biocontrol agent, and this in itself may reduce fruit decay by various degrees. In fact, site exclusion and simple competition for limiting nutrients are most frequently proposed putative mechanisms of biocontrol by yeasts in the fruit system (see Janisiewicz and Korsten 2002). Fruit wounds are a rich source of easily available carbon, and provide an excellent substrate for a variety of yeasts. High carbon content makes it less likely to be a limiting nutrient in most fruit systems, but other nutrients, including nitrogen and microelements, may be in short supply and therefore potential targets for nutrient competition. For example, depletion of iron has been shown to be the main mechanism of biocontrol by *Rh. glutinis* and *Metschnikowia* strains (Calvente et al. 1999, Sipiczki 2006). The addition to *Rh. glutinis* of rhodotorulic acid, a siderophore produced by yeasts belonging to *Rhodotorula* species, significantly improved control of gray mold on apple after harvest (Sansone et al. 2005). Inferences about competition for nutrients are often made where there is a lack of evidence of production of inhibitory substances, and the addition of an excess of nutrients to the wounds diminishes biocontrol effect (Castoria et al. 1997, Droby et al. 1989, Lima et al. 1997, Vero et al. 2002). Such inferences are also made in cases where an elucidated mechanism accounts only for a portion of the biocontrol (Droby et al. 1989, Wisniewski et al. 1991).

Production of lytic enzymes also has been implicated in various systems. This is because culture filtrates or the purified enzymes, such as β-1,3-glucanase and chitinase, produced by antagonists *C. oleophila* (Bar-Shimon et al. 2004), *C. guilliermondii* (Saligkarias et al. 2002), *Wick. anomalus* K (Grevesse et al. 1998, 2003, Jijakli and Lepoivre 1998), and *P. membranifaciens* (Fan et al. 2002), lysed conidia, germlings and hyphae of major postharvest pathogens of citrus, stone, and pome fruits, including *Pen. digitatum*, *Pen. expansum*, *B. cinerea*, and *Rhizopus stolonifer*. The best evidence has been presented by Jijakli's group (Friel et al. 2007) who used separate and combined disruption of two exo-β-1,3-glucanase-encoding genes *PAEXG1* and *PAEXC2* in *Wick. anomalus*. They demonstrated that control of gray mold of apple declined from 73% on fruit protected with the wild type, to as low as 8% on fruit protected with the mutant strains. The remaining portion of the control has been attributed to other potential mechanisms, including competition.

Killer toxins may play a significant role in biocontrol by some yeasts, but little work has been done on fruit and inferences must be made from related research. For example, killer toxins produced by *P. membranifaciens* CYC 1106 were active against *B. cinerea* and reduced the spread of the disease on grapevine (Santos and Marquina 2004). The optimum activity of the killer toxin *in vitro* was at pH 4, which is in the pH range of many fruits (see Chapter 6, Ecology, for other examples of killer yeasts).

Yeasts may also induce resistance to postharvest pathogens in fruit (De Capdeville et al. 2002, Forbes-Smith 1999, Wilson et al. 1994) but the role of this resistance in reducing postharvest decays is unclear, as the induction depends on fruit maturity, is transient, and occurs at a relatively slow rate, which may not be rapid enough to prevent establishment of the pathogen. For example, ethylene and PAL activity, as well as concentrations of the phytoalexins umbelliferone, scoparone, and scopoletin, increased in grapefruit peel tissue 24 hours after treatment with *C. oleophila* (Droby et al. 2002). Chitinase and β-1,3-glucanase concentration also increased after 24 and 48 hours, respectively. These increases correlated with increased resistance of grapefruit to green-mold decay. An application of the antagonist *Cr. laurentii* to jujube fruit increased expression of the *Glu-1* gene, which is responsible for the production of β-1,3-glucanase and the activity of this enzyme (Tian et al. 2007). These activities and the biocontrol of fruit decay increased as the concentration of the antagonist increased. Resistance of *Cr. laurentii* to reactive oxygen species (ROS) appearing after the oxidative burst which followed fruit wounding and yeast application was important for antagonistic activity against *B. cinerea* and *Pen. expansum* on apple. It may be an important mechanism in the fruit system generally (Castoria et al. 2003). A proteome approach to characterize proteins induced by the antagonist *P. membranifaciens* in peach fruit suggests that antioxidant and PR proteins, as well as enzymes associated with sugar metabolism, were involved in the induction of resistance to blue mold decay caused by *Pen. expansum* (Chan et al. 2007).

The ability of cells of a yeast antagonist to attach to surfaces of susceptible tissues of the host plant, or to the pathogen itself, will influence the strain's potential to colonize the surface successfully and impact the success of the biocontrol agent. This phenomenon was investigated by Buck and Andrews (1999) using the basidiomycetous yeast *Rhodosp. toruloides*, a common phylloplane epiphyte with biocontrol potential. Adhesion of wild-type *Rhodosp. toruloides* was transient and nonadhesive cells were observed to subsequently become adhesive with bud development. From studies using diverse approaches such as haptan competition assays, selective staining, lectin, enzyme, antibiotics, or chemical treatments, the authors concluded that compounds which are localized at sites of bud development (such as mannose residues) mediate adhesion of *Rhodosp. toruloides* to both polystyrene and barley leaf surfaces. Allen et al. (2004a) found that culture medium, but not culture age, significantly affected attachment of yeast cells to conidia of *B. cinerea in vitro,* with more effective attachment exhibited by cells grown in a liquid culture medium. Attachment may also, at least partially, explain the suppression of the production of conidia from mycelium of *B. cinerea* on kiwi fruit leaves after application of dried alpha-cellulose formulations of yeast isolates *C. sake*, *C. pulcherrima*, *Guehomyces (Gueh.) pullulans*, and *Galactomyces geotrichum* (Cook 2002a). In a separate study, Cook (2002b) found that *Gueh. pullulans* was capable of binding to *B. cinerea* conidia and was vectored with conidia harvested from a *B. cinerea* lesion. Both studies implied that yeasts could be applied effectively during advanced phases of epidemic development to potentially arrest or slow further epidemic development. Coculture of *Mey. guilliermondii* with *B. cinerea* resulted in the attachment of the yeast to the mycelium of the pathogen, erosion of the hyphal cell wall, and pitting of the hyphae (Wisniewski et al. 1991). The yeast produced β-1,3-glucanase that was greatly enhanced by growth on hyphal cell walls of *B. cinerea* and various other fruit-decaying fungi. Pretreatment of the pathogen with protease, trypsin, 0.1 N NaOH and 0.1 N HCl, or the yeast with trypsin or 0.1 N HCl greatly reduced this attachment, suggesting that lectins or other agglutinins may be involved. For *P. membranifaciens*, tenacious attachment to the pathogens *Monilinia fructicola*, *Pen. expansum*, and *Rhizopus stolonifer,* and the secretion of high amounts of lytic enzymes appear to be important in the biocontrol activity exhibited by this yeast (Chan and Tian 2005). However, the final determination of the significance of these attachments in biocontrol awaits experiments with attachment deficient mutants.

Yeasts may also interfere with pathogenicity factors. The antagonists *Cr. laurentii* and *Sp. roseus*, effective against gray mold of apple, utilized the apple volatile butyl acetate, which stimulated germination and adhesion to membranes of *B. cinerea* conidia (Filonow 1999, 2001). The exposure of apples inoculated with *B. cinerea* and *Sp. roseus* to an excess of butyl acetate significantly reduced, but did not totally eliminate, biocontrol by *Sp. roseus.* Thus, removal of butyl acetate can explain only part of the biocontrol mechanism(s).

1.6. Preserving Yeast Viability

Resistance of antagonistic yeasts to environmental stresses, whether physical or chemical, is essential for survival on the fruit, consistent biocontrol performance, enduring the process of formulation, and a long shelf life of the formulated yeasts. Inadequate resistance to various stresses may be responsible for declining yeast populations in formulations, which then results in reduced protection, or variable performance under fluctuating environmental conditions. The most important factors appear to be resistance to desiccation, growth at low temperature, and tolerance to chemicals used after harvest. Recent research has demonstrated that it is possible to select natural strains of antagonistic yeasts which have resistance to these stresses, and to manipulate them to further increase their stress tolerance. Great variability among *Metsch. pulcherrima* strains isolated from a single orchard allowed for the selection of antagonistic strains that grew well at 0°C and tolerated diphenylamine (DPA), a chemical used for preventing superficial scald of apple, a physiological disorder (Janisiewicz et al. 2001). The growth of *C. sake* in a medium with reduced water activity improved survival of the yeast at low relative humidity, and maintained biocontrol activity against *Pen. expansum* on apples (Teixidó et al. 1998a, b). The manipulation of growth conditions in cheap growth medium using molasses resulted in the production of water-stress-tolerant cells of *C. sake* (Abadias et al. 2001c). The use of appropriate rehydration media further improved survival and preserved the biocontrol potential of the yeasts (Abadias et al. 2001a, b). Also, growth of *Cr. laurentii* on media enriched with trehalose increased viability of this yeast after freeze-drying (Li and Tian 2006). The survival was further improved and the biocontrol potential of the yeast was maintained when the yeast cells were combined with skim milk and various sugars (Li and Tian 2007). S. Zhang et al. (2005, 2006) demonstrated enhanced survival and disease control by freeze- or air-dried cells after management of the C:N ratio and carbon loading of liquid production media for the yeast antagonist *Cr. flavescens*. Forcing cells of *Cr. flavescens* to adapt to a cold temperature change during cell production improved cell osmotolerance and altered the structure of the cell membrane (Dunlap et al. 2007). The survival of *Wick. anomalus* in a liquid formulation was significantly improved by the addition of trehalose and lactose, but trehalose was the most effective protectant at higher temperatures, such as 20°C and 30°C (Melin et al. 2006). The application of a liquid formulation of the antagonist *Rh. minuta* to mango trees controlled anthracnose caused by *Colletotrichum gloeosporioides* (Patino-Vera et al. 2005). Interestingly, survival of the yeast in a formulation containing 20% glycerol, alone or in combination with xanthan (5g/l), was higher when the initial concentration of the yeast was 10^9 rather than 10^{10} CFU/ml. This most likely resulted from greater accumulation of toxic compounds in formulations with a higher concentration of the yeast. The application of yeasts in orchards for the control of postharvest diseases presents additional challenges for improving the survival of the yeast in an environment that is harsher and more fluctuating than that encountered in storage.

1.7. Conclusions for Use of Yeasts in Biological Control

Advances in using yeasts for BCPD and the presence of yeast-based biocontrol products in the marketplace demonstrate the commercial feasibility of this approach to plant disease control. Variability in biocontrol can be at least partially overcome by combining yeasts with other alternative methods, stimulating the yeast antagonist with nutrients, using mixtures of different yeasts, manipulating mechanisms of biocontrol, optimizing fermentation production environments to produce effective and stress-tolerant yeast biomass, manipulating yeast physiology to increase tolerance to stresses, and by developing formulations that allow for rapid acclimatization and metabolic recovery of the yeast after application. It is also possible to improve biocontrol by genetically modifying yeast antagonists to increase the expression of genes responsible for biocontrol traits, or to use yeasts as a delivery system for foreign genes responsible for production of antifungal substances (Janisiewicz et al. 2008, Jones and Prusky 2002). In summary, the great versatility of yeasts makes them excellent candidates for utilization in the biological control of plant diseases. As the elucidation of whole genome sequences of biocontrol agents becomes more prevalent (Loper et al. 2007), along with powerful tools, such as bioinformatics analysis and whole

genome microarrays, for tracking the expression of groups of genes, further advances in the development of effective plant disease biocontrol products with yeasts as active ingredients appear to be assured.

2. INTRODUCTION TO YEAST PATHOGENS OF PLANTS

In the preceding sections, the importance of yeasts for biological control of pre- and postharvest diseases of crop plants was demonstrated. Other agriculturally important yeasts are those species which cause plant diseases. While few in number relative to other major groups of plant pathogenic fungi, yeasts occasionally cause significant losses to certain crops. Plant pathogenic yeasts are found among both the ascomycetes and the basidiomycetes, and examples from each of these groups are presented.

2.1. Ascomycetes

Taphrina and *Protomyces*, both members of the Taphrinomycotina, are perhaps the best known of yeast-like taxa that cause plant diseases. *T. deformans*, the cause of peach leaf curl, is worldwide in distribution and the most economically devastating of the diseases caused by species of *Taphrina* (Fonseca and Rodrigues, Chapter 73, Mix 1949). Young leaves, stems, and fruit are often severely distorted when infected by *T. deformans*. Early application of fungicides often controls peach leaf curl (Daughtrey et al. 2003), but failure to do so can result in significant crop losses. Other tree crops, such as almonds and pears, may also be severely affected by *Taphrina* infections. Trees, such as alders and poplars, are also susceptible to various *Taphrina* species (Fonseca and Rodrigues, Chapter 73, Mix 1949). The effect of these infections on tree health is generally limited, but the appearance of infected leaves and flowers can be distressing when these tree species are used in ornamental plantings.

Species of *Protomyces* cause symptoms similar to those seen from *Taphrina* infections. All known *Protomyces* species are plant parasitic and cause galls on stems, leaves and fruits of Compositiae, Umbelliferae, and certain other plants (Tubaki 1957). Economic losses are seldom great, but *P. macrosporus* infection of coriander (*Coriandrum sativum*) was reported to have damaged up to 11% of the crop during one growing season (Tripathi et al. 2003). *Protomyces* has also been examined as a plant biocontrol agent. Cartwright and Templeton (1988) tested *P. gravidus* as a mycoherbicide for control of giant ragweed (*Ambrosia trifida*), a major weed plant in some areas. Biocontrol of giant ragweed was only moderately successful in this test.

Several genera of the Saccharomycotina are the cause of sometimes severe plant diseases. Most notable are species of *Eremothecium*, some of which were previously classified in the genera *Ashbya*, *Nematospora*, and *Holleya*, but all of which are plant pathogens. *E. ashbyi* has a long history of causing cotton boll rot in various species of *Gossypium*, and cankers on citrus fruit (Batra 1973). Similarly, *E. gossypii* causes staining and rot of cotton bolls, as well as being pathogenic to coffee (*Coffea* spp.), soybean (*Glycine max*), and other crops. *E. coryli* also infects cotton, and it is also a pathogen of hazelnuts, tomatoes, and beans. Symptoms are generally disfigurement and disruption of the infected plant tissue. *E. sinecaudum* was discovered relatively recently (Holley et al. 1984), when it was found to be the cause of a major outbreak of seed infection in oriental and yellow mustard in Saskatchewan, Canada. The remaining known species of *Eremothecium*, *E. cymbalariae*, appears uncommon, but has been isolated as a pathogen of flax and other plants (Arnaud 1913).

Galactomyces candidus (anamorph *Geotrichum candidum*) and *G. citri-aurantii* (anamorph *Geotrichum citri-aurantii*) commonly cause sour rot of citrus, tomatoes, cantaloupes, peaches, lychee, and carrots (Butler et al. 1965, 1988, Morris 1985, Wells 1977, Wild 1992). Losses are sufficient to require treatment of the produce by a fungicide. Wild (1992) reported tests on the efficacy of guazatine for fungicidal control of these rots.

2.2. Basidiomycetes

Dikaryotic strains of *Itersonilia perplexans* (Cystofilobasidiales, Tremellomycetes, Agaricomycotina) are reported to be pathogenic to parsnip (*Pastinaca sativa*) and chrysanthemum (*Chrysanthemum* spp.) (Boekhout 1991b, Boekhout et al. 1991b, Channon 1956, 1963, Gandy 1966). Petal blight of the cut flower China aster (*Callistephus chinensis*) caused by *I. perplexans* was observed in 1997–1998 in southwest Florida. Interestingly, petal blight of chrysanthemum caused by *I. perplexans* in the early 1970s happened to occur in the same production plant as the disease on Chinese aster in the 1990s (McRitchie et al. 1973, McGovern and Seijo 1999). These latter authors noted that in both periods of disease the weather was unusually cold and wet, and they made a link to El Niño climate activity. In Hokkaido, Japan, *I. perplexans* was reported to be involved in black streak disease of edible burdock (*Arctium lappa*) since 1988 (Horita and Yasuoka 2002).

Among the Ustilaginomycetes, *Tilletiopsis minor* and *T. pallescens* have been isolated from apples which show a postharvest disorder named white haze. Most likely *T. pallescens* is one of the major causative species involved in this disorder (Boekhout et al. 2005). Species of *Pseudozyma* represent the monokaryotic and haploid state of Ustilaginales (Begerow et al. 2000, Boekhout 1987, 1995), but pathogenicity to plants has not been demonstrated for these states. However, it cannot be ruled out that after mating the resulting dikaryotic state may be pathogenic for specific plants.

Russetting of apples is found to be effected by population densities of species occurring in the natural communities that inhabit these fruits. Species reported to cause russetting are *Cr. victoriae*, *Erythrobasidium hasegawianum*, *Rhodos. babjevae*, *Rh. glutinis*, *Sporidiobolus pararoseus*, and an undescribed species of a *Tremella*-like fungus (Gildemacher et al. 2004, 2006, Matteson Heidenreich et al. 1997).

2.3. Conclusions for Yeasts as Plant Pathogens

Relative to examples of plant pathogenic filamentous fungi inciting such destructive diseases as stem rust and Fusarium head blight of wheat, yeasts seldom devastate crops. However, from the examples given, yeast infections of plants can be costly in some cases and may require control measures.

Chapter 5

Yeast Spoilage of Foods and Beverages

Graham H. Fleet

INTRODUCTION

Foods and beverages are spoiled when they no longer appeal to the consumer. Generally, they have objectionable odor, appearance, taste, or texture, or combinations of these defects. Microorganisms are well known as agents that cause spoilage. Microbial spoilage can occur at any stage throughout the production chain – from the raw material at the farm prior to harvest, during handling and processing, and to the final packaged product. The consequences of a spoilage outbreak can be substantial (Fleet 2001, Stratford 2006), and include:

- economic loss due to wasted product or product with inferior quality and value;
- cost of plant clean up, product recall, and product disposal;
- costly litigation and forensic investigation to determine cause, liability, and compensation, in the event of a large outbreak;
- adverse impact on company reputation and brand image;
- effect on human health if pathogenic bacteria develop following product spoilage by yeasts.

Although bacteria and molds (filamentous fungi) are most frequently perceived as the main organisms of spoilage, yeasts make a significant contribution. Yeast spoilage of foods is often predictable, principally occurring in those products where competition from faster growing bacteria is either retarded or prevented by the properties of the food and the conditions of processing and storage. Generally, high acid (low pH) foods, products with high sugar or high salt contents, products preserved with weak acids, and long-term frozen products are prone to spoilage by yeasts. While a great diversity of yeast species can be isolated from foods and beverages, only about 20 or so are frequently associated with spoilage outbreaks.

Food and beverage spoilage by yeasts is well documented in the literature and is covered in many early and recent reviews (Deak 1991, Fleet 1990a, 1992, Ingram 1958, Loureiro and Querol 1999, Mrak and Phaff 1948, Stratford 2006, Thomas 1993, Tudor and Board 1993, Walker and Ayres 1970), and in several specific texts (Boekhout and Robert 2003, Deak 2007, Deak and Beuchat 1996, Querol and Fleet 2006). Focused discussions of particular genera and species of spoilage yeasts have recently appeared, and these include *Saccharomyces* (Fleet 2006), *Zygosaccharomyces* (James and Stratford 2003, Kurtzman and James 2006), *Candida* (Deak 2006), *Dekkera/Brettanomyces* (Loureiro and Malfeito-Ferreira 2006), *Debaryomyces* (Breuer and Harms 2006, Praphailong and Fleet 2000), *Schizosaccharomyces* (Fleet 2000), *Yarrowia* (Heard and Fleet 2000), and *Wickerhamomyces* (*Pichia) anomala* (Passoth et al. 2006). This chapter outlines the principles underlying the ecology, physiology, and biochemistry of yeast spoilage, and discusses spoilage management through quality control and quality assurance strategies.

1. RECOGNITION OF YEAST SPOILAGE AND ITS ECOLOGICAL STUDY

Spoilage is a consequence of yeast growth in the product. Food components are utilized as growth substrates by the yeasts and are transformed into a vast array of metabolic end products. In this way, the chemical, physical, and sensory properties of the food are changed. Yeast spoilage becomes evident to the consumer in many ways, depending on the product (Stratford 2006, Tudor and Board 1993).

Carbon dioxide (gas) production by yeasts causes the containers of packaged products to swell, distort, and eventually explode as a consequence of the internal pressures that develop, which can be as high as 5–10 atmospheres. As yeasts grow on the surfaces of solid products they become visually evident as individual colonies, or as a film of dull, dry, or slimy biomass that can cause discoloration. In liquid products, yeast growth is seen as a film of biomass that covers or floats on the surface of the product, or as haze, turbidity, and sediments of cells within the product. These visual signs of spoilage are usually accompanied by the development of yeasty, alcoholic, and other off-odors and off-flavors in the product (Fleet 1992, Stratford 2006). These defects first become noticeable when yeast growth reaches approximately 10^4–10^5 cells or colony forming units (cfu) per gram or milliliter, and are evident at 10^7–10^8 cfu per g/ml.

The ecological principles that govern the occurrence and growth of microorganisms in foods in general, also apply to yeast spoilage of foods (Fleet 1999). To understand and manage food and beverage spoilage by yeasts, a systematic process of investigation and knowledge acquisition is required.

This information includes:

- isolation, enumeration, and taxonomic identification of the species and strains responsible for the outbreak;
- ecological study of the total production chain ("farm to fork"), to determine the source of the spoilage yeasts and their potential to grow at different stages throughout production;
- physical location and spatial distribution of yeasts within the product;
- biochemical, physiological, and molecular explanation of how yeasts colonize products and change their chemical and physical properties;
- understanding how food properties, food processing, and food storage conditions affect the survival, growth and metabolic activity of yeasts; and
- correlation between the presence and activity of yeasts and their impact on the sensory properties of the product.

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2. THE DIVERSITY OF YEASTS CAUSING FOOD AND BEVERAGE SPOILAGE

The ubiquitous occurrence of yeasts in the environment ensures that most foods become contaminated with yeasts during some stage in the production chain. Fortunately, most of these chance contaminations do not result in spoilage, because the food does not present a habitat that is conducive to yeast survival and growth. Several authors have compiled extensive tables that report the frequency of isolation of specific yeasts from particular foods or food groups (Deak 1991, 2007, Deak and Beuchat 1996, Fleet 1992, Tudor and Board 1993). These data have enabled some broad conclusions to be made about yeasts and their association with food and beverage spoilage. First, of the 1,500 or so yeast species recognized in current taxonomic classifications, only about 100–150 are usually isolated from foods and beverages. Secondly, only about 10% of these species (i.e., 15–20 species) are frequently implicated in outbreaks of spoilage. Table 5.1 lists several yeast species most commonly associated with food and beverage spoilage. However, some of these species can also have beneficial roles at other stages of food and beverage production. For example, *Saccharomyces cerevisiae* is well known for its key role in the alcoholic fermentation of wine and beer, but it can easily re-ferment the final, packaged product, leading to turbidity and gassiness that is now considered as spoilage (Fleet 2006, 2008). Consequently, spoilage by yeasts must be viewed in the context of the total production chain. It is also important to note that the spoilage response may vary between strains within a species. Hydrogen sulfide production by yeasts, for example, is a notable spoilage reaction, but the extent of its production varies significantly among the strains within each species (Mendes-Ferreira et al. 2002). Thus, some strains within a species could be significant spoilage organisms, while other strains may not be detrimental.

2.1. Meat Products

The occurrence of yeasts in meat products has been specifically reviewed by Dillon and Board (1991) and Samelis and Sofos (2003). Freshly slaughtered beef, lamb, pork, poultry, and seafood meats harbor low populations (10^1–10^3 cfu/g) of yeasts that generally represent about 5–10% of the total microbiota. Yeasts grow during storage of meats at 5°C, but bacteria eventually spoil these products because they grow much faster than yeasts in these high protein, high water activity, and neutral pH habitats. The most frequently isolated yeasts from fresh meats are species of *Candida*, *Rhodotorula*, *Cryptococcus*, and *Debaryomyces*. High populations (10^3–10^7 cfu/g) of yeasts may be found in minced and ground meats, but they remain insignificant compared with bacteria. *Candida zeylanoides*, *Yarrowia lipolytica*, *Cryptococcus* (*Cr.*) *laurentii*, *Debaryomyces hansenii*, and *Pichia membranifaciens* have been isolated from such meats. Storage and processing of meats under conditions that restrict the growth of bacteria will lead to growth and dominance of yeasts. Long-term frozen storage of beef, lamb, and poultry gives a yeast-dominated spoilage, characterized by off-flavors and off-odors. Species isolated from such products presumably have good ability to grow at these low temperatures, and include *Cr. laurentii*, *C. zeylandoides*, and *Y. lipolytica* (Fleet 1992). Similar species develop on refrigerated poultry products (Hinton et al. 2002, Ismail et al. 2000). Cured and brined meat products processed with salt, sodium nitrite/nitrate, sulfur dioxide, and various acidulants present habitats where bacterial growth is restricted. Consequently, products such as fresh and fermented sausages, bacon, frankfurters, corned beef, hams, and other delicatessen meats are prone

TABLE 5.1 Yeasts Frequently Associated with the Spoilage of Foods and Beverages

Yeast	Significant Properties
Debaryomyces hansenii (Candida famata)[a]	Highly salt-tolerant; frequently found in salted meat products, cheeses, brined vegetables, causing surface biofilms and off-flavors.
Dekkera/Brettanomyces[a] (e.g., *D. anomala, D. bruxellensis)*	Slow-growing, ethanol and carbon dioxide tolerant; mostly associated with spoilage of alcoholic and carbonated beverages, causing turbidity and acetic, phenolic, and mousy off-flavors.
Hanseniaspora uvarum (Kloeckera apiculata)[a]	Very acid-tolerant; frequently associated with fermentative spoilage of fresh and processed fruits and fruit products.
Kluyveromyces marxianus (Candida kefyr)[a]	Fermentation of lactose, pectinolytic, proteolytic, growth at 40–45°C and refrigeration temperatures; spoilage of dairy and plant products.
Wickerhamomyces (Pichia) anomalus (Candida pelliculosa)[a]	Acid- and salt-tolerant, produces high levels of ethyl acetate; causes spoilage of dairy, fruit, and bakery products.
Pichia kudriavzevii (Issatchenkia orientalis, Candida krusei[a]*)*	Acid-tolerant, preservative-resistant; causes fermentative spoilage and surface biofilms in low pH products.
Pichia membranifaciens (Candida valida)[a]	Oxidative, ethanol-tolerant, preservative-resistant; causes surface biofilms and off-flavors in many products.
Rhodotorula spp.	Oxidative, red-pink colonies, lipolytic, proteolytic, pectinolytic; frequent surface contaminant of dairy, meat, fruit, vegetable, bakery products.
Saccharomyces cerevisiae	Fermentative spoilage of a diversity of foods and beverages containing monosaccharide and disaccharide sugars.
Kazachstania exiguus (Candida holmii)[a]	Moderately tolerant to preservatives, acetic acid, and salt; fermentative spoilage of fruit juices, carbonated beverages, mayonnaise, vegetable salads, dairy and meat products.
Schizosaccharomyces pombe	Tolerant of high sugar and ethanol concentrations, preservative-resistant; fermentative spoilage of high sugar products and alcoholic beverages.
Yarrowia lipolytica (Candida lipolytica)[a]	Oxidative, strong proteolytic and lipolytic activities, moderately tolerant to low pH, and high concentrations of salt and preservatives; causes off-flavors and textural changes in meat and dairy products.
Zygosaccharomyces bailii	Preservative-resistant, acid and ethanol-tolerant; fermentative spoilage of fruit juices, fruit and syrup concentrates, sauces, alcoholic beverages.
Zygosaccharomyces bisporus	Properties and fermentative spoilage somewhat intermediate to *Z. bailii* and *Z. rouxii*.
Zygosaccharomyces rouxii	Tolerant of very high sugar and salt concentrations, preservative-resistant; fermentative spoilage of juice concentrates, sugar syrups, honey, jams, confectionary products, dried fruits.

[a]*Anamorphic name*

to yeast spoilage (i.e., surface slimes, off-odors) if stored too long at 5°C. *Debaryomyces hansenii* generally predominates on these products, especially if they are salted, but species of *Rhodotorula*, *Candida*, and *Pichia* may also occur. It should be noted that some yeasts play a positive role along with lactic acid bacteria in the fermentation of salami type sausages and country cured hams. *Debaryomyces hansenii* and, to a lesser extent, *Y. lipolytica* are significant in this context but strain influences are important as well (Andrade et al. 2006, Cocolin et al. 2006, Romano et al. 2006).

2.2. Dairy Products

The role of yeasts in the production and spoilage of dairy products has been reviewed by Fleet (1990b), Jakobsen and Narvhus (1996), and Frohlich-Wyder (2003). Yeasts are found in raw and pasteurized milks at 10^1–10^3 cfu/ml. However, their growth in milk during refrigerated storage is limited, as they are quickly overgrown by psychrotrophic bacteria. Nevertheless, milk is an excellent substrate for their growth and, in the absence of bacterial competition, they readily develop populations of 10^8–10^9 cfu/ml (Roostita and Fleet 1996a). Fermented dairy products, however, are prone to spoilage by yeasts, because their increased acidity restricts bacterial competition. Yogurts undergo gaseous, fermentative spoilage, usually from yeast contaminants that originate from raw materials, such as fruits, and from ineffective cleaning and sanitation of processing equipment. Yeasts isolated from spoiled yogurts include *S. cerevisiae*, *Kluyveromyces marxianus*, and various species of *Pichia* and *Candida* (Caggia et al. 2001, Vasdinyei and Deak 2003). In semi-soft and soft cheeses, yeast spoilage causes off-flavors, softening, gas production, discoloration, and swollen packages. *Debaryomyces hansenii, Y. lipolytica, K. marxianus, P. membranifaciens*, *Candida*, *Rhodotorula*, and *Cryptococcus* spp. are frequently implicated. Brown spot discoloration on the surface of some cheeses is caused by *Y. lipolytica* due to oxidation of tyrosine (Carreira et al. 1998). High populations of *D. hansenii, Y. lipolytica, K. marxianus*, and *S. cerevisiae* may develop in soft, semi-soft, and even Cheddar-style cheeses during the stage of maturation, and are considered to have positive influences on cheese quality. Consequently, yeasts are now considered to be an important component of the maturation microbiota in many cheeses. However, the difference between a beneficial and spoilage outcome may be determined by the strain that grows (Addis et al. 2001, Romano et al. 2006). Other dairy products that have potential for yeast spoilage include sweetened-concentrated milks, sour cream, and butter. The occurrence and growth of yeasts in dairy products is favored by their possession of one or more of the following properties: fermentation of lactose (e.g., *K. marxianus*); production of extracellular proteases or lipases (e.g., *Y. lipolytica*, *D. hansenii*); tolerance of salt; utilization of lactic and citric acids; and growth at low temperatures (Fleet 1990b, Corbo et al. 2001, Hansen and Jakobsen 2001, Roostita and Fleet 1999, Vasdinyei and Deak 2003). In a study of 513 yeasts isolated from dairy products marketed in Austria, the most frequently occurring species were *D. hansenii, Geotrichum candidum, K. marxianus, Y. lipolytica,* and *C. zeylanoides* (Lopandic et al. 2006).

2.3. Fruit Products

Yeasts are present as part of the surface flora of healthy, undamaged fruits, at populations of 10–10^3 cfu/cm^2. Species of *Cryptococcus*, *Rhodotorula*, *Sporobolomyces*, *Aureobasidium* (a dimorphic, ascomycete mold), and *Metschnikowia* are generally found, and they have probably evolved mechanisms to tolerate the extremes of desiccation, exposure to sunlight and irradiation, temperature fluctuations, and poor availability of nutrients associated with this habitat (Fleet 1992, 2003a). These yeasts rarely cause spoilage of fresh fruits, which is largely caused by filamentous fungi. However, some of these phylloplane yeasts have strong anti-fungal properties and could naturally function in the biocontrol of these fungi (Fleet 2003a, Spadaro and Gullino 2004). Some cultivars of apples may develop a condition termed "russeting" or corking of their skin layer which significantly depreciates their appearance and commercial value. While the physiological basis for this condition is still under investigation, there is evidence that *Aureobasidium pullulans*, *Rhodotorula* species, and other surface yeasts may contribute to its development by degrading the skin cuticle (Gildemacher et al. 2006). Damage to the structural integrity of fruits exposes their sugary, acidic tissues which are ideal for the growth of fermentative yeasts and eventual product spoilage. Similarly, processed fruit products, such as fruit juices, juice and pulp concentrates, canned fruits, dried fruits, glacéd fruits, ready-to-eat fruit slices, and fruit salads are all prone to fermentative spoilage by yeasts in the genera *Saccharomyces*, *Zygosaccharomyces*, *Hanseniaspora/Kloeckera*, *Candida*, and *Pichia*. Some products (e.g., juice concentrates, fruit syrups, dried fruits, glacéd fruits) also have high sugar concentrations, and are likely to be spoiled by osmo-tolerant species such as *Zygosaccharomyces bailii*, *Z. rouxii*, *Hanseniaspora valbyensis*, and *Schizosaccharomyces pombe* (Arais et al. 2002, Fleet 2003a, Heras-Vazquez et al. 2003, Shearer et al. 2002, Thomas 1993). Fruit and fruit products are used as ingredients in the preparation of many other commodities such as yogurts, jams, syrups, pies, cakes, and various beverages, and they can be a primary source of yeast contamination and spoilage of these products.

2.4. Vegetable Products

Low populations of basidiomycetous yeasts (*Cryptococcus, Rhodotorula*, and *Sporobolomyces* spp.) are usually isolated from the surfaces of fresh vegetables (Edgar and Aidoo 2001). However, vegetables are more prone to spoilage by bacteria than by yeasts, because of the proteinaceous nature and neutral pH of their tissues (Nguyen-the and Carlin 2000). Nevertheless, there are occasional reports that yeasts have caused problems, such as the growth of *Rhodotorula glutinis* on frozen peas, the rotting of onions by pectolytic strains of *K. marxianus*, and spoilage of tomatoes by various species (Fleet 1992, Wade et al. 2003). Spoilage is more frequently associated with fermented vegetables, such as the pink discoloration of sauerkraut by *Rhodotorula* species, and the softening and bloating of olives and pickles by species of *Saccharomyces*, *Debaryomyces, Pichia, Candida*, and *Rhodotorula* (Fleet 1992). Ready-to-eat vegetable salads (coleslaw, potato salad, lettuce/mixed salads) mixed with vinegar-based mayonnaise or salad dressings are most prone to yeast spoilage during refrigerated storage because of their decreased pH. *Naumovozyma* (*Saccharomyces*) *dairenensis*, *Kazachstania* (*Saccharomyces*) *unisporus*, *S. bayanus*, *Kazachstania* (*Saccharomyces) exiguus, Z. bailii*, *P. membranifaciens*, and various *Candida* species have been isolated from such products (Fleet 1992, 2006, Kurtzman and James 2006).

2.5. Non-Alcoholic Beverages

Carbonated and non-carbonated soft drinks, energy drinks, sports drinks, and various health beverages are typical non-alcoholic beverages. They are generally characterized by the presence of sugar concentrations up to 10% as well as having components that include organic acids (e.g., citric, malic, lactic, and acetic acids), fruit juices, vegetable extracts, colorants, flavors, antioxidants, vitamins, carbonation, etc. Their sugary, acid (pH 3.0–3.5) and relatively oxygen-free conditions make them highly susceptible to fermentative yeast spoilage. Their microbiological stability is usually due to heat processing and the addition of permitted levels of preservatives such as sorbic

and benzoic acids, sulfur dioxide, and, more recently, dimethyl dicarbonate (Stratford et al. 2000, Thomas 1993). Failure in manufacturing hygiene and process control leads to contamination and spoilage by yeasts that are usually resistant to the added preservatives. *Zygosaccharomyces bailii* is the ?A3B2 tlsb?> most problematic species, but other *Zygosaccharomyces* species are often implicated, as well as *Dekkera* (*Brettanomyces*) species, *S. cerevisiae*, *S. bayanus*, *K. exiguus*, *P. membranifaciens*, *Pichia kudriavzevii* (*Issatchenkia orientalis)*, and *Candida* species such as *C. davenportii* and *C. parapsilosis* (James and Stratford 2003, Stratford and James 2003, Thomas 1993).

2.6. Alcoholic Beverages

These products present another specialized habitat for yeast spoilage. Ethanol tolerance and ability to grow at low pH values are the key properties that enable yeasts to selectively grow and spoil these products (Fleet 1998, Thomas 1993). Packaged beers that have been properly processed by filtration and/or heat pasteurization rarely undergo spoilage. When spoilage does occur, species of *Saccharomyces* are often responsible, and include carry-over of *S. cerevisiae* strains used to ferment the beer, or contaminants such as forms of *S. cerevisiae* previously classified as *S. cerevisiae* var. *diastaticus* that have the ability to ferment residual starch dextrins in the beer and produce undesirable phenolic off-flavors (Dufour et al. 2003, Jespersen and Jakobsen 1996). Usually, beer is at higher risk of spoilage during production. Many different strains of *S. cerevisiae* are used to conduct beer fermentations according to the type of beer that is wanted. Use of an incorrect strain, or contamination with killer strains of *S. cerevisiae* or wild, non-*Saccharomyces* species, can lead to unsatisfactory outcomes. Some beers are subject to processes of maturation and conditioning after the primary fermentation, where lapses in hygiene control may lead to spoilage with wild yeasts (e.g., *Pichia*, *Dekkera*, *Debaryomyces*, *Candida* species) (van der Aa Kuhle and Jespersen 1998).

Like beer, packaged wines occasionally undergo spoilage. Many wines contain small amounts of residual glucose and fructose that are good fermentable substrates for yeasts. Re-fermentation by carry-over strains of wine yeasts (*S. cerevisiae, S. bayanus*) is usually the cause, but other species may occur (Fleet 1998, 2007, Louriero and Malfieto-Ferreira 2003, Nisiotou and Gibson 2005). Wines are more likely to be spoiled by yeasts before packaging. The alcoholic fermentation of grape juice by yeasts is an ecologically complex process involving the sequential growth of various species and strains, in addition to the principal wine yeasts, *S. cerevisiae* and *S. bayanus,* and must be properly managed to ensure a product with an acceptable quality (Fleet 2003b, 2007, 2008). After this fermentation, wines are frequently stored in tanks, barrels, etc., according to their style. Effective management of hygiene at this stage is essential to prevent the growth of spoilage yeasts. Problematic yeasts include fermentative species such as *Z. bailii*, *Dekkera* (*Brettanomyces*) *bruxellensis,* and oxidative species such as *P. membranifaciens* that cause a diversity of off-flavors (Curtin et al. 2007, Louriero and Malfieto-Ferreira 2003, 2006, Silva et al. 2004). Cider and other fruit wines experience spoilage problems similar to those described for grape wines (Thomas 1993). Distilled alcoholic spirits (e.g., whisky, rum, gin) and fortified wines, such as ports and sherries, are not usually spoiled by microorganisms because of their higher alcohol contents (Fleet 1998).

2.7. Bakery Products

Although yeasts are primarily responsible for the fermentative production of bakery products (e.g., baker's yeast, *S. cerevisiae*), they can also cause spoilage of these products (Bonjean and Guillaume 2003, Jenson 1998, Legan and Voysey 1991). During storage, breads can develop alcoholic, fruity, and acetone-like off-flavors, and some may show visible yeast growth as white, chalky, or other colored spots. The main species associated with these defects have been *S. cerevisiae*, *Hyphopichia burtonii*, and *Wickerhamomyces* (*Pichia) anomalus* (Magan and Aldred 2006). Yeasts can grow to spoilage levels during the refrigerated storage of unbaked doughs for bread, pastry, biscuit, and pizza production, and in the jam, fruit, and cream fillings of pastry products. Sour dough breads and similar products are becoming increasingly popular. A diversity of yeast species, including *S. cerevisiae*, *K. exiguus*, *Candida milleri*, *C. humilis*, *C. krusei, W. anomalus*, *P. membranifaciens*, and *Y. lipolytica* may contribute to these fermentations, but careful management of this ecology is necessary to obtain acceptable products (De Vuyst and Neysens 2005).

2.8. Products With High Contents of Sugar or Salt

Foods containing high concentrations (40–70%) of sugar include sugar cane, sugar syrups, molasses, honey, malt extract, fruit juice concentrates, jams, jellies, confectionery products, and dried fruits. Their spoilage by yeasts is not uncommon, with *Z. rouxii* being most frequently implicated because of its unique ability to tolerate the high osmotic stresses and low water activity condition of these products (El Halouat and Debevere 1996, Martorell et al. 2007, Membre et al. 1999). Occasionally, other yeasts are found and these include *Z. bailii*, *Z. bisporus*, *Z. mellis*, *Schiz. pombe*, *Torulaspora delbrueckii*, *D. hansenii*, and various *Candida* species (Martorell et al. 2007, Stratford 2006, Tokuoka 1993). High salt (5–15%, NaCl) environments occur in cured meat products (e.g., bacon, hams, corned beef), fermented, brined vegetables, dried and salted meats and fish, and fermented soy products such as soy sauce and miso. The aqueous phases of many cheeses, margarines, and mayonnaises represent less obvious high salt habitats, where 10–12% salt may occur. Spoilage of these products is usually dominated by *D. hansenii*, *Z. bailii*, and *Z. rouxii*, but *Y. lipolytica* and some species of *Pichia* and *Candida* may also be involved (Breuer and Harms 2006, Fleet 1992, Hanya and Nakada 2003, Heard and Fleet 2000, Praphailong and Fleet 2000).

2.9. Other Products

High-value cash crops, such as cocoa beans and coffee beans, undergo processes that involve the action of yeasts (Schwan and Wheals 2003). Cocoa beans must be fermented to generate the precursors of chocolate flavor, and various species of *Saccharomyces, Hanseniaspora, Candida,* and *Pichia* (including species formerly assigned to *Issatchenkia*) contribute to the process (Ardhana and Fleet 2003, Schwan and Wheals 2004). Coffee beans are processed to remove pulp and other mucilaginous materials that surround the seeds, and species of *Candida*, *Saccharomyces, Kluyveromyces, Saccharomycopsis, Hanseniaspora, Pichia*, and *Blastobotrys* (*Arxula*) have been associated with these fermentations (Masoud et al. 2004, Schwan and Wheals 2003). Growth of unwanted species during cocoa and coffee bean processing can lead to chocolate and coffee products with significantly inferior quality. A vast array of traditional fermented foods and beverages is produced in African, Asian, and South American countries from raw materials such as maize, wheat, cassava, rice, soy beans, and fruit (Aidoo et al. 2006, Naumova et al. 2003a, Nout 2003). While details of the microbial ecology of these fermentations are still emerging, yeasts have prominent roles in both beneficial and spoilage contexts.

3. YEASTS AND FOOD SAFETY

With respect to the field of food safety, yeasts have a good record. Unlike bacteria, viruses, and some filamentous fungi, yeasts are rarely associated with outbreaks of food-borne gastroenteritis or other food-borne infections and intoxications. As part of daily food consumption, humans ingest large, viable populations of a diversity of yeast species without adverse impact on their health. Nevertheless, some caution and vigilance are required. Fleet and Balia (2006) have reviewed issues relating to yeasts and food safety. For some individuals, yeast presence in foods leads to the onset of a broad range of allergic and hypersensitive reactions. Migraines, respiratory problems, chronic fatigue, dysfunctional gut and irritable bowel syndromes, and gut dysbiosis are prominent among these disorders. The underlying mechanisms of these responses require systematic scientific research, and could reflect adverse human reactions to yeast cell wall polysaccharides, cell proteins, or yeast metabolites (e.g., proteins, sulfur dioxide, biogenic amines). Most yeast species are not aggressive, infectious organisms, but two species, namely *Candida albicans* and *Cr. neoformans*, are well known as opportunistic pathogens that cause a range of muco-cutaneous, cutaneous, respiratory, central nervous, systemic, and organ infections in humans (see also Chapter 2). These two species are not usually associated with foods. In recent years, however, there have been increasing reports of human infections with other yeast species, including many that are commonly found in foods (e.g., *S. cerevisiae*, *C. krusei*, *W. anomalus*, *Y. lipolytica*, *K. marxianus*, *Rhodotorula* spp.) (Fleet and Balia 2006, Jaques and Casaregola 2008). Usually, healthy individuals are not at risk, because infections are mainly confined to those with weakened health and immune functions, such as cancer, AIDS, and hospitalized patients, and those being treated with immunosuppressive drugs and broad spectrum bacterial antibiotics. These trends, however, are raising increasing questions about the safety of yeasts in general, and properties related to their acquisition of pathogenicity (Enache-Angoulvant and Hennequin 2005, Fleet and Balia 2006, Murphy and Kavanagh 1999).

4. FACTORS AFFECTING THE GROWTH AND SURVIVAL OF YEASTS IN FOODS AND BEVERAGES

Control of commodity spoilage by yeasts depends on the application and maintenance of processing and storage conditions that either kill the cells or prevent their growth. Many environmental factors (e.g., temperature, pH, water activity, addition of chemical preservatives, physical matrix) determine the physical and chemical limits for survival and growth of yeasts, but precise limits are difficult to define, since the impact of one factor may be influenced by other factors (Deak 2006b, 2007, Deak and Beuchat 1996, Fleet 1992). For example, the minimum temperature for yeast growth varies, depending on the pH of the medium or the concentration of any sugar or salt that may be present. The impact of combined environmental stresses may be difficult to predict because their effects may be additive or synergistic (interactive), where the outcome is significantly greater or less than that obtained by adding the responses to single stresses (Battey et al. 2002, Betts et al. 1999, 2000, Evans et al. 2004, Praphailong and Fleet 1997). Two other concepts are also important in determining the yeast survival and growth response, namely, the physiological status of the cell and any adaptive behavior (Fleet 1999). Stationary phase cells are, generally, more resistant to physical and chemical stresses than cells from the exponential growth phase. Cells exposed to sub-lethal stresses may initiate adaptive reactions to enhance their survival and growth. Most foods and beverages present ecosystems where yeast cells are exposed to multiple stresses for relatively long time frames. Consequently, there is good opportunity for adaptive responses to occur (Fleet 1999, Querol et al. 2003). Detailed discussions of factors affecting yeast growth and survival are given elsewhere (Deak 2006b, 2007, Deak and Beuchat 1996, Fleet 1992, Ingram 1958, Walker and van Dijck 2006).

4.1. Temperature

Most yeasts exhibit optimal growth in the range 20–30°C, but the upper and lower limits are not well defined for individual species. Very few species grow above 40–45°C, but many grow at 2–10°C, including spoilage species of *Saccharomyces* and *Zygosaccharomyces* (Betts et al. 1999, Fleet 1992, 2006a, Guerzoni et al. 1993, Kurtzman and James 2006, Martorell et al. 2007, Steels et al. 1999a). Consequently, yeasts can be significant in the spoilage of refrigerated foods. Some species of *Candida*, *Cryptococcus*, and *Rhodotorula* and some strains of other species grow at temperatures less than 0°C, and spoil frozen foods (Davenport 1980a, Fleet 1992, Walker 1977). Temperature not only affects the limits and rate of growth, but also influences other physiological and biochemical properties, such as tolerance to ethanol, growth in the presence of high concentrations of sugar and salt, resistance to preservatives, and production of spoilage metabolites (Deak and Beuchat 1996, Fleet 1992, Papouskova and Sychrova 2007, Tudor and Board 1993).

Outbreaks of yeast spoilage in heat-processed products, such as soft drinks, syrups, fruit juices, and fruit concentrates, have drawn attention to the susceptibility of yeasts to destruction by heat. Thermal death curves and decimal reduction (D) values have been published for numerous yeasts (Fleet 1992, Shearer et al. 2002, Stratford 2006, Thomas 1993). Under normal environmental conditions, yeast cells are quickly inactivated at 60–65°C. The D60 values (i.e., time required for 10-fold decrease in viable population at 60°C) for *S. cerevisiae*, *Z. bailii*, *Z. rouxii*, for example, are in the range 0.1–0.4 minutes, but can be 5–10 minutes or longer, depending on the food matrix, pH, solute concentration, etc. (Martorell et al. 2007). *Saccharomyces cerevisiae* is regarded as one of the most heat-resistant yeast species, and its ascospores are about 100 times more resistant than budding cells (Fleet 2006).

4.2. Solute Concentration and Water Activity (A_w)

Yeasts are more tolerant of low water activity than bacteria, and most species grow in the range A_w 0.90–0.95. Some species are particularly osmo- or xerotolerant, and grow at A_w values of 0.65–0.85, depending on the solute (Table 5.2, Lages et al. 1999, Tokuoka 1993, van Eck et al. 1993). As mentioned previously, such yeasts are most frequently associated with the spoilage of high sugar and high salt foods. *Debaryomyces hansenii* is particularly salt-tolerant, with some strains surviving in the presence of 20–24% (w/v) NaCl (Breuer and Harms 2006, Butinar et al. 2005, Papouskova and Sychrova 2007, Praphailong and Fleet 2000). The upper limit for *S. cerevisiae* is about 10–12% NaCl, but this varies with the strain, and is affected by other factors such as pH. For example, a strain of *S. cerevisiae* grew in the presence of 7.5% NaCl at pH 5.0–7.0, but could not grow at this concentration when the pH was decreased to 3.0 (Hansen and Jakobsen 2001, Praphailong and Fleet 1997). Similar observations have been reported for other yeasts, including *D. hansenii*, *Y. lipolytica*, *Z. bailii*, and *H. uvarum* (Betts et al. 1999, Praphailong and Fleet 1997). The most sugar-tolerant yeast is *Z. rouxii,* which readily grows in foods containing 60–70% (w/v) sugars (Table 5.2) (Martorell et al. 2007,

TABLE 5.2 Comparison of Growth Responses of Food and Beverage Spoilage Yeasts

Yeast	Temp. Range°C	pH Range	Max. Sucrose (% w/v)	Max. NaCl (%w/v)	Min. Aw
Debaryomyces hansenii	0–37	2.5–9.0	50–60	12–24	0.81–0.91
Hanseniaspora uvarum	3–35	1.5–7.5	50–60	12	0.90–0.95
Kluyveromyces marxianus	1–47	2.5–8.0	50	10	0.96
Wickerhamomyces anomalus	3–37	2.0–10.0	60	10–15	0.85–0.92
Pichia membranifaciens	5–30	2.5–7.5	50	5–12	0.84–0.93
Saccharomyces cerevisiae	0–45	2.5–8.0	50–60	5–8.0	0.89–0.92
Yarrowia lipolytica	5–37	2.0–8.0	50	10–12	0.85–0.89
Zygosaccharomyces bailii	2–37	2.5–7.0	70	5–12	0.87–0.94
Zygosaccharomyces rouxii	4–40	2.5–7.5	70	7–20	0.65–0.86

Values in Table are taken from Praphailong and Fleet (1997), Betts et al. (1999), van Eck et al. (1993), Guerzoni et al. (1993), Lages et al. (1999) Steels et al. (1999), Butinar et al. (2005), Martorell et al. (2007). The values represent a comparative guide only. Absolute values vary with yeast strain and influence of other environmental factors.

TABLE 5.3 Minimum Concentration of Preservatives Required to Prevent the Growth of Food and Beverage Spoilage Yeasts

Yeast	Benzoic Acid (mg/l)	Sorbic Acid (mg/l)	Sulfur Dioxide (mg/l)	Acetic Acid (g/l)
Debaryomyces hansenii	100–200	100	–	–
Dekkera bruxellensis	–	950	75	10–15
Hanseniaspora uvarum	100–200	200	7	6
Kluyveromyces marxianus	100–200	150	50	6
Pichia membranifaciens	200	200	–	15
Wickerhamomyces anomalus	100–200	150	50–75	6
Saccharomyces cerevisiae	100–200	200	75–100	10–20
Yarrowia lipolytica	300–400	300	–	–
Zygosaccharomyces bailii	600	600	200–500	25
Zygosaccharomyces rouxii	200	500	–	9

Values in Table are taken from Fleet (1992), Guerzonni et al. (1993), Praphailong and Fleet (1997), Steels et al. (1999), Fredlund et al. (2002), Stratford (2006), Loureiro and Malfieto-Ferreira (2006) and Martorell et al. (2007). The values represent a comparative guide only. Absolute values vary with the yeast strain and influence of other environmental factors. The values shown are given for pH 3.5.

Membre et al. 1999). Some other species notable for sugar tolerance include *Z. bailii*, *C. versatilis*, and *Schiz. pombe* (Martorell et al. 2007, Tokuoka 1993).

4.3. pH and Acidity

Yeasts grow best in the range pH 4.5–7.0. They prefer acid environments, and many species grow at pH values as low as 2.0–2.5 (Fleet 1992, Martorell et al. 2007). Some strains of *H. uvarum* grow at pH 1.5 (Praphailong and Fleet 1997). The stronger growth of yeasts at low pH when compared with bacteria leads to their predominance in acid foods. Very few species grow at pH 9.0, and some species show weak or no growth at pH 7.0–7.5 (e.g., *Z. bailii*, Table 5.2) (Betts et al. 1999, Praphailong and Fleet 1997, Steels et al. 1999a). Acidity and pH synergistically interact with many other factors affecting yeast growth, such as temperature, water activity, sugar and salt concentration, and this is a most important concept that determines product stability and shelf life (Battey et al. 2002, Betts et al. 1999, 2000, Evans et al. 2004, Praphailong and Fleet 1997).

4.4. Antimicrobials

A range of preservatives may be added to foods and beverages to control yeast growth. Many of these are weak organic acids such as sorbic, benzoic, acetic, and propionic acids. Sulfur dioxide is also used. The effectiveness of these agents depends on their concentration, the pH of the food, and other food properties such as sugar and salt concentrations (Deak and Beuchat 1996, Fleet 1992, Maimer and Busse 1992). Most are only effective at pH values around 5.0 or lower, when a greater proportion of the molecule is present as the undissociated form, which is able to diffuse into the cell. Susceptibility to these agents varies with the yeast species (Table 5.3). *Zygosaccharomyces* species are notoriously resistant to these preservatives, especially *Z. bailii*, which can tolerate the maximum concentrations permitted by some food legislations (Martorell et al. 2007, Steels et al. 1999a). Other species that exhibit relatively high resistance include *C. krusei, P. membranifaciens*, *Y. lipolytica*, and *Schiz. pombe*, as well as some strains of *S. cerevisiae* (Fleet 2006, Praphailong and Fleet 1997. Stratford 2006). The two major end products of yeast growth and metabolic activity, ethanol and carbon dioxide, also have anti-yeast activity. Yeasts vary in their tolerance to these substances. Some yeasts are known for their ability to tolerate higher concentrations of ethanol, and become significant in the spoilage of alcoholic beverages. These include species of *Saccharomyces*, *Zygosaccharomyces*, *Dekkera* (*Brettanomyces*), *Pichia*, (*Issatchenkia)* and *Saccharomycodes* (Fleet 1998, du Toit and Pretorius 2000, Louriero and Malfieto-Ferreira 2003, Thomas 1993). Similar yeasts are also tolerant to higher concentrations of carbon dioxide (El Halouat and Debevere 1996, Fleet 1992, Stratford 2006).

Dimethyl dicarbonate is another preservative that has recently been approved for the control of spoilage yeasts, and it is usually effective at concentrations of 200–250 mg/l (Martorell et al. 2007, Steels et al. 1999a, Threlfall and Morris 2002). Several plant extracts are inhibitory to yeasts and other microorganisms, and are often considered as more "natural" alternatives to conventional preservatives (Araujo et al. 2003, Conner and Beuchat 1984). The essential oils of garlic and onion are particularly effective, with concentrations of approximately 20 ppm sufficient to control *S. cerevisiae*. Moreover,

these extracts exhibit their anti-yeast activity across a wide range of pH (e.g., pH 3.0–8.0) (Kim et al. 2004). Vanillin (4-hydroxy-3-methoxy benzaldhyde), which is extracted from vanilla beans, is inhibitory to *S. cerevisiae* and other yeasts at concentrations of 20 mM, but lower concentrations can be effective when combined with other hurdles such as low temperature and low pH (Fitzgerald et al. 2004). Many plant extracts are also powerful flavorants, so there is a challenge to obtain yeast control without adversely compromising the sensory acceptability of the product.

5. NEW PROCESSING TECHNOLOGIES

New technologies are being developed for food processing to minimize the use of heat, and these exploit the use of electric fields and high hydrostatic pressure (Raso and Barbosa-Canovas 2003). Yeasts are inactivated by exposure to low-intensity electric fields and high-intensity pulsed electric fields but, so far, most studies have been done with *S. cerevisiae* (Elez-Martinez et al. 2004, Geveke and Brunkhorst 2003, Guillou and El Mur 2002). High hydrostatic pressures around 300–400 MPa inactivate *S. cerevisiae* and *Z. bailii*, with D-values in the range of 1–3 minutes. Stationary phase cells and ascospores are more resistant, and there are significant influences of the substrate matrix, such as sugar content, on inactivation rates (Basak et al. 2002, Goh et al. 2007, Palou et al. 1997, Zook et al. 1999).

6. MICROBIAL INTERACTIONS

Yeasts rarely occur in food and beverage ecosystems as single species cultures. Exceptions occur in highly processed products where spoilage outbreaks by single, well-adapted species are known, e.g., *Z. rouxii* in high sugar products (Stratford 2006). Generally, most habitats are comprised of a mixture of yeasts, bacteria, filamentous fungi, and their viruses, and product spoilage is determined by the interactive growth and metabolic activity of the total microbiota. Even within yeasts themselves, there can be significant species and strain interactions that impact on the population dynamics of the ecosystem and hence on product quality. The diversity and complexity of these microbial interactions are beginning to emerge (Deak 2006, Fleet 2003b, Viljoen 2006).

A network of yeast–yeast interactions occurs in many food ecosystems, and is seen as the successive growth and death of different yeast species and strains within each species, throughout the food production chain. Such sequential development of yeasts occurs in the fermentation of wines, production of salami-style sausages, maturation of cheeses, various bread fermentations, and fermentations of cocoa and coffee beans, where growth of an inappropriate species or strain can be detrimental to product quality (Romano et al. 2006, Viljoen 2006). The physiological mechanisms underlying these ecological shifts are numerous (Palkova and Vachova 2006). Explanations include the different rates of nutrient transport and uptake by different species and strains, the sensitivities of different yeasts to metabolic end products (e.g., ethanol), and the production and sensitivity to killer toxins (Schmitt and Breinig 2006).

The concept of quorum sensing has recently been observed to occur in populations of yeast cells, and is a mechanism that could determine how populations evolve and change (Hogan 2006). Quorum sensing is a mechanism of cell communication that occurs during the growth of microbial cultures or colonization of a habitat. As cells proliferate they excrete metabolites into the surrounding environment. The concentration of these metabolites increases in proportion to cell density. At certain threshold levels, after a quorum population has been reached, some metabolites become signaling molecules that regulate gene expression and subsequent cell behavior. The transition from budding to filamentous growth in *S. cerevisiae* and *C. albicans* is now thought to be a quorum response, with the triggering or signal metabolites being tryptophol and phentlethyl alcohol, and farnesol, respectively (Hogan 2006, Ramage et al. 2002). The physical proximity of one cell in relation to another could also affect the cell response (Arneborg et al. 2005). The metabolic outcomes of these interactions and their impacts on product quality are complex, as demonstrated by the mixed culture of strains of *S. cerevisiae* and *S. bayanus* in grape juice fermentation and their effect on chemical composition and flavor of wines (Howell et al. 2006).

Yeast–bacterial interactions are often seen as the inhibitory effects of yeasts on bacteria through ethanol production. However, broader relationships occur. The death and autolysis of yeast cells releases vitamins and other nutrients that stimulate the growth of bacteria, as seen in the spoilage of alcoholic beverages (Alexandre and Guilloux-Benatier 2006, Fleet 1998). Some yeasts utilize the organic acids that occur in cheeses, fruit products, and salad dressings, causing an increase in product pH, and growth of spoilage and pathogenic bacteria (Viljoen 2006). Some bacteria are antagonistic towards yeasts. Excessive growth of lactic and acetic acid bacteria on grapes produces acetic acid and other substances that inhibit the growth of yeasts in grape juice, causing stuck or sluggish wine fermentations, loss of process efficiency, and, generally, a spoiled product (Fleet 2003b).

Interactions between yeasts and filamentous fungi have not been widely studied, but do occur. Fungal growth on wine grapes produces substances that inhibit the growth of yeasts during grape juice fermentation (Fleet 2003b). In contrast, some yeasts encourage the growth of *Penicillium* spp. during the maturation of cheeses (Hansen et al. 2001). Several species within the genera *Candida, Pichia, Metschnikowia, Cryptococcus*, and *Pseudozyma* have strong antifungal properties through elaboration of lytic enzymes, toxic proteins, toxic fatty acids, and ethyl acetate, and have potential for use in the biocontrol of fungi. Commercial preparations of some yeast species are now available for the pre- and postharvest control of fruit, vegetable, and grain spoilage fungi (Breuer and Harms 2006, Fleet 2003a, Passoth et al. 2006, Spadaro and Gullino 2004).

7. BIOCHEMISTRY AND PHYSIOLOGY OF FOOD SPOILAGE BY YEASTS

Yeasts utilize food constituents as substrates for their growth, metabolizing them into a vast array of end products that change the food's chemical, physical, and sensory properties. The type and concentration of products that are generated depend upon the yeast species and strain (Lambrechts and Pretorius 2000, Romano et al. 2003), and how the environment of the food habitat affects the biochemistry and physiology of the yeast response (Fleet 1999, Walker and van Dijck 2006).

7.1. Carbohydrates

Because sugars, such as glucose, fructose, sucrose, and maltose, are frequently found in foods and beverages, fermentative spoilage by yeasts is not uncommon. These sugars are converted principally to ethanol and carbon dioxide, causing the product to lose sweetness, and acquire distinctive alcoholic aromas and flavors, along with gassiness. In addition, many hundreds of secondary end products, such as higher alcohols, organic acids, glycerol, esters, aldehydes, ketones, and sulfur volatiles are produced. Although produced in relatively, low concentrations, many of these substances have low flavor and

aroma thresholds and, therefore, have high impact on sensory quality. However, there is significant diversity between yeast species and strains in the production of these metabolites (Heard 1999, Romano et al. 2003). The biochemical pathways and mechanisms for producing these metabolites are generally well known (Berry and Slaughter 2003, Dickinson and Kruckeberg 2006, Rodrigues et al. 2006, F. Romano et al. 2003, Sweigers et al. 2005). Many yeasts are facultative anaerobes and also metabolize sugars aerobically, but some (e.g., *Rhodotorula* and *Cryptococcus* spp.) only exhibit aerobic metabolism.

7.2. Polysaccharides

Apart from species in genera such as *Aureobasidium*, *Galactomyces*, and *Trichosporon*, yeasts do not degrade cellulose, and only a few species are known to degrade xylan. Pectin- and starch-degrading yeasts are more common (Fleet 1992). A diversity of species degrade pectin, including strains of *S. cerevisiae, K. marxianus, Cr. albidus, W. anomala, A. pullulans, Rhodotorula* spp., and *Candida spp.* (Buzzini and Martini 2002, Charoenchai et al. 1997, Masoud and Jespersen 2006, Nakagawa et al. 2004, Oliveira et al. 2006, Radoi et al. 2005, Strauss et al. 2001). Pectins mainly occur in fruit and vegetable products, where their degradation gives a loss in texture, firmness, and viscosity. Starch-degrading (i.e., amylolytic) yeasts are potentially significant in the spoilage of cereal products and those products where starch is used as an ingredient (e.g., meat sausages, yogurts, fruit pulps, salad dressings, sauces). Amylase production has been reported in various species of *Cryptococcus*, *Candida*, *Pichia*, *Schwanniomyces*, *Saccharomycopsis*, *Aureobasidium*, and *Galactomyces*, but their significance in food spoilage has not been demonstrated (Buzzini and Martini 2002, Charoenchai et al. 1997, Fleet 1992, Strauss et al. 2001, Wanderley et al. 2004). However, *S. cerevisiae* (var. *diastaticus*) can be troublesome in the brewing industry, because it produces a glucoamylase that enables it to ferment residual starch dextrins in packaged beer (Fleet 2006).

7.3. Nitrogen Compounds

The main nitrogen substrates used by yeasts during growth in foods are free amino acids and inorganic ammonium compounds. They are assimilated and metabolized by well-known biochemical processes which also determine the production and concentrations of higher alcohols, organic acids, and esters, mentioned earlier (Berry and Slaughter 2003, Lambrechts and Pretorius 2000, Messenguy et al. 2006, Sweigers et al. 2005). Decarboxylation of amino acids leads to the production of amines that could impact on flavor, and could initiate adverse health responses in some consumers. Amine production varies with the yeast species (Fleet and Balia 2006). Yeast metabolism of some amino acids such as arginine and citrulline gives urea, which can react with ethanol to give ethyl carbamate, a potential carcinogen (Fleet and Balia 2006, Uthurry et al. 2006).

Metabolism of lysine and ornithine by *Dekkera* (*Brettanomyces)* species leads to the production of tetrahydropyridines that give distinctive, mousy odors and taints (Loureiro and Malfieto-Ferreira 2006, Sweigers et al. 2005). Sodium nitrite and sodium nitrate are assimilated by some species (e.g., *Pichia*, *Cryptococcus* spp.), and this reaction could be significant in foods (e.g., meat products) where nitrites/nitrates are used as curing agents (Dillon and Board 1991). Proteolysis is a key spoilage reaction in foods, and leads to the production of ammoniacal, bitter flavors, and loss of texture. The majority of yeasts do not produce extracellular proteolytic enzymes. *Yarrowia lipolytica*, *A. pullulans*, and various species of *Rhodotorula* and *Cryptococcus,* however, are notable for the production of these enzymes, but protease-producing strains also occur within *Saccharomyces*, *Hanseniaspora*, *Metschnikowia*, *Debaryomyces*, and *Candida* spp. (Buzzini and Martini 2002, Charoenchai et al. 1997, Fleet 1992, Roostita and Fleet 1996a, Strauss et al. 2001).

7.4. Organic Acids

Yeasts either produce or utilize organic acids, thereby changing the acidity and flavor profile of the product (Radler 1993). Succinic and acetic are the main acids produced from sugar fermentation, with acetic acid having the stronger sensory impact. At concentrations exceeding 1–2 grams per liter, acetic acid has a detrimental effect on quality, and some yeasts, such as *Kloeckera apiculata*, *W. anomalus*, *C. krusei*, and *Dekkera* (*Brettanomyces*) species, can produce these amounts. However, there is notable variation between strains in acetic acid production and, even in *S. cerevisiae,* some strains can give unacceptable levels (du Toit and Pretorius 2000, Fleet 1992, Radler 1993, Romano et al. 2003, Swiegers et al. 2005). Many yeasts oxidatively metabolize organic acids, leading to a decrease in acidity of the product and a rise in pH, which could encourage the growth of spoilage and pathogenic bacteria. This activity is of particular concern in fermented dairy products where yeast species such as *D. hansenii* and *Y. lipolytica* utilize lactic acid (Fleet 1990b, Roostita and Fleet 1999). *Schiz. pombe* and *Z. bailii* strongly metabolize malic acid under fermentative conditions and this activity could significantly de-acidify some fruit juices (Gao and Fleet 1995, Radler 1993).

7.5. Sulfur Compounds

Yeasts produce a range of volatile sulfur compounds which, above certain thresholds, have negative impacts on product odor and flavor (Swiegers et al. 2005). The most predominant substances are hydrogen sulfide, sulfur dioxide, and dimethyl sulfide, but lesser amounts of other organic sulfites, mercaptans, and thioesters are also formed. Most studies have focused on the production of these substances by *S. cerevisiae,* where the amounts formed vary greatly with the strain (Spiropoulos et al. 2000). Further studies suggest that other species, such as *W. anomalus*, *P. membranifaciens*, *Dekkera* spp., and various basidiomycetous yeasts (e.g., *Cryptococcus* and *Rhodotorula* species), may also produce significant quantities of these sulfur metabolites (Buzzini et al. 2005a, Mendes-Ferreira et al. 2002,).

7.6. Lipids

Enzymatic degradation of food lipids produces free fatty acids that give rancid, soapy, cardboardy off-flavors, as well as acidification of the food. Food texture is also altered. Lipolytic species mostly occur in *Candida*, *Cryptococcus*, *Geotrichum*, and *Rhodotorula,* and have been implicated in the breakdown of fats in dairy and meat products, and in olive oil. Notable lipolytic species include *Y. lipolytica*, *Cr. diffluens*, *C. zeylanoides*, *Cr. albidus*, and *Cr. laurentii* (Buzzini and Martini 2002, Charoenchai et al. 1997, Roostita and Fleet 1996a, Strauss et al. 2001) but lipolytic strains of *Barnettozyma* (*Williopsis*) *californica* and *S. cerevisiae* that spoil olive oil have been reported (Ciafardini et al. 2006).

7.7. Lysis

Cell lysis is an overlooked response that, nevertheless, impacts on food quality. The disruption of yeast cells releases their intracellular constituents into the food matrix. This will include an array of active enzymes, such as peptidases, proteases, lipases, nucleases, esterases, and decarboxylases, which may react with food components. Lysis

can occur by two mechanisms. First, it may be caused by the disruption of yeast cells by enzymes or substances produced by other microorganisms, as mentioned in a previous section. Secondly, yeast cells enter into a process of self degradation or autolysis after they die. Intracellular components such as nucleic acids, lipids, and proteins are extensively degraded by endogenous enzymes, giving a diversity of products that transfer to the food and so affect flavor and aroma. In addition, some of these products may act as nutrients for the growth of spoilage bacteria (Alexandre and Guilloux-Benatier 2006, Hernawan and Fleet 1995, Zhao and Fleet 2005).

8. STRESS, ADAPTATION, AND GENOMICS

The control of food and beverage spoilage by yeasts generally depends on the maintenance of chemical and physical conditions that prevent yeast growth. Such conditions include low temperature, low pH/high acidity, high concentrations of sugar or salt, and addition of chemical preservatives. Essentially, these represent stress barriers to the yeast cell. Continual exposure to these stresses, however, provides opportunities for yeast cells to adapt and acquire resistance to the stress and, indeed, this behavior is seen in practical situations. The wine industry, for example, has used sulfur dioxide as an antimicrobial for over a hundred years, so it is not surprising to find wine strains of *S. cerevisiae* that have developed enhanced ability to resist this substance (Aa et al. 2006, Querol et al. 2003). Similarly, it would not be unusual to find more osmotolerant strains of *S. cerevisiae* in the fruit juice concentrate industry (Erasmus et al. 2003), or benzoate- and sorbate-tolerant yeasts associated with the carbonated beverage industry where these preservatives are routinely used (Stratford 2006). Enhanced osmotolerance of *Zygosaccharomyces* species by adaptation has been demonstrated by Martorell et al. (2007). The ability of yeasts to resist and develop resistance to food processing hurdles poses a major challenge to the prevention of spoilage. Consequently, it is important to understand the biological mechanisms that control these responses.

Yeasts react quickly to changes in the external environment by shifting their metabolic and physiological behavior to tolerate the new conditions. For example, an array of protective, heat shock proteins is produced in response to temperature stresses, and the fatty acid composition of membranous lipids also changes. Intracellular glycerol is produced as an osmo-protectant against increases in external sugar and salt concentrations, and proton and anion pumping mechanisms are activated to accommodate acid and pH stresses (Tanghe et al. 2006, Walker and van Dijck 2006). Genomic studies based on DNA-microarray and proteomic analyses now enable the linkage of these responses to the expression and regulation of individual genes (Bond and Blomberg 2006). Few studies of this nature have been done with food and beverage yeasts, but during wine, beer, and sake fermentations, *S. cerevisiae* exhibits sequential expression and regulation of many genes associated with carbon, nitrogen, and sulfur metabolism, as well as other genes required to tolerate stresses, such as high sugar concentration, low pH, ethanol, rehydration, and nutrient deficiency (Brejning et al. 2005, Novo et al. 2007, Rossignol et al. 2003, Varela et al. 2005, Wu et al. 2006, Zuzuarregul et al. 2005). Similar analyses are providing molecular and genetic insights into the remarkable tolerance of some yeasts to the extremes of high salt and high sugar contents in some foods (e.g., *D. hansenii* in cheese brines, *Z. rouxii* in sugar syrups and fruit juice concentrates), and resistance to organic acid preservatives (e.g., *Z. bailii* in salad dressings and soft drinks) (Ando et al. 2006, Gori et al. 2007, Piper et al. 2001, Tanghe et al. 2006). Cell flocculation, adhesion to solid surfaces, and biofilm formation are further stress responses of yeasts that are likely to affect their growth and survival in food and beverage ecosystems (Verstrepen and Klis 2006).

9. ISOLATION, ENUMERATION, AND IDENTIFICATION

The isolation, enumeration, and identification of yeasts from foods and beverages follow the same principles and strategies that are used for yeasts in general. These involve the sequential operations of rinsing or maceration of the sample, dilution of the suspension, enumeration of yeast cells in suspension by agar plating, most probable number, membrane filtration, microscopic or electronic methods, purification of isolates, and identification of isolates to either genus, species or strain level. Details of these procedures have been reviewed by Fleet (1992), Beuchat (1993), Deak (2003, 2007), Deak and Beuchat (1996), Kurtzman et al. (2003), and Kurtzman (2006a).

9.1. Isolation and Enumeration

Media used for the general isolation and enumeration of yeasts include malt extract agar, glucose-yeast extract-peptone agar, tryptone-glucose-yeast extract agar, WL-nutrient agar, and dichloran-rose bengal-chloramphenicol (DRBC) agar. Bacterial growth on these media can be controlled by the addition of antibiotics (e.g., oxytetracycline, gentamicin, streptomycin, chloramphenicol, penicillin) at concentrations of approximately 100 mg/l. Overgrowth by filamentous fungi can be controlled by addition of biphenyl, propionic acid, or dichloran (Deak et al. 2001, Fleet 1992). DRBC and WL media contain dyes that cause some species to give different colored colonies, enabling a degree of yeast differentiation to be made when mixtures of species are likely to occur in the habitat (Deak 2003, Pallmann et al. 2001). Selective-differential media have been developed for the isolation and enumeration of specific yeasts from foods and beverages (Beuchat 1993, Deak 2003, Fleet 1992, Kurtzman et al. 2003, Loureiro and Querol 1999). Lysine agar is used to isolate non-*Saccharomyces* species when they occur in conjunction with high populations of *S. cerevisiae*, since the latter species cannot use lysine as a nitrogen source. Ethanol-tolerant yeasts may be isolated in the presence of less tolerant species by plating onto media supplemented with ethanol. Species, e.g., *Z. bailii,* that are resistant to weak organic acid preservatives, such as benzoic, sorbic, and acetic acids, can be selectively cultured on media that incorporate these acids into their formulation. Xerotolerant yeasts that dominate in high sugar or high salt (i.e., low A_w activity) products can be selectively cultured in media containing 50–60% sucrose, 10–15% NaCl, or other solutes such as glycerol. Various chromogenic media have been developed for the targeted detection of yeasts such as *D. hansenii*, *K. marxianus*, *Y. lipolytica*, and some species of *Candida* and *Dekkera* (Loureira 2000). Specific media can be designed to detect amylolytic, proteolytic, lipolytic, and pectolytic yeasts. Formulations for many of these media are given in Kurtzman et al. (2003).

Selection of media and cultivation conditions for the isolation and enumeration of yeasts should not overlook the fact that many foods and beverages are processed to varying extents, and are likely to harbor a proportion of sub-lethally injured cells that require resuscitation before analysis. These injured cells might not form colonies under some of the selective culture conditions mentioned previously, and consequently their presence may be overlooked. Nevertheless, they have the potential to resuscitate in the product and eventually cause spoilage. The concept of sub-lethal injury and its significance in the spoilage of products by yeasts has not been widely studied, but the phenomenon does occur (Deak and Beuchat 1996, Fleet and Mian 1998). Shipments of heat-processed fruit juices, wines, and other beverages sometimes develop spoilage many months after packaging, and this is probably a consequence of not detecting injured yeast cells at the time of production. Studies to

date suggest that injured cells can be resuscitated and repaired by incubating them in 2% malt extract broth for 2–3 hours at 25°C prior to culture on selective media (Fleet and Mian 1998).

A somewhat related issue is the possible presence of viable, but not culturable (VBNC) species of yeasts in foods and beverages (Divol and Lonvaud-Funel 2005, Fleet 1999, Palkova and Vachova 2006). Detection of these organisms requires a culture-independent strategy, based on extraction and analysis of the habitat DNA. One approach that is finding increasing application is PCR-denaturing gradient gel electrophoresis (DGGE) or PCR-temperature gradient gel electrophoresis (TGGE). Total DNA is extracted from the food, and yeast DNA is specifically amplified using PCR and primers targeting regions of ribosomal RNA genes. The yeast DNA is then resolved into amplicons for individual species by DGGE or TGGE. These amplicons are extracted from the gel, and their species identity is determined by sequencing. PCR-DGGE/TGGE has been applied to the analysis of yeast communities associated with grapes, wines, sourdoughs, cocoa beans, coffee beans, and meat sausage fermentations (reviewed in Beh et al. 2006, Fernandez-Espinar et al. 2006). There is good agreement between yeasts detected by cultural and PCR-DGGE/TGGE methods but, in some cases, species have been recovered by PCR-DGGE but not by agar culture, suggesting the presence of non-culturable zymobiota, or that the spoilage yeasts have died, leaving behind only DNA. However, the reverse also occurs, where PCR-DGGE has not detected yeasts that were isolated by culture. Many factors affect the performance of PCR-DGGE/TGGE analyses and further research is required to understand and optimize the assay conditions (Beh et al. 2006, Prakitchaiwattana et al. 2004).

9.2. Identification

In the past, yeast taxonomy and the identification of yeast isolates were based upon phenotypic properties that were determined by performing a vast array of physiological and cultural tests. These included: colony, cell, and sporulation morphology; fermentation of sugars; assimilation of various carbon and nitrogen substrates; vitamin requirements; growth at different temperatures; and growth in the presence of various concentrations of sugars and salt (NaCl) (Kurtzman et al. 2003, Kurtzman 2006a). The workload, time, costs, and general impracticality of this approach has led to the development and commercial availability of various diagnostic kits for yeast identification. Generally, these kits assay the growth and reactivity of yeasts on a few carefully selected substrates, and enable computer processing of results in reference to established databases. Such kits include the API 20C, ATB 32C, SIM, RapID yeast Plus, Yeast Ident-Food, and BIOLOG systems, and have been evaluated by many researchers (Deak and Beuchat 1996, Praphailong et al. 1997, Robert 2003, Velazquez et al. 2001). Although kits provide a first stage, convenient, and rapid diagnosis of yeast identity, they should be followed up by confirmation with more definitive phenotypic and molecular tests. Fatty acid profiling is another rapid method that has shown some success for identification of food related yeasts (Loureiro 2000).

Advances in understanding the molecular biology of yeasts have led to major revisions of yeast taxonomy and classification, and the development of numerous molecular technologies for yeast identification, differentiation, and detection (Fell et al. 2000, Kurtzman and Fell 2006, Kurtzman and Robnett 1998a, Kurtzman et al. 2003, van der Vossen et al. 2003). Specific applications of these methods to food and beverage yeasts have been reviewed in Beh et al. (2006) and Fernandez-Espinar et al. (2006).

Yeasts are now routinely identified to species by sequencing regions of the SSU and LSU ribosomal RNA (rRNA) genes, and the internal transcribed spacers (ITS) of the ribosomal RNA repeat. Most of these sequences can be accessed through public databases, e.g., GenBank. Sequences have been determined for the D1/D2 domains of the LSU ribosomal RNA gene for all currently accepted ascomycetous and basidiomycetous yeasts (Fell et al. 2000, Kurtzman and Fell 2006, Kurtzman and Robnett 1998a, 2003, Scorzetti et al. 2002) (see Chapter 10, Molecular Identification of Yeasts). The basic procedure involves extraction of the DNA from the yeast culture, PCR amplification of the selected gene sequence, separation and isolation of the amplified DNA, sequencing of this product, and comparison of the sequence with the database to give the species identification. Usually, the entire operation can be completed within 24–48 hours. A less definitive but simpler and faster method for species identification is based on PCR-RFLP (restriction-enzyme fragment length polymorphism) analysis of the ITS and other regions of ribosomal RNA genes. The profile of DNA fragments so produced (size and number of fragments) is characteristic of many species, and databases for comparative analyses have been established (Esteve-Zarzoso et al. 1999, Granchi et al. 1999, Naumova et al. 2003). This method has received widespread application to food and beverage yeasts (see Beh et al. 2006, Fernandez-Espinar et al. 2006).

Nucleic acid probes and real time PCR detection methods have been described for some species, such as *S. cerevisiae* (Martorell et al. 2005), *Brettanomyces/Dekkera bruxellensis* (Phister and Mills 2003), and *Z. bailli* (Rawsthorne and Phister 2006), and have been adapted to enumerate and quantify yeast populations (Hierro et al. 2006b). Species-specific DNA probes for yeasts have been immobilized in the wells of microtiter plates or onto the surfaces of microspheres and used in hybridization assays for the rapid detection of target species. DNA of the yeast under test is amplified by PCR, labeled with a reporter tag, and then used in the assay. Positive signals can be measured colorimetrically or by automated flow cytometry (Diaz and Fell 2005a, Kiesling et al. 2002, Page and Kurtzman 2005).

The spoilage potential of yeasts not only varies with the species, but can also be a strain-related response. For example, some strains of *S. cerevisiae* produce objectionable levels of acetic acid and hydrogen sulfide, while others may not (Fleet 2006). Consequently, differentiation of yeasts at the sub-species level is an important requirement in quality assurance programs. Molecular methods which have been developed for this purpose include pulsed field gel electrophoresis (PFGE) of chromosomal DNA, and PCR-based methods such as random amplification of polymorphic DNA (RAPD), amplified fragment length polymorphism (AFLP), RFLP, and profiling of microsatellite DNA. A simpler, faster method is based on RFLP analysis of mitochondrial DNA, where no PCR amplification of DNA is required (Andrade et al. 2006, Beh et al. 2006, Fernandez-Espinar et al. 2006, Lopandic et al. 2006, Schuller et al. 2004, van der Vosssen et al. 2003). Various combinations of these methods have been applied to trace the sources of yeast contamination during fruit nougat production (Martorell et al. 2005) and carbonated orange juice production (Pina et al. 2005).

10. QUALITY ASSURANCE AND CONTROL

As mentioned earlier, yeasts are widely distributed in the environment and, consequently, contaminate most foods and beverages. Prevention of spoilage requires good manufacturing practices, including application of the principles of Hazard Analysis Critical Control Point (HACCP) analysis, other quality management programs (Jouve 2000), and good hygienic practices (Lelieveld 2000). Since most yeasts grow well at low temperatures, refrigeration does not prevent spoilage, only slows down its occurrence. Prevention and minimization of contamination are, therefore, key requirements in the management of yeast spoilage. Raw materials and ingredients

used in food and beverage processing (e.g., fruit pulp, flavors, sugar syrups, sugar, salt, spices) should be free of yeast contamination through the adoption of appropriate specifications (e.g., yeasts may not be detected in 1–10 g of product). If possible, ingredients should be heat processed to kill any contaminants. Insects such as bees and fruit flies are significant sources of yeast contaminants (Rosa et al. 2003, Stratford and James 2003), and their access to foods should be prevented. Effective cleaning and sanitation of equipment and process lines to eliminate yeast contamination is another basic requirement. Although preservatives, such as benzoates, sorbates, and sulfur dioxide, are frequently used to control yeast spoilage, it is important to recall that several yeast species (e.g., *Z. bailii*) can tolerate and grow quite well at maximum concentrations permitted by most legislations. Routine monitoring of end products to ensure that they conform to appropriate specifications is usually part of an overall strategy to manage yeast spoilage, but reliable and sensitive yeast detection methods need to be used. Just one viable yeast cell in a 750 ml bottle of wine or in a 1 liter package of fruit juice can eventually cause product spoilage (Deak 2007, Louriero and Malfeito-Ferreira 2003, Stratford 2006).

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Chapter 6

Yeast Ecology

William T. Starmer and Marc-André Lachance

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1. INTRODUCTION

Yeasts participate in a number of complex processes in ecosystems. In the classical food chain model, free-living yeasts are primarily decomposers. Typically, yeasts are among the earlier colonizers of nutrient rich substrates, where they are followed by a succession of organisms that degrade dead organic matter. However, yeasts are not just decomposers but can assume a diversity of forms and functions in the natural world. Along with their role in the transformation of nutrients, they can engage in intimate relationships with other organisms as mutualists, competitors, parasites, or pathogens. They occur together in communities or guilds linked together through intricate interrelationships. Yeasts are widely distributed throughout all biomes of the world. They have been found in the upper levels of the atmosphere (above the clouds in the stratosphere), in the deepest parts of the oceans, in aquifers under the sea, in ancient glacial ice, and are abundant throughout the phyllosphere. Associates of yeasts include viruses, bacteria, other fungi, algae, vascular plants, and animals of almost any sort. The ubiquity of yeasts on earth is complemented by their diversity, specificity for habitats, obligate relationships with other organisms, and the means by which they propagate. Understanding the ecology of yeasts has been and will continue to be an important but challenging endeavor. Yeast ecology shares a dual history; that of fungal ecology and that of microbial ecology, which may differ in many ways.

Microbial ecology can be approached in two complementary ways. One involves the description of where microorganisms propagate in nature, the types of substrates used, interactions with other organisms, and microbial influences on the habitats themselves. The other perspective applies the description and understanding of where and how microbes live and interact to gain insights into general ecological concepts, problems, and questions (Andrews 1991, 1992b). Both perspectives aid in fitting traditional yeast studies into an ecological framework that allows a comprehensive examination of basic ecological ideas and also provide insights into applied problems. In this chapter we offer both viewpoints, and thus we use complementary approaches to provide a perspective that might guide future studies in yeast ecology. We rely heavily on previous reviews of yeast ecology (Lachance and Starmer 1998, Phaff and Starmer 1980, and chapters in Rose and Harrison 1987). In the present compilation we make extensive use of the information given by Phaff and Starmer (1987) as well as Hagler and Ahearn (1987).

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Furthermore, we find two general treatments of fungal community ecology (Carroll and Wicklow 1992, Wicklow and Carroll 1981) very useful. Throughout this chapter, we shall frequently refer to information and ideas presented in those reviews and collections of articles.

The chapter is organized in four sections, each of which can to a large extent be read independently of the others. However, to avoid repetition, some material that is common to multiple sections is cross-referenced. The four sections progress from the ecology of the individual organism (autecology), to studies on the relationships of yeasts with other organisms (symbioses), competitive interactions involving the yeast-killing phenomenon (interference competition), and finally a treatment of yeast community ecology.

We do not include general recommendations for yeast isolation, purification, and identification, or sampling strategies. Although these practical considerations are fundamental in the recovery of yeasts from nature, they were effectively covered in our last review of yeast ecology (Lachance and Starmer 1998). Nonetheless, we must again stress the necessity of obtaining sufficiently large samples and the desirability of multiple isolates, not only for ecological studies, but also for the description of new taxa. This will be particularly important for future comparative ecological studies where a taxon based on the description of single or very few isolates will be almost useless. Equally important is the need to document the source material and geographic origin of yeast isolates and to preserve the information in retrievable form. Documentation of the location where an isolate was collected is now facilitated by the widespread availability of the global positioning system (GPS). When isolation substrates consist of plants or animals, they should be identified correctly and completely. Stahl and Tiedje (2002) deplored the lack of such information in the very large and frequently accessed DNA sequence databases, which they see as both a cause and a consequence of neglect of ecological data in many current studies that claim an interest in biodiversity.

2. THE NICHE AND THE HABITAT OF YEASTS

The traditional methods used to identify yeasts are rapidly being supplanted by sequence-based approaches. However, the former are essential to acquire an understanding of yeast autecology. Laboratory observations on physiological abilities, metabolic capacities, and physical-chemical limitations can be used to predict where a species might or might not be able to live. A corollary to this proposition is that growth responses can be used to infer the actual circumstances that a yeast experiences in its natural habitat. Both the proposition and the inference can be useful in autecological studies of yeasts. Three broad areas are usually observed in the laboratory:

1. catabolic activities or the capacity to acquire energy by exploiting small molecular weight organic carbon sources through alcoholic fermentation or respiration;
2. anabolic activities, or the ability to use small compounds such as nitrate to make larger ones; and
3. the tolerances to physical challenges that could preclude growth in an otherwise suitable habitat (e.g., exposure to antibiotics and the extremes of pH, temperature, osmotic pressure, and concentration of ethanol, CO_2, or other simple toxic substances).

Knowledge of all intrinsic characteristics (chemical, physical, and physiological) that describe an organism's ability to exist and persist in a habitat allows the description of its fundamental niche (Hutchinson 1957, 1959). The fundamental niche localizes a species in an abstract multi-dimensional space that defines a potential habitat. This potential can be limited by other factors, such as competing species that share the same fundamental niche. Beneficial relationships with other organisms (e.g., mutualism) can enhance the potential influence of a yeast upon its habitat. The sum of these interactions ultimately determine where a yeast actually lives, in other words, its realized niche. Ever since Wickerham (Wickerham and Burton 1948, Wickerham 1951) introduced the wide array of growth tests used in describing and identifying yeast species, the fundamental niches of different yeasts have been approximated in the laboratory. The ever-expanding surveys of yeasts in their natural habitats complement this knowledge. The information resulting from these efforts provides insights on the realized niches of yeasts and helps us understand why various species live in particular habitats.

2.1. The Niche of Yeasts

The small size of yeast cells results in a high surface/volume ratio that favors the rapid acquisition of essential nutrients by yeasts. Even though the fermentative metabolism of sugars (e.g., fructose, glucose, sucrose, maltose, melibiose, raffinose, lactose) is important to many yeasts, the oxidative utilization of a much broader variety of organic carbon compounds substantially expands the number of dimensions included in the fundamental niche. Commonly non-fermentable organic molecules, for example pentose sugars (D-xylose, L- and D-arabinose, D-ribose), methylpentoses (L-rhamnose, D-fucose), primary alcohols (methanol, ethanol, propanols), sugar alcohols (glycerol, erythritol, ribitol, D-arabitol, galactitol, mannitol, glucitol), amino sugars (D-glucosamine, *N*-acetyl-D-glucosamine, D-galactosamine), organic acids (lactic, succinic, citric, malic), and other compounds (e.g., acetone, ethyl acetate, meso-inositol, glucuronic acid), as well as straight or branched chained hydrocarbons and aromatic compounds (including anthracene, phenanthrene, and other cyclic aromatic hydrocarbons, Lahav et al. 2002) are all examples of sources of carbon that yeasts might use (Phaff and Starmer 1987).

Fungi cannot fix nitrogen. Nevertheless, some may efficiently scavenge combined forms of nitrogen from the atmosphere (Wainwright 1992). Yeasts obtain their nitrogen from either reduced or oxidized forms and use them for anabolism of proteins, nucleic acids, and other essential nitrogenous components of the cell. The ability to assimilate various nitrogen sources (e.g., nitrate, nitrite, ethylamine, lysine, creatinine, creatine) as in laboratory tests adds another set of dimensions to the yeast fundamental niche and provides further insight into the types of habitats that yeasts occupy.

Yeasts are usually tolerant to broad pH ranges and are often found at the acidic end of the scale where many bacteria are not able to compete. However, truly thermophilic yeasts remain unknown. Rarely can they grow above 42°C and those that do may occupy specialized habitats such as the intestine of warm-blooded animals (Watson 1987). There is little doubt that tolerance to high osmotic pressure or high salinity is an important niche dimension, as this single factor can determine the occupation of broad habitat types, namely marine versus fresh water, and high versus low sugar materials. Tolerances to antibiotics and some surface-active compounds have also provided useful fundamental niche descriptors that help us understand why certain yeasts can or cannot occupy a habitat.

Narrow fundamental niches define physiological specialists. For example, yeasts that initially colonize fruit, such as *Hanseniaspora* species, have limited physiological abilities. They ferment and respire glucose vigorously, utilize cellobiose as a source of carbon, and require an external supply of vitamins. In spite of the physiological specialization imposed by this narrow fundamental niche description, these species have a wide distribution in nature, due to the common occurrence of the corresponding habitat (i.e., decaying fruit are numerous, available from many different plants, and exist in many different places). The realized niche, the place where *Hanseniaspora* species are actually found, is relatively narrow in terms of habitat type (fruit), but the physiological specialization described by the fundamental niche leads to a general realized

distribution in space and time. A similar example of specialization resulting in a general distribution would be an insect that eats only the growing point (apical meristem) of plants because this tissue has not grown sufficiently to accumulate chemical deterrents. As a consequence this feeding specialist becomes a host-plant generalist.

Alternatively, physiological specialization (a narrow fundamental niche) in conjunction with vector behavior or host distribution can lead to a narrow realized niche. The yeast *Cyniclomyces guttulatus* has restricted nutritional requirements and unique requirements that limit the species to growth in the stomach lining of domestic and feral rabbits, guinea pigs, and chinchillas (Zierdt et al. 1988). The coprophagous habits of the hosts confines the yeast further to a narrow realized niche.

Some yeasts with broad fundamental niches are also broadly distributed. For example, the polytrophic species *Debaryomyces hansenii* is found in many habitats (soil, water) in association with plants and animals, and as a consequence is broadly distributed. This species is the most common ascomycetous yeast found in marine waters where its fundamental tolerance to high salinity (Prista et al. 2005) potentially contributes to it being found in that habitat (Hagler and Ahearn 1987).

These examples illustrate the fact that the dimensionality of the fundamental niche may not always translate directly into an equivalent realized niche (McNaughton and Wolf 1970, McNaughton 1981). It is thus useful to supplement information on the fundamental niche of a yeast with a knowledge of its means of dispersal and its interactions with other microorganisms.

Lachance and Starmer (1998) emphasized the importance of distinguishing yeasts that actually reside in a habitat from those that are transient or fortuitously found there. Those that grow and persist in a habitat (originate within the system) are referred to as autochthonous whereas those that are "accidental" are allochthonous (originate outside the system). Yeast species that are recovered repeatedly from the same habitat in such numbers that it is clear that they grow in that habitat can be considered autochthonous. This distinction may be difficult to draw, especially when general habitats that can serve as reservoirs (e.g., soil and water) are the only reported source of isolation without much additional information.

There is no doubt that the future of yeast ecology is aided by results of surveys and by descriptions of new taxa that emerge from exploring new habitats and previously unsampled regions of the world. Descriptions that include conditions, habitats, locations, co-inhabitants, and the distribution of similar forms are critical for the advancement of our understanding of yeast ecology. New areas of research are facilitated by the possibility of obtaining in-depth knowledge of a yeast's fundamental niche, realized niche, habitat, biogeography, and phylogenetic history. For example, knowledge of a yeast's phylogeny allows us to address new issues, such as the effect of habitat history on the present fundamental and realized niches of a yeast. Co-mapping yeast habitats and fundamental niche dimensions onto phylogenies or clades can study this question. It is now possible to infer the origins of the members of yeast communities. This has been investigated in the cactophilic yeast community by mapping habitats onto the phylogeny of each community member (Starmer et al. 2003). One may ask whether there is a relationship between phylogeny and community organization. Anderson et al. (2004) approached this question by comparing abundance relationships of yeasts in a community as a function of their phylogenetic distance inferred from cladograms. These newly emerging areas are discussed in the yeast community ecology section of this chapter.

2.2. Yeast Habitats

Broadly speaking, habitats can be characterized as atmospheric, aquatic, or terrestrial. Further subdivision of these types into biotic realms would include associations with plants, animals, and other fungi. Additional abiotic divisions include surfaces, soil, and subsurface habitats in the terrestrial category, or marine, estuarine, fresh water, and ice habitats for the aquatic type. Many yeasts occur in close associations in mixed communities. These are described and discussed in the sections on yeast symbioses and yeast communities. In this section we shall only outline generalities applicable to the broad habitat types and point out the conditions that make them suitable for occupation by yeasts.

2.2.1. Atmospheric Yeasts

Yeasts have been recovered from the atmosphere. This outer layer of the earth is clearly a reservoir or a place of transition rather than a site for growth and reproduction. For example, red yeasts have been recovered from the upper layers of the atmosphere, 18–30 km in the stratosphere (Bruch 1967), but they are unlikely to grow there. Records of this sort show the extraordinary survival abilities of some taxa, particularly the pigmented yeasts. Interestingly, some studies have suggested that some yeasts reproduce in fog (*Rhodotorula* species, Fuzzi et al. 1997). The atmosphere is undoubtedly much more important as an element of dispersal for basidiomycetous yeasts than for ascomycetous yeasts, due to differences in dispersal adaptations by the two yeast types. In general ascomycetous yeasts rely on vectors such as insects to move from habitat to habitat while basidiomycetous yeasts may use vectors (e.g., insects) or in some cases ballistocondia are discharged to passively disperse in air currents.

2.2.2. Aquatic Yeasts

Yeasts exhibit excellent survival in water. Storage in distilled water is an easy and sometimes a suitable means of preserving a yeast culture (McGinnis et al. 1974). In 1972, cells of *Rhodotorula rubra* were transported to outer space on the Apollo 17 mission. The cells were exposed to the vacuum of space and subsequently stored in sterile water for return to earth. After 27 years in aqueous suspension the cells were shown to be viable (Volz and Parent 1998). Cells of *Rhodotorula mucilaginosa* exhibited a mean survival of over 600 days in river water (Peter and Peter 1988). *Rhodotorula* species have been isolated from deep igneous rock aquifers, 200–400 m below the surface in the Baltic Sea (Ekendahl et al. 2003) and also from deep ice cores of Greenland glaciers at extraordinary depths (2000 m below the glacial surface). These ice yeasts had survived in frozen water under extreme pressures for more than 140,000 years (Starmer et al. 2005a).

Yeast densities in water are astonishing. Hagler and Ahearn (1987) reported average counts of 500 cells per liter for rivers, 100 for lakes, and 10–50 for seawater, whereas urban estuaries can have considerably more (2.8×10^3). Large amounts of glacial ice have yet to be examined, but a limited sampling from the Greenland ice sheet recovered 1–10 colony-forming units per liter (Starmer et al. 2005a). Using a conservative estimate of one yeast cell per liter of water and calculated volumes of water in its major sources on earth (Debenedetti and Stanley 2003), we estimate the total number of yeast cells to be in the order of a quadrillion (10^{15}) in rivers to a sextillion (10^{21}) in the oceans. Somewhat unexpectedly, polar ice caps are second to oceans with 10 quintillion (10^{19}) yeast cells, and lakes are third with 10^{17} cells. To place this in perspective, global annual precipitation (rain, snow, freezing rain, sleet, and hail) involves approximately 2.2×10^{17} liters of water per year.

Interestingly, the global number of yeast cells in water (10^{21}) is comparable to the numbers estimated to occur on leaf surfaces. The global leaf area index (LAI) is a dimensionless number used to express leaf area coverage in m^2 per m^2 of land area. Data gathered

over a 68-year sampling period (summarized by Scurlock et al. 2001) generate LAI values that range from 1.31 for deserts to 8.71 for tree plantations. The mean LAI across biomes is approximately 5. Assuming a value of 5 for LAI and a value of 1.5×10^8 km^2 for the total land area on earth (Coble et al. 1987), there are approximately 10^{16} cm^2 of leaf surface available on the earth at any one time. Typical yeast counts on leaves range from ca. 10 to 10^4 per cm^2 (e.g., Shivas and Brown 1984) and thus the total number of yeast cells in the phylloplane is ca. 10^{17} to 10^{20}. This is comparable to the number estimated for the major water sources of the earth. Most phylloplane yeasts are basidiomycetes that move from leaf to leaf by passive air dispersal.

Hagler and Ahearn (1987) emphasized the common occurrence of red yeasts in aquatic environments. Most of these yeasts are in the genus *Rhodotorula* but species of *Rhodosporidium* and *Sporobolomyces* are often found. The authors reasoned that some of the red yeasts may be washed into water from terrestrial sources, especially the phyllosphere, and suggest also that some of the marine yeasts may be associated with marine plants. Factors that may favor abundance of *Rhodotorula* species in the oceans include their osmotic tolerances (Gupta 1996, Hernandez-Saavedra et al. 1994, 1995) and their ability to withstand the high pressures (40 MPa) characteristic of the abyssal depths of the ocean (Gross et al. 1994, Lorenz and Molitoris 1997). As mentioned earlier, the most common ascomycetous yeast in marine waters is *Debaryomyces hansenii*. The broad salinity tolerance (as part of its wide fundamental niche) of this yeast is probably important to its widespread distribution in the ocean. *Debaryomyces hansenii* is often recovered as an occasional member of plant yeast communities and was the major ascomycetous yeast species recovered in fresh frass of various leaf-eating caterpillars in Costa Rica (M. A. Lachance and D. Jansen, unpublished data), which again points to a connection between the phylloplane and marine waters as yeast habitats.

Yeasts in water have both negative and positive associations with plants and animals that live there (Hagler and Ahearn 1987). Yeast numbers in plankton-rich waters exceed those in other areas of the open ocean, and yeasts are numerous in decaying macroalgae, including kelp. However, algae produce and excrete not only nutrients that support yeast growth, but also compounds that interfere with yeast growth (Hagler and Ahearn 1987).

The list of aquatic animals from which yeasts have been isolated is long (clams, mussels, shrimps, isopods, amphipods, crabs, sponges, sea urchins, polychaete worms, fish, dolphins, whales, penguins, gulls, and terns; see Hagler and Ahearn (1987) for references) and no doubt would be longer if more animal associations were studied. The yeasts from these sources are also typically found in water, but not always. This latter observation suggests possible symbiotic relationships between yeasts and aquatic animals. For example some yeasts, such as species in the genus *Metschnikowia,* may be pathogenic to planktonic crustaceans (Lachance et al. 1976, Ebert et al. 2000a, 2000b) and have been implicated in the infection and ultimate death of fish (Chen et al. 2003, Moore and Strom 2003). However, yeasts involved in the mutualism and parasitism of aquatic animals have not been as extensively studied as they have for terrestrial animals.

Fell (1967, 1974a, 1976) and colleagues (Fell and Statzell 1971) have extensively studied yeasts in specific water masses in the Indian and Antarctic Oceans. These observations are detailed in a comprehensive review of yeasts in oceanic regions (Fell 1976). Among the findings are the notable ubiquity of some species (e.g., *D. hansenii*) in all oceanic regions and the specificity of others in particular water masses (e.g., *Leucosporidium antarcticum*). This review emphasizes our lack of knowledge on the role of yeasts in the oceans and provides interesting pathways for investigations into the ecological reasons for the observed broad scale and restricted distributions of oceanic yeasts. The potential for abiotic influences such as temperature and salinity are discussed along with biotic factors, such as productivity, algal blooms, and proximity to coastal regions, where estuaries and the drainage of rivers may have significant influence on the yeast communities near the shore.

2.2.3. Terrestrial Yeasts

Land plant tissues (stems, flowers, and fruits) are rich in organic compounds and moisture, and consequently provide a favorable environment for yeast growth. Likewise, exudates of leaves, roots, flowers, and tree trunks are good habitats in which yeasts flourish. Many yeast species that are found in live or decaying plant parts are associated with insects that also use these habitats as feeding or breeding sites. In general these three-part associations (insect–yeast–plant) are maintained by reliance on reciprocal benefits exchanged by the insect–yeast partners. Often the yeast supplies essential nutrients or beneficial supplements to the insect while the insect provides transportation of the yeast to new habitats. However, when the insect–yeast partners are obtaining their needed nutrients from dead, moist, organic material, the system is part of the saprotrophic channel of the ecosystem and thus the plant is not a part of the symbiosis.

Previous reviews (Lachance and Starmer 1998, Phaff and Starmer 1987) provide additional information on yeasts in soil, tree exudates, tanning liquors, necrotic cactus tissue, flowers and fruits of higher plants, as well as yeasts that are pathogenic to plants. The section on symbiotic associations in this chapter describes and discusses yeast–insect mutualisms that often involve plant tissues, whereas the section on yeast communities details our knowledge of several well-studied systems (cactophilic yeasts, flower yeasts, phyllosphere yeasts, and yeasts associated with bark and ambrosia beetles).

Soil has been extensively sampled for yeasts because of its general importance in ecosystem processes and because of its easy access. Nevertheless, the diversity of soil types and environmental conditions make soil a complex and difficult habitat to study. Soils occur in diverse climates, have different chemical compositions, can vary across microscopic as well as geographic scales, and are differentially influenced by the activities of local plants and animals that live in them. Phaff and Starmer (1987) pointed to the early review of soil yeasts by do Carmo-Sousa (1969a) as a "fairly up-to-date picture of yeasts found in soils". Even now we find that the earlier reviews capture the essence of yeast soil-ecology. Some generalities about soil yeasts include:

1. Yeasts occur in small numbers relative to bacteria and other fungi. Many studies relegate the yeasts to the status of minor contributors to soil ecological processes such as carbon recycling and mineralization.
2. Capsulated forms of yeasts (*Cryptococcus*, *Lipomyces*, and *Rhodotorula* spp.) survive better than other forms found in soil. For instances, *Cryptococcus vishniacii* is indigenous to the dry valleys of Antarctica (Vishniac and Hempfling 1979a). This species is psychrophilic and its phenotype shows an adaptation to the highly stressed soils present there.
3. Yeasts are limited to the upper surface of soil (5–15 cm) and are rare in deeper layers. Species of *Lipomyces* are exceptional by being more abundant in lower moist mineral horizons of soils collected from a diversity of sites (Danielson and Jurgensen 1973). The distribution of *Lipomyces* spp. was thought to result from the inability to compete for readily available nitrogen near the surface of soil. In addition, *Lipomyces* species were judged to favor conditions where organic matter is relatively well decomposed.
4. Sporulating taxa have an advantage in soil due to their higher tolerance to desiccation and temperature extremes.

5. Some taxa appear to be specific to soil and are likely autochthonous. These include *Lipomyces* spp., the monotypic genus *Schizoblastosporion*, and *Schwanniomyces* spp.
6. Many taxa that are found in soil also live above the soil surface (e.g., in decaying fruits, on leaves, and in association with trees) and are incorporated into soil by a variety of mechanisms (e.g., passive dispersal, wash water, and insects). These allochthonous yeasts are not likely to be important to the nutrient cycling that occurs in soil and as such they have less importance to the study of yeast ecology. However, some yeasts that reside in soils may become important to soil processes when soil amendments are added, naturally or by human intervention. For example, heterotrophic nitrification occurs when sugars are added to soils containing *Barnettozyma* (*Williopsis*) *californica* (Wainwright and Falih 1996). Thus the importance of these yeasts in agricultural soils should not be overlooked.

Because of the diversity and abundance of terrestrial arthropods, it is no wonder that they should enter into numerous associations with yeasts and that their relationships with yeasts should be diverse and complex. We discuss several of these in detail in the sections on symbiosis and yeast community ecology. Nevertheless it is appropriate to emphasize the availability of a multitude of opportunities for insightful studies on many aspects of yeast ecology by investigating natural biological systems involving animals and yeasts. For example, we chose to study the cactus–yeast–*Drosophila* and the flower–yeast–beetle systems because they held potential answers to fundamental questions about ecology, evolution, and ecological genetics. Some of the attributes of an appropriate and useful system are the ability to obtain adequate samples in space and time, the possibility of bringing them into the laboratory, and their suitability for making inferences about natural processes and functions. Three of the outstanding features of using a plant–yeast–insect system are; 1) their discrete nature, 2) the ability to examine several magnitudes of scale, i.e., from micro samples to global distributions, and 3) the ability to compress the time dimension. These features allow the ecological and evolutionary time scales to be merged and thus provide a means of studying evolutionary ecology.

The famous essay by Theodosius Dobzhansky (1973) "Nothing in Biology makes sense except in the light of Evolution" is often quoted to remind us of the importance of understanding evolution when asking questions about causal factors in biology. A corollary to this notion is: "Nothing in Evolution makes sense except in the light of Ecology". Such a connection is possible when studying microbial systems. Those involving yeasts are certainly appropriate and investigations that link both sciences deepen our comprehension of the ecology and evolution of all organisms. Recent conceptual ideas about "niche construction" (Odling-Smee et al. 2003) provide a framework for understanding how organisms influence their own niches and thus their own evolution. This dynamic connection between niche and organism throws a different light on the evolutionary process and thus offers an interesting perspective for future studies on yeast ecology. In the next section we review yeast symbiosis, which provides an important perspective on how the fundamental niche is influenced by relationships with other organisms.

3. SYMBIOSIS

Anton de Bary (1879) described symbiosis as an intimate relationship between different species living together. The influence of the relationship on an individual in the partnership can be positive (+), negative (−), or of no consequence (0). These influences are usually taken to be constant over the lifetime of the association. However, if the relationship changes, then the overall cost or benefit to both participants will determine if the symbiotic relationship is mutualistic (+, +), parasitic (+, −), commensal (0, +) or amensal (0, −). Free-living species that experience competitive (−, −) or predator–prey/pathogen–host (+, −) interactions are not usually treated as symbionts. However, the distinction may be clouded by circumstances where, for example, a parasite becomes a lethal predator, or roles are reversed during the lifetime of the participants. Even mutualism and parasitism are thought to be part of a continuum in certain ecological circumstances (Johnson et al. 1997) and mutualism is thought to evolve in some cases from an initial parasitic association. Yeast–yeast competitive interactions that involve the killer-yeast phenomenon are treated in a separate section.

Ultimately the net population-level cost or benefit of a symbiotic interaction will determine the significance of a species–species relationship. A symbiosis may change its character from direct to indirect as a consequence of dynamic habitat modifications or when other organisms join the interaction. Indeed some old complexes of organisms have evolved three-part, or even four-part, complex symbiotic interactions. For example, the attine ant–microbe symbiosis involves ants that have an obligate mutualistic relationship with fungi (Basidomycotina) that they transport, cultivate, and protect as a garden crop (Currie et al. 2003, Gerado et al. 2004). Worker ants cut young leaves or flower parts and transport them to their underground gardens. Leaf segments are chewed into a pulp and inoculated with drops of the ant's anal exudates. This mixture is used to start, supplement, and maintain the fungal crop. The garden provides the ants with nutrition but is sometimes parasitized by microfungi in the genus *Escovopsis* (Ascomycotina). This parasite invades and consumes the fungal cultivar. The parasite is detrimental to both the ants and the fungal garden, and even though the parasite is removed from the gardens by the ant, it can persist. The ant, however, is aided by a filamentous actinomycete bacterium (*Streptomyces* sp.) that is distributed over the ant's exoskeleton (Currie et al. 1999). The bacterium produces antibiotics that are specifically active against the *Excovopsis* parasite of the fungal garden. These symbiotic relationships (direct and indirect) have evolved over 50 million years and represent a complex interplay of microorganisms and insects. Figure 6.1 depicts the relationships among the four organisms representing three Kingdoms (Animalia, Fungi, and Bacteria) and if one considers the plant material that is required for the gardens, then four Kingdoms are involved.

Three questions are central in understanding the ecology and evolution of species–species interactions:

1. Who are the participants and what are their phylogenetic origins?
2. What is the nature of the relationship that causes the interactions and how does it work (i.e., what is the mechanism)?
3. How is the relationship between the participants maintained over generations?

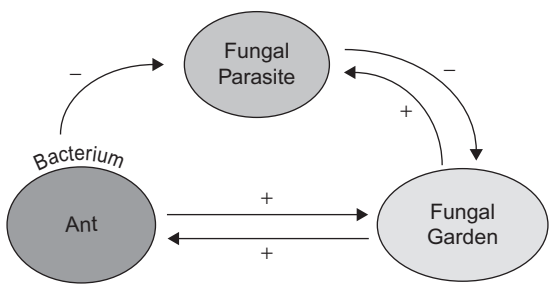


FIGURE 6.1 Symbiotic relationships among four organisms (ants, fungi, bacteria, plants) involved in ant–fungal mutualism.

These three questions (origins, mechanisms, and maintenance) have not been studied in a balanced fashion in yeasts because of several difficulties. In some cases separating the species involved in a symbiotic relationship is desirable because by studying each species in isolation we may discover the nutritional requirements of each species and thus the potential mechanisms responsible for the relationship. When the relationship is obligate this study has not been possible. Furthermore, until recently, the evolutionary origins of obligate symbionts would have been a matter of pure speculation as cultures were not available for study. Finally, understanding maintenance requires detailed investigations on physiological and behavioral traits in nature and the laboratory.

3.1. Mutualism (+, +)

Carroll (1992) discusses the benefits received and provided by fungi involved in mutualistic associations. He emphasizes harvest mutualisms as a common mode of symbiosis where heterotrophic fungi receive fixed carbon and often nitrogen (as in the case of cyanophycophilous lichens), but benefits at the level of dispersal may also be important, especially in fungus–insect mutualisms that involve the saprophytic use of plant tissues.

Benefits provided by the fungus to its partner are categorized by Carroll (1992) as

1. harvest mutualisms: benefits are supplied by decomposing, concentrating, and liberating substances such as essential nutrients necessary for growth, survival, and reproduction;
2. protective mutualisms: the fungus provides protection (either by mechanical or chemical means) from toxins, parasites, predators, or abiotic hazards;
3. combative mutualisms: the fungus produces deterrents that mitigate intra- or interspecific competition;
4. physiological enhancement: benefits come from inducing greater tolerance to climatic condition such as drought; and
5. habitat conditioning: the fungus enhances the habitat for successful occupation by its partner.

Harvest mutualisms are probably common between insects and yeasts because arthropods often require nutrients that they cannot synthesize on their own (Buchner 1965). Molecules such as sterols are not synthesized by insects, but are needed for membrane construction and as precursors of hormones. As a consequence an exogenous source of these important molecules is required. Symbionts may provide the necessary sterols (Pant and Fraenkel 1958), a supply of vitamins (Fraenkel and Blewett 1943), or other required components of the diet such as essential amino acids (for a review see Cooke 1977, Douglas 1989).

The qualitative needs of an organism can translate into quantitative needs when essential nutrients are scarce or distributed homogenously at low levels in the habitat. For instance, insect larvae that forage on substrates with low levels of nitrogen can benefit from filter feeding and in effect concentrating the nitrogen that fungal or yeast cells have assimilated during their growth in the substrate. An example of this comes from studies of yeasts associated with the larval substrate of cactophilic drosophilids. The larvae forage on decaying cactus tissues that generally have a homogeneous nitrogen content of 0.3 to 0.5% (dry weight). The yeasts that grow in the decaying tissue take up and accumulate nitrogen from their immediate vicinity to a final concentration of ca. 8% (dry weight). Larvae can increase their nitrogen intake 16–26 times by selectively feeding on yeast cells in the decaying tissue (Starmer and Aberdeen 1990). In some cases adults can concentrate yeast cells during feeding by harvesting hydrophobic yeasts that rise to the surface of the rotting tissue (Vacek et al. 1979). As a consequence, the nutrients required by females for egg formation are concentrated. Adult drosophilids have, on the end of their proboscis, a spongy labellum that is used to rasp and collect liquid and suspended particles from semi-liquid decaying tissues or exudates. The labellum is constructed of pseudotracheae that apparently serve as a sieve when the proboscis is retracted and the food is directed to the insect crop. A study of cactus rot juices ingested by adults in nature showed that the ratio of bacterial cells to yeast cells in the juice was about 10:1, whereas the crop contents of adults feeding on the same juice was reversed (1:10). Thus the more nutritious yeasts are concentrated by filter feeding (W. T. Starmer, unpublished data). This feeding strategy is employed by diverse organisms (e.g., baleen whales, clams) that consume scarce or widely distributed nutrients.

Not all symbiotic relationships between fungi and insects are harvest mutualisms. For example *Septobasidium* sp. (Septobasidiales, Basidiomycota) is an obligate symbiont of scale insects. The fungus grows over the top of the insect that has pierced the plant surface with its stylet to suck phloem sap. The living chamber made of fungal hyphae provides protection for the scale insect from parasitoids such as wasps (Seifert 1981), so it is an example of habitat conditioning. As the scale insect gains nutrients from the plant phloem, individuals that are infected by the fungal haustoria provide nutrients to the fungus. Those individuals are rendered non-reproductive as a consequence of the infection. Ultimately the fungus produces basidiospores (Couch 1938) in the form of yeast-like buds that stick to the bodies of scale insect nymphs. The nymphs start new colonies and disperse the fungus (Paracer and Ahmadjian 2000). In summary, the scale insect gets nutrients from the plant and protection from the fungus, whilst the fungus gets nutrients from some of the insects and is also dispersed by them. The reproductive sacrifice by the insect is seen as an example of kin selection, whereby the inability of infected individuals to reproduce is compensated by their role in propagating a fungus that protects the uninfected kin.

3.1.1. Yeast-like Symbionts (YLS)

Yeasts and yeast-like symbionts have been found in association with many different animals, particularly in the phylum Arthropoda. This includes diverse orders of the class Insecta (Coleoptera: beetles; Diptera: flies and mosquitoes; Homoptera: aphids, planthoppers, and scale insects; Hymenoptera: ants, bees, and wasps; Isoptera: termites; Lepidoptera: moths and butterflies; Neuroptera: lacewings; Orthoptera: roaches) as well as the classes Arachnida (spiders), Diplopoda, and Crustacea. Much of the attention has focused on the members of the insect orders Homoptera and Coleoptera that carry many interesting intracellular yeast-like fungi (Shankar and Baskaran 1992, Fukatsu and Ishikawa 1995, Jones et al. 1999, Nasir and Noda 2003, Noda et al. 1995, Noda and Kawahara 1995, Noda and Kodama 1996, Sasaki et al. 1995).

Most yeast-like symbionts are carried by insects in specialized cells termed mycetocytes that are grouped together in mycetomes located in evaginations of the midgut, in alimentary tract epithelia, or other body parts of the insect. The transfer of the yeast endosymbionts to new individuals can be accomplished by several methods, namely 1) licking and stroking of offspring, 2) coating the external egg surfaces during oviposition (via structures in the ovipositor), and 3) egg cell cytoplasm carrying the symbiont (Paracer and Ahmadjian 2000).

Until recently, descriptions of many yeast-like symbionts were only based on their morphologies in the host because they could not be independently cultivated. Modern molecular techniques, especially sequence amplification by PCR, have now made it possible to sequence their DNA and thus compare them with free-living fungi.

Now that the symbionts can be compared, we are learning that similar forms can have different origins and are the result of convergent evolution (Jones et al. 1999). Many of the symbionts provide nutritional benefits to their host and are thus harvest mutualists, although some provide additional benefits.

The yeast-like endosymbionts of planthoppers (Homoptera) are most likely evolved from filamentous ascomycetes (Pezizomycotina) even though their morphology might suggest an affinity with the Saccharomycotina (Suh et al. 2001). Aphids (Homoptera) all possess symbiotic microorganisms. Most have bacterial intracellular symbionts contained in mycetocytes, but some aphids (tribe Cerataphidini) have extracellular yeast-like symbionts that are phylogenetically related to those found in planthoppers (Fukatsu and Ishikawa 1996, Suh et al. 2001).

Honeydew-excreting aphids and their symbiotic yeasts are linked to honeydew-feeding insects and their yeast symbionts. For example, certain species of Chrysopidae (Neuroptera) depend on honeydew for sustenance and egg production (Hagen et al. 1970, Hagan and Tassan 1972). However, the honeydews lack certain amino acids required by the adults and yeasts are required to make up that deficiency in their diet. In adult *Chrysopa carnea* (green lacewings) the extracellular yeast symbionts are found in the adult crop, where they propagate at the expense of the honeydew ingested by the insect. Interestingly the larval stages of *C. carnea* are carnivorous predators on other insects that visit the plant leaves and the larvae do not carry the symbiotic yeasts. The yeasts in the adult crops are transferred from adult to adult by trophallaxis via regurgitation of droplets containing yeasts. The adult-to-adult transfer occurs before mating and thus provides a potential means of propagating yeast populations from generation to generation. This behavior may be necessary because *C. carnea* overwinters in the adult stage and not as eggs, larvae, or pupae. Notable is the observation that other predaceous *Chrysopa* spp. that do not overwinter as adults do not have symbionts.

In many situations mutualisms are based on a combination of benefits that solve one or more problems. For example it has been suggested that yeast-like endosymbionts in brown planthoppers convert nitrogenous waste products of the insect into useful compounds (Saski et al. 1996). In this case the honeydew-feeding insect does not excrete the uric acid that it synthesizes, but stores it in tissues where it is recycled by the yeast-like endosymbiont into compounds with nutritional value. This is similar to the process used by symbiotic bacteria associated with cockroaches and termites (La Fage and Nuttings 1978). Even the hindgut of millipedes (diplopods) has been shown to contain yeasts that are presumed to use carbon sources in the leaf-litter and also may hydrolyze uric acid (Byzov et al. 1993).

An interesting example of a potential combative mutualism is the case of two yeasts, *Kuraishia* (*Pichia*) *capsulata* and *Ogataea* (*Pichia*) *pini*, associated with the bark beetle *Dendroctonus ponderosae*. In this case both yeasts can convert the female aggregation pheromone (cis- and trans-verbenol) into verbenone. The yeast product (verbenone) is an anti-aggregation pheromone and thus the microbial symbionts terminate aggregation and the mass attack on the host tree (Hunt and Borden 1990). Ultimately the reduction in aggregation of beetles diminishes population growth and intra-specific competition.

3.1.2. Phyllosphere Mutualisms

Even though the yeasts present on leaves are considered either epiphytes (commensals) or saphrophytes (decomposers), some species may act as protective mutualists under some circumstances because of their negative influence on potential pathogens (Lockwood 1992, Fokkema 1976, Fokkema et al. 1983, Martin et al. 1993, Warren 1972, Dik and Van Pelt 1992). The presence of aphid honeydew on leaf surfaces stimulates an increase in the abundance of phylloplane yeasts (e.g., *Sporobolomyces roseus*) and in pathogens such as the ascomycetous mold *Cochliobolus sativus*. Under experimental conditions Fokkema et al. (1983) showed that the naturally occurring phylloplane yeasts prevented establishment of pathogens. The mechanism for this competitive inhibition is probably the consumption of carbohydrates by the saprophytes and thus the yeast serves as a nutrient sink. Competition for space could also be a factor. However, because only a small proportion (1 to 10%) of the leaf surface is colonized by leaf microbes, space may or may not be important (Macauley and Waid 1981).

The yeasts that inhabit leaf surfaces may also affect insects. Martin et al. (1993) showed that the European corn borer was deterred from ovipositing on maize leaves when increasingly large populations of *Sporobolomyces roseus* were experimentally sprayed on leaf surfaces. The authors concluded that the change in egg laying behavior was possibly a result of the removal, by yeast, of nutrients that are important for the induction of oviposition, chemical deterrence, or interference with adequate access to the leaf surface. Not all saprophytic yeasts on leaf surfaces provide protection. Parker and Blackeman (1984) showed that some yeasts enhance the growth of rusts on broad beans, such that the yeasts and rust may be mutualistic partners.

Phylloplane yeasts may represent a life form that changes from one type of ecological interaction to another as its habitat changes. For instance, epiphytes residing on leaves of deciduous trees are joined by other fungi and become saprophytes when the leaves drop and start to decay in the upper layer of the forest floor. The subsequent process of nutrient recycling in the saprophytic channel of the ecosystem is an important indirect role of many fungi that are associated with leaves. Fungal decomposers are thought to drive the global carbon cycle and phylloplane yeasts ultimately participate in that process in one way or another. However, the role of phylloplane yeasts in soil processes may not be significant because many only join the upper layers of soil and do not persist in soil after leaves fall (di Menna 1959).

The examples given above involve a potentially complex set of symbiotic interactions taking place on the surfaces of plant leaves. The diagram (Fig. 6.2) summarizes these interactions and shows how three different types of yeast symbionts can influence the system and, indirectly, one another. The arrows in the diagram indicate beneficial (+) or detrimental (−) influences on the organism at the tip of

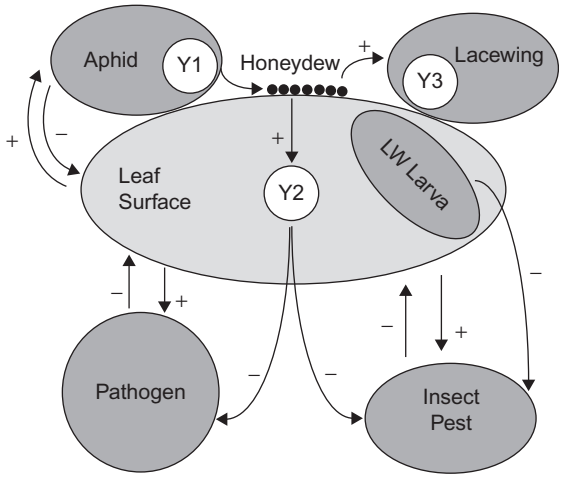


FIGURE 6.2 Complex set of potential symbiotic interactions taking place on the surfaces of plant leaves.

the arrow. In this diagram the leaf or plant is the ultimate source of energy for all participants and the leaf status will influence the health of the plant. Aphids on the leaf initially will have a detrimental effect on the plant due to extraction of fluids that could be used for growth and survival of the plant. Aphids generally have bacterial symbionts (Baumann et al. 1995, Douglas 1998) but some also have yeast symbionts (Y_1) that supply beneficial nutrients (Fukatsu and Ishikawa 1996). The honeydew that is excreted by the aphid is a carbon-rich waste product which accumulates on leaf surfaces. This potential source of energy affects the phyllosphere microbiota (e.g., Stadler and Müller 1996). The honeydew is particularly beneficial to both epiphytic yeasts (Y_2, e.g., *Sporobolomyces* spp.) that grow on the leaf surface, and to honeydew-feeding insects such as the green lacewings mentioned above. The lacewings also have symbiotic yeasts (Y_3) associated with the adults, whereas the larval stages are free of yeasts. The epiphytic yeasts (Y_2) can deter both fungal pathogens and insect pests of the plant, while the larval stages of the lacewing are predaceous on insects that come to the leaves (e.g., insect pests of the leaves). Depending on which other organisms are present on the leaves, the symbiotic yeasts have diverse influences on the ultimate health (survival and reproduction) of the plant and thus the processes in the phyllosphere ecosystem.

Phyllosphere fungi have been used to study ecological theories rather than just ecological relationships. For example, John Andrews and his colleagues (Andrews et al. 1987, Kinkel et al. 1987, 1989a, 1989b) used apple leaves as islands to study the predictions of the Theory of Island Biogeography (MacArthur and Wilson 1967). They found that a species turnover occurs and an equilibrium number of species ($\sim$12) is achieved. These results are consistent with what is predicted by the theory. However, they did not find the relationship between leaf area (island size) and the number of species predicted by the theory.

3.1.3. Diffuse Mutualisms

Research on the association of *Drosophila* and yeasts has uncovered a number of symbiotic relationships. The prevalence of yeasts in the diet of *Drosophila* was recognized early in the last century (Baumberger 1917, 1919, Delcourt and Guyenot 1910, Northrup 1917). These observations on yeasts and *Drosophila* were followed by two lines of inquiry, namely studies of the nutritional value of yeasts to larvae and adults (Sang 1956, 1978) and surveys of yeasts in the natural habitats of the flies (reviewed by Begon 1982). The general conclusion was that yeasts associated with *Drosophila* rely on the flies for dispersal and the flies rely on the yeasts for nutrients. Beneficial nutrients supplied by the yeasts to the flies are primarily sterols, vitamins, and concentrated nitrogen needed during larval development and maturation of eggs in adults. Thus, *Drosophila* species and their yeasts are engaged in a mutualistic relationship. However, because the mutualism is not species-specific, as a community of yeasts is associated with one or more *Drosophila* species, the mutualism is diffuse.

Investigation of the cactophilic yeasts and their associated drosophilids was initiated in the mid-1940s by Wagner (1944, 1949). Subsequent interest by W. B. Heed, H. J. Phaff, and their colleagues (Barker and Starmer, 1982, Barker et al. 1990, Lachance et al. 1988b) has revealed a complex set of interactions between the flies and their yeasts that link them in multiple mutualistic categories. In addition to the direct nutritional benefits provided to the flies (i.e., harvest mutualism), other factors contribute to mutualism:

1. *Drosophila* larvae disperse yeast cells within the decaying tissue of the host during their foraging activity. Even though the larvae are consuming the yeasts, their activity encourages yeast growth in new areas of the expanding rot, and the yeasts benefit by the resulting increase in numbers. This behavior is not random but selective, as demonstrated by the larval feeding preference for certain yeasts, in nature and the laboratory (Fogleman et al. 1981, 1982). Adult drosophilids disperse yeasts from host to host in a cactus-specific manner and, even though other insects can be involved, the cactophilic *Drosophila* carry a more diverse array of yeast species in larger numbers when compared to other cactophilic insects (Ganter 1988, Starmer et al. 1988a).
2. *Drosophila* adults use yeast products as attractants and cues for oviposition (Armstrong 1992, Barker et al. 1994, Barker and Starmer 2000, Vacek 1982). Yeast volatiles seem to be used in two different manners. One is as a cue for available habitats (rot pockets) locally or attractants for long-distance dispersal. The other is a cue for selecting an appropriate patch within the rot pocket for egg laying (Barker et al. 1994). The differential response to alternate types of yeasts for oviposition is heritable in *Drosophila buzzatii* (Barker and Starmer 2000), i.e., some prefer to lay eggs on tissue with *Pichia cactophila* colonies, while others are selective for tissue with *Sporopachyderma cereana* growth present. This genetic linkage provides possibilities for evolutionary diversification of the symbiotic relationship between the two organisms via habitat selection.
3. Yeasts in the cactus rots can modify or eliminate toxic secondary chemicals which form during the decay process. Two situations have been investigated. The first is the unusual medium-chain length fatty acids (C_8 to C_{12}) that are present in organ pipe cactus tissue (Kircher 1982). There are no higher-chain length (normal) fatty acids in the tissue, and the C_8 to C_{12} fatty acids are bound as esters in the live stem tissue. When the tissue decays, the bound fatty acids are released and in the protonated form (i.e., at low pH) they are toxic to most yeasts and to fly larvae. The common cactus yeast, *Candida ingens* [teleomorph *Magnusiomyces* (*Dipodascus*) *starmeri*], is capable of metabolizing the fatty acids, and experiments have shown that the yeast can alleviate the detrimental effect of these toxic compounds (Starmer et al. 1982). The second circumstance is the detoxification of toxic volatiles that are also produced during the decay process. Decaying cactus stems of *Stenocereus* species have high levels of 2-propanol and acetone in their rot-pockets (Starmer et al. 1986). These substances are detrimental to larvae foraging in the decaying tissue, but both dominant cactus-specific yeasts (*Candida sonorensis* and *Sporopachydermia cereana*) can metabolize and use 2-propanol and acetone as carbon sources, and thus eliminate the toxic effects experienced by the *Drosophila* (Starmer et al. 1986). Both of these examples can be categorized as mutualisms due to habitat conditioning.
4. Laboratory experiments have shown that yeasts in the diets of cactophilic flies can influence mate acceptance behavior, and that males and females can exchange their yeast communities during courtship and mating (Starmer et al. 1988b). The ultimate result of this behavior is not known, but because females inoculate yeasts onto the tissues in which they lay eggs, the process could be relevant to larval nutrition.

In other *Drosophila* species, yeasts have been shown to influence sexual selection (Norry and Vilardi 1996), parasitoid attraction (Wertheim et al. 2003), and the immune response to parasitoids. In the latter situation, Vass and Nappi (1998) showed that larvae transferred to a yeast-rich medium are more susceptible to cynipid wasp parasitoids compared to larvae deprived of yeasts after being parasitized. This finding indicates that yeasts in the diet can diminish the immune response of the fly to parasitoids. An early report (Gigioli 1897) claimed that yeasts in the crop of flies increase in numbers if the flies are fed sugars. This is an intriguing possibility but our attempts to repeat this experiment were not successful (W. T. Starmer and V. Aberdeen, unpublished observations).

Although the direct nutritional benefit of the yeast to the fly is not in question, mixed cultures of cactus-specific yeasts growing in cactus tissue are better for larval development and survival than the corresponding yeast monocultures (Starmer and Barker 1986, Starmer and Fogleman 1986, Moreteau et al. 1992). This mixed-culture effect, coupled with the finding that the effect seems to be host-specific (e.g., mixed cactus-stem specific yeasts growing in cactus fruits do not provide additional benefits), argues that the harvest mutualism is not only diffuse (involves several yeast species, Starmer and Aberdeen 1990) but also depends on the host-tissue to benefit the fly. Interestingly, the cactus yeasts found in *Stenocereus* stems show mutual growth enhancement in the rotting tissue (Starmer and Fogleman 1986) and thus the yeast community itself is mutualistic.

An unusual case of an arthropod–yeast association involving *Drosophila* is the placement of carcasses of yeast-infected flies by the social spider, *Mallos gregalis*, in its web. The odor produced by the yeasts in the dead flies apparently attracts more prey (Tietjen et al. 1987) for the spider. The benefit to the yeast is not clear, and consequently this may be an example of a commensal association.

Similar in many ways to the yeast–*Drosophila* partnership is the association between certain yeasts and small flower-visiting beetles in the family Nitidulidae (Lachance et al. 2001c). Nitidulid or sap beetles are found in many of the same habitats as *Drosophila* species, namely sap fluxes, fermenting fruit, or ephemeral flowers. Beetles collected from the latter are of particular interest because they contain an unusual array of yeasts with affinities in the genera *Metschnikowia*, *Kodamaea*, and *Wickerhamiella*, represented mostly by species that are not found anywhere else. This leads one to suspect a strong symbiotic relationship. The nature of the symbiosis is not clear, however. Preliminary experiments (C. Mueller and M.A. Lachance, unpublished data) suggest that adult beetles can survive without yeasts if given a rich, soluble diet, but that larvae depend on yeasts for their development. Flower-visiting beetles may benefit from the transformation of scarce and poorly digestible components of flowers into a richer diet by the yeasts.

The yeast community found in bees and their habitats consists largely of members of a clade centered around the genus *Starmerella* (Rosa et al. 2003, Teixeira et al. 2003). Again, the nature of the possible symbiosis is not known with certainty, but a role in pollen maturation is suspected.

3.2. Parasitism (+, −)

Yeasts can be parasites or predators on other fungi (Lachance and Pang 1997, Lachance et al. 2000b) and they can be parasitized by other fungi (Hutchison and Barron 1995). Yeasts in the genus *Saccharomycopsis* and related *Candida* species have been found to share the ability to form infection pegs that penetrate the wall of various other yeast species as well as some molds. In addition, all species in the group are deficient in sulfate transport, leading to the initial hypothesis that organic sulfur was the principal benefit of the interaction (Lachance and Pang 1997). Comparison of the response of various predacious species to different nutrient regimes disputed this idea (Lachance et al. 2000b), suggesting instead that the necrotrophic destruction of prey is a form of competitive exclusion.

Attack of yeasts by filamentous fungi is common among the wood-decaying Basidiomycota where over 50% of isolates tested by Hutchison and Barron (1995) attacked the yeast *Candida ernobii* (target organism). In these cases the filamentous fungi use different forms of necrotrophic mycoparsitism (Barnett 1964) to obtain nutrients either by cell lysis or by direct hyphal penetration of the yeast cells.

Parallel tests with Ascomycota and their anamorphs, previously classified as Deuteromycota, showed only about 10% of the representative fungi attacked yeasts. The authors noted that those that could not parasitize yeasts were predominately short-lived, opportunistic species that live in the soil. Overall the propensity to attack yeasts appears to be driven by low levels of nitrogen or other scarce nutrients that characterize the wood habitat of wood-decaying fungi.

3.3. Other Types of Symbiosis

Yeast symbionts of coccids have important influences on the reproductive status of individuals. An unusual case is that of yeast symbiont of the brown scale insect, *Stictococcus diversisetae*. If an ovary of the female scale insect is infected by the symbiont, the egg develops into a parthenogenetic female, whereas uninfected eggs become males (Buchner 1965, Hughes-Schrader 1948).

The major role that termites play in recycling fixed carbon by degrading cellulose and hemicellulose implicates a strong influence of their gut microbiota. This complex community includes gram-positive and gram-negative bacteria as well as yeasts (Prillinger et al. 1996, Shaefer et al. 1996).

Nutritional cooperation amongst the different members of a community is probably common, but is infrequently reported. Thanh et al. (2002) described *Debaryomyces mycophilus* based on isolates recovered from the gut of the woodlouse, *Armadillidium vulgare* (Isopoda). The yeast could not be cultured on conventional media but grew well in the presence of certain filamentous fungi or their culture filtrates. A stimulating agent purified from *Fusicoccum* sp. was identified as a siderophore, which led to the demonstration that *D. mycophilus* is deficient in iron uptake.

The study of symbioses from the perspective of ecology or evolution contributes to our knowledge of the nature and frequency of relationships among organisms. Understanding how these interactions come into being, change, and persist is central to our overall knowledge of yeast ecology. In the next section we continue our review of symbiosis by exploring the widely distributed killer yeast phenomenon.

4. THE KILLER YEAST PHENOMENON

Yeast killer toxins or mycocins have been known since the middle of the last century (Bevan and Makower 1963). Their genetics, molecular structure, synthesis, secretion, and mode of action have been extensively studied and reviewed (Magliani et al. 1997, Schmitt and Breinig 2002, Tipper and Bostian 1984, Volkert et al. 1989, Wickner 1986, 1992 1996). The phenomenon of "yeasts killing other yeasts" has been used to investigate:

1. the diversity of the molecular processes used in systems that produce killer activity,
2. their use in systematics for biotyping,
3. their industrial application in biocontrol,
4. their use in the clinical setting, and
5. their ecological function in natural populations.

Studies of ecological aspects of mycocin-producing yeasts have been limited to surveys that reveal patterns of killer activity and sensitivity profiles of different yeast species within and among habitats. We will review contributions to these five areas and highlight recent contributions since Golubev's review chapter (Golubev 1998a) on yeast mycocins in the previous edition of *The Yeasts*.

4.1. Diversity

The diversity of yeast killer systems can be viewed from several perspectives, including the extent of toxin production across taxa, the variety of toxin types, the different modes of inheritance, and the various mechanisms used to effect killing. All of these points of view provide insights into the biological diversity of the killer phenotype. Golubev (1998a) listed 14 genera and 79 species of yeasts that exhibit mycocinogenic activity. Since that list was generated an additional 7 genera and 28 species have been added to the total. This glimpse of the extent of killing ability among the yeasts is no doubt a conservative estimate given the restricted environmental conditions (e.g., pH, osmotic pressure, temperature) and the small number of sensitive tester strains used in the detection of toxins. Weak killers and slightly sensitive strains can also be overlooked when the lawn densities and growth rates of the killer and target yeasts differ substantially. Another potentially important factor is the loss of killing activity due to the stress of preservation in culture collections (e.g., the loss of plasmids and virus-like particles that are often responsible for making toxins, Magliani et al. 1997, Starmer et al. 1987b).

Killer genetic systems can be categorized as cytoplasmic (either dsRNA virus-like particles or linear DNA plasmids) or chromosomal. The toxins produced are proteins or glycoproteins, and can be monomers, heterodimers, or heterotrimers. The killing activity occurs following four different general modes, namely disruption of the plasma membrane causing formation of ion channels and thus ion leakage, inhibition of DNA synthesis, cell cycle arrest in G1, or inhibition of β-1, 3-glucan synthesis.

Mycocins such as K1, K2, and K28 of *S. cerevisiae* are encoded by different cytoplasmically inherited, dsRNA virus-like particles. They have been extensively studied and reviewed (recently by Magliani et al. 1997, and Schmitt and Breinig 2002). The three toxins, although different in terms of their mode of activity and amino acid composition, do share similarities in their synthesis and secretion, and all use a two-step receptor-mediated process to kill other yeasts.

The molecular mechanism by which the K1 toxin acts is the best known of the three. After the K1 protein is processed and secreted, it binds to the sensitive cell at a cell-wall receptor (β-1, 6-D-glucan), and then to a plasma membrane receptor (Kre1p, an O-glycosylated cell surface protein, Breinig et al. 2002). A transmembrane channel allows the leakage of ions resulting in the death of the sensitive cell. Modification of the ion gradient at the cell–environment interface is a common method of killing. However, the modification that disrupts the electrochemical potential across the cell membrane may be achieved by several methods, some of which are not yet understood.

The K28 toxin initially binds to an α-1,3-linked mannose residue of the cell wall mannoprotein and then to a receptor in the plasma membrane. The toxin enters the cell by endocytosis and follows the secretory pathway in reverse to enter the cytosol and ultimately the nucleus, where it inhibits cell division at the early G2 stage and is directly or indirectly involved in the inhibition of DNA synthesis (Eisfeld et al. 2000, Schmitt and Radler 1987, 1988, Schmitt et al. 1989, Smitt and Breinig 2002).

Other yeasts that use cytoplasmic dsRNA virus-like particles include *Hanseniaspora uvarum*, *Zygosaccharomyces bailii* (Radler et al. 1990, 1993, Schmitt et al. 1997, Schmitt and Neuhauen 1994, Weiler and Schmitt 2003, Zorg et al. 1998) and *Phaffia rhodozyma* (Castillo and Cifuentes 1994).

Two other killer toxins, KHR and KHS, have been found in *S. cerevisiae* (Goto et al. 1990, 1991). These toxins are not produced by virus-like particles in the cytoplasm but are chromosomally encoded. The toxins differ in their pH optima and thermostability (KHR, heat resistant; KHS, heat sensitive). They are both proteins and appear not to be homologues of other killer genes of *S. cerevisiae*. The KHS mycocin may operate by a similar killing mechanism to that of the K1 toxin by increasing membrane permeability to ions (Goto et al. 1991).

Killing activity in *Kluyveromyces lactis* is inherited through cytoplasmic linear dsDNA plasmids (Gunge et al. 1981, Gunge 1995, Schaffrath and Meinhardt 2005, Stark et al. 1990). The plasmids have a number of open reading frames that are involved in making killer toxin subunits and immunity factors, as well as participating in plasmid replication and maintenance. The toxin (zymocin) consists of three different subunits, and acts through independent mechanisms to decrease cell viability and by arresting the unbudded G1 phase of the cell cycle and thus prevents cell division (Butler et al. 1991, White et al. 1989). The *K. lactis* toxin has an unusual effect on the sexual reproduction of *S. cerevisiae* (Klassen et al. 2006). The novel influence essentially prevents mating and is independent of the toxin's effect on cell division. The consequence of this action is to block entry into the diploid state and thus prevents the target yeast from escaping into a phase that is less vulnerable to the toxin's function as an inhibitor of growth (Klassen et al. 2006). Fukuhara (1995) surveyed 1,800 strains of about 600 yeast species for linear DNA plasmids. He found that 1–2% had linear plasmids with similar properties to killer DNAs of *K. lactis*.

Toxins produced by *Pichia* species are diverse in terms of their inheritance. Some [*Babjeviella* (*Pichia*) *inositovora*, *Millerozyma* (*Pichia*) *acaciae* and *Schwanniomyces* (*Pichia*) *etchellsii*] are produced by dsDNA plasmids (Hayman and Bolen 1991, Klassen et al. 2001, Ligon et al. 1989, Worsham and Bolen 1990). These toxins are similar in structure and function to the *K. lactis* zymocin toxin (Bolen et al. 1994, Klassen et al. 2001, Klassen and Meinhart 2003). Also sharing similarities with the extensively studied *K. lactis* dsDNA plasmid killer system are the killer strains of *Debaryomyces* (*Wingea*) *robertsiae* (Klassen and Meinhart 2002). The *Pichia kluyveri* mycocin, however, is probably encoded by nuclear genes. The toxin is an acidic glycoprotein that forms ion channels in the membrane of sensitive cells, i.e., similar in action to the K1 toxin activity of *S. cerevisiae*, (Kagan 1983). Likewise, the salt-tolerant yeast *Millerozyma* (*Pichia*) *farinosa* makes a toxin that also seems to increase membrane permeability and cause the loss of ions (Suzuki et al. 2001), thus also resembling the K1 toxin of *S. cerevisiae*. However, there is no sequence similarity between the two toxin types. The *M. farinosa* toxin has high activity in media containing 2M NaCl and is thus termed a salt-mediated killer toxin (SMK). *Wickerhamomyces* (*Pichia*) *anomala* toxins function to kill a broad range of organisms, including bacteria, hyphomycetes, and yeasts (Cailliez et al. 1994, Polonelli and Morace 1986, Polonelli et al. 1989a). Apparently, two toxin types can be secreted by *W. anomala*, but little is known about how they kill susceptible cells. The mode of action probably involves a β-glucan receptor, which is a common yeast toxin receptor in the cell wall and is used also by killer toxins of *P. membranifaciens* (Santos et al. 2000).

Species formerly classified in *Williopsis* apparently make four toxins (HM-1 or HMK, K-500, WmKT and Wicaltin). HM-1 is unusual as it is a basic, unglycosylated protein with high pH stability (2–11) and is thermotolerant (Yamamoto et al. 1986). *Lindnera mrakii* (*Williopsis saturnus* var. *mrakii*) may use its toxin to target the cell wall β-1, 3-glucan skeleton during budding or the growth of conjugation tubes. This results in lysis of sensitive cells (Takasuka et al. 1995). The second toxin produced by a strain termed *Williopsis* (K-500) is an acidic polypeptide that may act by influencing ion gradients across the plasma membrane. *Lindnera mrakii* toxin WmKT has similarities to killer toxin-like proteins produced by bacteria. For example, the soil bacterium *Streptomyces* sp. F-287 causes cytocidal effects in yeasts, and may have a parallel mode of action to the *L. mrakii* toxin. In this case the bacterium and yeast toxins have similar structural elements, i.e., a Greek key β-barrel fold that may be involved in target binding of the toxin (Ohki et al. 2001). The WmKT

toxin was originally attributed to *Wickerhamomyces anomala* (see Guyard et al. 2002b). Guyard et al. (2002b) suggest that WmKT alters cell wall structure through hydrolytic activity that targets β-glucans in the cell wall, resulting in cell death. *Barnettozyma* (*Williopsis*) *californica* makes a broad-spectrum toxin, Wicaltin, which has similar properties to HM-1 (Theisen et al. 2000). Earlier attempts to cure (i.e., convert a killer strain into a non-killer strain) *Lindnera* (*Williopsis*) *saturnus* with cycloheximide or high temperature were unsuccessful, although Moriya et al. (1995) reported that high hydrostatic pressure (60 MPa) did cure some strains.

Characterization of the killer protein produced by *Schwanniomyces occidentalis* (Chen et al. 2000) suggests that it is chromosomally encoded, and functions by binding to cell wall mannoprotein receptors with subsequent damage to the plasma membrane. The toxin shares a broad spectrum of killer activity with *L. mrakii* toxin (HM-1) but does not have similar biochemical properties (the *S. occidentalis* toxin is a heterodimer, has restricted pH stability, and is only moderately thermostable).

Three toxins (KP1, KP4, and KP6) are produced by dsRNA viruses in the maize smut fungus *Ustilago maydis* (Koltin and Day 1975, 1976). A variety of dsRNA segments of different sizes are responsible for producing the toxin and capsid-related polypeptides, and are involved in both virus replication and maintenance. The KP1 and KP6 toxins are likely to function by binding to the cell wall (KP6, Steinlauf et al. 1988) and may act by disruption of sensitive cell membranes, causing ion leakage and cell death. The K4 toxin is nonglycosylated (Park et al. 1994) and has 10 cysteines (of 105 amino acids) in its polypeptide. Involvement of disulfide bonds in toxin activity is possibly important to the mechanism responsible for killing susceptible cells. Enrichment of the protein with cysteine is common to the HM-1 toxin produced by *L. mrakii*, where 10 out of 88 amino acids are cysteines. In the case of "*Williopsis*", the cysteines may also be responsible for toxin activity as well as the unusual stability of the toxin.

4.2. Systematics, Taxonomy, and Discrimination of Biotypes

Killer phenotypes have been successfully used as a method of biotyping different genera of eukaryotic and prokaryotic microorganisms, especially for epidemiological purposes (Polonelli et al. 1997). The use of killer sensitivity/resistance profiles of a set of "unknown" yeasts challenged by a known killer yeast (or panel of killer yeasts) is a typical method used to sort and discriminate among unknowns. This method can be limited in general taxonomic value when resistance to a particular toxin has a high selective value in the natural environment, and if the resistance mechanism is similar for phylogenetically distant taxa. For example, if diverse toxins all use a common cell wall receptor to concentrate toxin and thus promote transfer to a secondary receptor, then a common resistance mechanism would be to reduce the number of receptors (e.g., β-1, 6-D-glucan) and thus decrease the cell wall affinity to achieve resistance (Boone et al. 1990, Brown et al 1993). Likewise, two yeasts can be resistant to a given toxin through different mechanisms, such as the presence of plasmids that carry immunity factors, or nuclear gene mutations that alter binding sites in the wall or membrane. In such situations convergent evolution is likely and therefore resistance profiles cannot be expected to be a valuable tool for either biotyping or classification. A possible solution to this problem is to use a set of killer yeasts in the panel that employ different killing mechanisms. This strategy has been put into practice for detecting pathogenic species such as *Candida albicans* (Buzzini and Martini 2000a, 2000b, 2001a, 2001b, Buzzini et al. 2003, Caprilli et al. 1985, Lehmann et al. 1987, Stenderup 1986, 1990), varieties of *Cryptococcus neoformans* (Boekhout and Scorzettii 1997), and for biotyping indigenous *S. cerevisiae* strains in winery populations (Sangorrin et al. 2002). Furthermore, Vaughan-Martini et al. (1996) report that sensitivity to killer is a valuable tool for fingerprinting wine yeast strains and that the profiles have a good potential for biotyping important industrial yeasts.

General rules that can be applied to the use of killer yeasts to facilitate identification were outlined by Golubev (1998a), as follows:

1. Basidiomycetous killers kill basidiomycetes and ascomycetous yeasts kill ascomycetes;
2. Broad-range mycocins should be used to evaluate distantly related species and narrow-range mycocins should be used to evaluate closely related forms;
3. Anamorphic genera are more heterogeneous in their response to killer toxins compared with teleomorphic taxa.

Perhaps the typically greater phylogenetic diversity of anamorphic genera accounts for this generalization.

No extensive comparison has explicitly evaluated the potential for killer ability profiles (in contrast with sensitivity profiles) to be included in the properties used for general yeast characterization and identification. In one comparison that used cross-killing profiles of four closely related cactophilic species in the genus *Phaffomyces*, a cladogram based on killer sensitivity was congruent with cladograms based on physiology and rDNA sequence comparisons (Starmer et al. 2001). The congruence did not extend, however, to a cladogram based on the killing ability profiles. These results suggest that killer ability profiles may not be taxonomically useful at the level of closely related species. However, this single comparison may not be representative of all yeasts, especially given the unusual reciprocal killing phenomenon exhibited by species of *Phaffomyces*. Golubev (1998a) discussed the utility, pitfalls, and problems associated with using killer phenotypes in yeast systematics. He concluded they may have utility as an additional tool in yeast classification.

4.3. Biocontrol (Industrial)

Killer yeasts have been used in the food industry for several different purposes. Although most applications have aimed at using killers to control fermentation (primarily wine and beer), they have been used also to protect the final product from refermentation and film production (Hara et al. 1983), and they have been used as effective biopreservatives in wine (Ciani and Fatichenti 2001). Killer yeasts are important to olive fermentation where they are associated with olive brines (Marquina et al. 1992, 1997) and with green-olive fermentation bloaters (Asehraou et al. 2000). The use of killer yeasts in sake fermentation has also been suggested as an effective means of biocontrol (Ouchi 1981, Yoshiuchi et al. 2000). Likewise, given their osmotic tolerance, killer yeasts in the genus *Kluyveromyces* have been evaluated as natural preservatives in salted fermented foods (Kono and Himeno 1997). Considerable attention has been given to the killer species *Millerozyma farinosa*, a halotolerant yeast with novel killer properties (Suzuki et al. 1989, 2001, Suzuki and Nikkuni, 1989, 1994).

Spontaneous sugar cane fermentations experience a succession of yeast populations where killer yeasts may be involved in competitive exclusion of contaminants and transient species (Morais et al. 1997). Natural tequila fermentations also show changes in yeast community membership where the heterogeneity is reduced over time. However, it would seem that killing abilities are overshadowed by other factors in determining the yeast community structure (Lachance 1995).

Agricultural applications include the use of killer yeasts [*Wickerhamomyces anomalus*, *Meyerozyma guilliermondii*, and *S. cerevisiae*] to control damaging mold growth in high-moisture wheat,

rye, barley, and oats stored under airtight conditions (Petersson and Schnürer 1995, 1998, Petersson et al. 1999). In this regard *Aspergillus niger* has been engineered for the heterologous production of the HMK toxin of *L. mrakii*, which can then be used to control spoilage of mature maize silage (Lowes et al. 2000). Killer yeasts also occur in wounds of maize, where they may be important in attracting insects to the ears before harvest (Nout et al. 1997). Even home-made bread dough shows a high incidence of killer yeasts (25%), including strains of *W. anomala* endowed with a broad activity spectrum (Almeida and Pais 1996). In the dairy industry Jakobsen and Narvhus (1996) suggest a link between killer activity and probiotic starter cultures. Likewise, yeast–yeast interactions have been implicated in the maturation of Camembert and blue-veined cheeses (Addis et al. 2001). In addition, the yeast toxin HMK (see above) was shown to be useful in preventing yoghurt spoilage (Lowes et al. 2000).

The brewing industry has considerable interest in either preventing undesirable killer yeasts from contaminating their fermentation processes or using killer yeasts in the fermentation to prevent contaminations by unwanted yeasts. As a consequence, the starter culture that is most desirable would satisfy both requirements, by being widely resistant to toxins and making a broad-spectrum super-killer toxin. However, caution against engineering super-resistant super-killers should be exercised due to the risk that the organism could escape into natural environments and later become a threat to other fermentation processes (Magliani et al. 1997). Two of the main problems with killer yeasts as contaminants of wine fermentation are that they can modify the sensory quality of wine (Fleet 2003), and cause protracted or stuck fermentation (van Vuuren and Wingfield 1986, Carrau et al. 1993). Some of the factors that influence these outcomes are the initial ratio of killer to susceptible yeasts (Perez et al. 2001), the growth rate of sensitive yeasts in comparison to the killer yeasts (Da Silva 1996), and the composition of the indigenous community. As indigenous killer yeasts associated with wineries vary markedly from region to region (Vazquez and Toro 1994) and in view of the high incidence (88%) of killer yeasts in different spontaneous fermentations (Vagnoli et al. 1993), a strategy based on one solution for all problems seems unlikely and perhaps undesirable.

The many studies that give suggestions and advice on which yeast is useful in any particular situation collectively suggest specific rather than general solutions to the use of biocontrol to keep killers out, or how to employ killers to keep other yeasts out of fermentation processes.

4.4. Biocontrol (Clinical Applications)

The use of killer yeasts in the prevention and control of pathogenic yeasts has obvious appeal because of the specificity of the toxins for yeasts and not for other organisms. However, the use of active yeasts to deliver the toxin is fraught with the potential for opportunistic infections by the killer strains. The use of purified toxin instead may not be a good solution, since killer toxins are often large, foreign glycoproteins expected to induce an immune response and thus render the therapy useless or even dangerous.

The toxin from *L. mrakii* is similar in mechanism to some antifungal compounds (e.g., aculeacin A, Komiyama et al. 1998, Yamaguchi et al. 1982, Yamamoto et al. 1986), has activity against *Candida* spp. (Hodgson et al. 1995, Michalcakova et al. 1993, Walker et al. 1995), and is stable to changes in pH and temperature. For this reason, it has been singled out as potentially valuable in the therapeutic treatment of mycoses. To circumvent the antigenicity of killer toxins, one strategy has been to identify and synthesize small peptides that retain the killer activity without the antigenic properties (Magliani et al. 1997). Luciano Polonelli and colleagues (Polonelli et al. 1993, 1994, 1996, 1997, 2003 and Magliani et al. 2003) have taken an approach that attempts to develop an idiotypic vaccination that would provide an immunoprotection which mirrors a microbicidal toxin. The method uses a monoclonal antibody bearing the killer receptor-like idiotype to immunize animals, and thus mimic the activity of killer toxins against pathogenic yeasts (Pollonelli et al. 1991). More recently, Weiler and Schmitt (2003) have identified in *Zygosaccharomyces bailii* an antifungal toxin, zygocin, which effectively kills pathogenic yeasts such as *Candida albicans*, *C. glabrata*, and *C. krusei*. The activity of the toxin is analogous to that found in other dsRNA encoded toxins that disrupt membrane ion gradients but, in contrast to the *S. cerevisiae* toxins, it has a rapid killing action and a broader activity spectrum that extends to other fungi such as *Sporothrix schenckii*. As a consequence zygocin has attracted attention for potential clinical use.

4.5. Killer Yeast Ecology

The widespread occurrence of the killer phenomenon suggests that it plays an important role in the ecology of yeasts (Starmer et al. 1987b, Stumm et al. 1977). In fact, the abundance of killer yeasts in nature indicates that killing ability functions as a significant competitive mechanism. The observation that killer toxins often change the gradient of ion flow in their target cells has two mechanistic implications. One is that this manner of effecting killing evolves easily, and the other is that resistance is not easily developed, as it would require changes in the cell envelope that would result in the loss of other critical cellular functions. In any case, the general mechanism whereby growth is inhibited by disrupting membrane integrity points unambiguously to interference competition as the principal ecological role. Indeed, production of toxin is likely to occur early after the colonization of new habitats, and as a result, the growth of simultaneous or subsequent colonists that would compete for the same resources can be curbed without delay.

In conjunction with our studies on the population biology and ecology of cactophilic yeasts, we have conducted a broad survey of yeasts associated with slime fluxes of trees, decaying fruits, and cactus necroses (Starmer et al. 1987b). The study compared killer activity and sensitivity profiles within and across yeast community types, within one region (near Tucson, Arizona, USA), across localities and hosts, over seasons, and as a function of habitat characteristics (pH). Several general conclusions emerged from the comparisons:

1. Killer yeasts (22 of 81 species in the study) occurred in about 10% of the isolates, with the highest incidence, 27%, among isolates in decaying fruits.
2. Each community, defined by the host plant species, had at least one killer present.
3. Cross-killing tests for the region showed that 7 of 21 species were killers while 18 of the 21 species had at least one sensitive response, suggesting that sensitivity to toxins is more widespread than killer ability.
4. Although there were some exceptions, killer-sensitive responses were more prevalent across community types and across localities as compared to killer-sensitive responses within localities or of the same community types. This result implies that local communities have evolved resistance to local killers.
5. Killer yeasts found in fruits not only occur more frequently than in other hosts, they occur more commonly at low pH where many toxins have optimal activity. The mature fruit habitat is a valuable non-toxic source of abundant nutrients and energy, especially free sugars. When these free sugars are available they become

a significant resource for competition among microorganisms and many sorts of animals. Microbes that have either good colonization ability or that use mechanisms that interfere with their competitors (i.e., interference competition) are likely to succeed.

6. Seasonal distribution of killer yeasts shows that some killer species (e.g., *Phaffomyces thermotolerans*) are more abundant during certain seasons. The reason for seasonality in *P. thermotolerans* is not known, as it only occurs in columnar cactus necroses. The depression in frequency occurs during the summer.

In general the common pattern observed in cross-killing studies is that sensitive strains outnumber killer strains. This pattern is readily explained by considering the geographic (spatial) and host range of the species cross-tested. Given that evolutionary adaptation to a particular toxin type should require exposure to that toxin, those yeasts living in different areas or in different hosts will be sensitive to toxins from other areas and other hosts, but resistant to toxins in their own host and locality. Ganter and Starmer (1992) analyzed within-community patterns of killing activity in decaying cactus to test this hypothesis: yeasts found together in the same host with a killer should show the least sensitivity to the killer, when compared to a yeast not found alongside it. The correspondence with killer-sensitive responses was tested using a scale of decreasing likelihood of encounter, from yeasts occurring together in the same rot, to yeasts found in separate rots but in the same host, to yeasts occurring in separate rots of different hosts. The likelihood of encounter was positively correlated with killer resistance, supporting the idea that toxins do affect community composition and that the communities are distinct. These results are consistent with the theoretical results of Czárán and Hoekstra (2002), who addressed the general problem of explaining the widespread occurrence of killers and killer-sensitive strains by using simulation of stochastic cellular automata models of metapopulations. They concluded that polymorphisms for killer and killer-sensitive systems, such as those documented for yeasts, can be maintained by a slight tradeoff between toxin production and population growth rate. Their results implicate local killing phenomena in small habitat patches in conjunction with regular extinction–recolonization cycles as most important for maintenance of these types of systems.

Not all strains of a known killer yeast species from a natural habitat are killers (Abranches et al. 1998, Starmer et al. 1987b). Polymorphism in killer abilities can be explained by postulating a cost associated with the production of killer toxin. If there were no cost then one would expect all strains to retain the trait even when there is no local benefit in the absence of competitive conditions. Pintar and Starmer (2003) demonstrated the expected cost–benefit tradeoff by studying haploid clones of the yeast *Pichia kluyveri*, which is polymorphic for killer toxin production in nature. The polymorphism is found across the United States (Starmer et al. 1992), and appears to be under control of one to three genes. When clones derived from a single ascus (i.e., sister spores of the same meiotic event) were compared, non-killer clones initially grew faster than did their toxin-making sisters. This tradeoff between intrinsic growth rate and toxin production was used to explain the maintenance of both killer and non-killer genotypes in natural conditions. Microcosm experiments using the two types of *P. kluyveri* gave results that were consistent with this hypothesis.

Although correlational evidence indicates that killer toxin production is a meaningful ecological variable, experimental demonstration of a direct influence on community structure is lacking. Starmer and Aberdeen (unpublished observations) conducted several field experiments using tomato fruits inoculated with killer and non-killer genetic segregants of *P. kluyveri*. The fruits were surface sterilized, cut open, and set out in the environment where insect visitors vectored the local yeasts and affected colonization. The three treatments consisted of pre-inoculation with a killer genotype (K+) or a non-killer genotype (K−), as well as a control that was not inoculated. Each treatment was replicated six times. The fruits were subsequently sampled by plating and the yeasts were counted and identified. Variables such as the density of *K. apiculata*, the community composition (indigenous yeasts), and species diversity metrics were studied by analysis of variance. In three separate trials, each at a separate locality, three different results were obtained. In one case the killer-inoculated fruits showed decreased cell numbers of *K. apiculata* compared to the other two. In another case the opposite was demonstrated and in the third case no effect was detected. Furthermore, species diversity was not significantly affected by the treatments. One possible reason for these mixed results may be that differences between the sensitivities of indigenous yeasts present at each locality resulted in different responses to the treatments. Thus a better experimental design might compare local and non-local killer yeasts in the treatments in each locality.

The killer yeast phenomenon may well influence higher levels of ecological organization. In the next section we review yeast community ecology with the goal of understanding community organization and the determinants of community structure from a general ecological perspective.

5. YEAST COMMUNITY ECOLOGY

Yeasts normally do not grow as monocultures in their natural habitats. They typically occur as members of communities that involve other yeasts, other fungi, bacteria, protozoans, and other small organisms. In ecology, a collection of species of the same general type, for example the yeast species in a community, is called a guild. In this section we will refer to collections of yeasts that live together as communities. In other words, other organisms (such as bacteria) that could be considered part of the same community will be disregarded. As a consequence, we will be concerned mainly with the structure, origins, membership, and maintenance of yeast guilds. However, because past studies of this type have referred to these assemblages as communities, we shall preserve that terminology to maintain continuity with the literature.

Taxonomic descriptions of yeast species include “sources” of the isolates used as part of the description. These sources often indicate the natural habitat of the species, especially when a specific habitat (e.g., decaying fruit) has been the focus of a survey or investigation. However, yeasts occur in diverse habitats that are broadly defined over the major abiotic and biotic partitions of the world. These include water (oceans, ice, rivers, lakes), soil (mixtures of sand, silt, and clay), the atmosphere (clouds, fog, snow, hail, and rain), plants (leaves, stems, flowers, bark, fruit, and seeds), and animals (surfaces and intracellular or extracellular spaces). Some of the places where yeasts occur are not necessarily where they live (i.e., where they grow and reproduce) but can be where they survive and persist during the transition between habitats where they can grow. For example, a soil sample may contain yeast cells that have fallen to the ground with a decaying fruit. Likewise, phylloplane yeasts can be incorporated into the soil when the leaves on which they live fall to the ground. The yeasts may persist in the soil, but do not necessarily grow there, nor interact with other yeasts that do grow in the soil. Survival in reservoirs such as water, soil, or insect surfaces depends on resistance to temperature extremes, tolerance of desiccation, pressure extremes, or the harmful effects of UV irradiation, and other challenges to their survival. With this possibility in mind our discussion of yeast community ecology will be limited to well-studied

habitats where the resident yeasts are known to grow and live together.

Loosely defined, a community is a set of organisms that live together in a common area. In some situations the common area is a discrete entity. A decaying flower, a rot pocket in a cactus stem, the surface of a leaf, and the hindgut of an insect are all examples of common areas where yeast communities might live.

Community ecology has focused on understanding two properties of assemblages, namely the species that are present and the relative proportions of those species in their habitat. These features are referred to as community structure. They provide insights into species diversity. For example the species richness (**S**) or number of species in the community may be an appropriate statistic used to describe the diversity of member species. If the relative proportions of the species in the assemblage is known, then other diversity indices, e.g., **H′**, a measure of the uncertainty of species identity (Pielou 1975), can be calculated.

Community structure has been postulated to result from interactions among populations of different species in a small confined area (MacArthur 1972). Interactions consist of competitive, mutualistic, prey–predator, and commensal relationships that are collectively termed "local processes". However, the local-process postulate often fails to provide an explanation for changes in diversity observed at larger geographic scales. Over larger geographic areas, knowledge of historical processes (Brooks 1985, Endler 1982, Ricklefs 1987) such as speciation, extinction, and large-scale dispersal adds to our overall understanding of changes in diversity from local patches to large collections of localities, or across regions, or even over the entire globe.

5.1. Local Communities

Because the temporal scale relevant to yeast communities is compressed compared to that of macroorganisms, the time frame and cycle of yeast habitat occupation must be taken into account when investigating the factors that influence yeast community diversity. It is often possible to study the cycle of habitat occupation and as a consequence we have adopted a sequential filter–amplifier model to document and explain how communities are organized at the local level. In this model a large, local community of yeast species has the potential to occupy a new habitat, but the species are *filtered* by sequential events (arrival, habitat chemistry, competition) and *amplified* by their ability to exploit resources (i.e., grow). This in turn determines the ultimate likelihood of their occupation of another, new habitat. The filter–amplifier approach is useful in dissecting the salient features of the micro-ecosystems in which yeast populations reside and persist.

The dynamic cycle, depicted in Fig. 6.3, captures the important challenges facing the yeasts. These challenges ultimately influence inclusion, persistence, and relative numbers of particular yeast species in the habitat over the long term (many cycles) and the short term (during a cycle). Viewed in this manner, the community may appear never to be in equilibrium except in terms of community composition at the same phase of the cycle over long periods of time. However, in some cases one stage may be prolonged to the extent that an equilibrium phase can be studied. To endure and become a predictable member of the community a yeast species needs 1) to arrive at the habitat, 2) to be capable of growing in the chemical environment it encounters, 3) to be a successful competitor, and 4) to grow successfully and increase its likelihood of dispersal to a new habitat. If this cycle is stable, then the yeast community structure will continue to exist as a part of a dynamic process that can be studied at specific points or during periods where the process is in a quasi-equilibrium state.

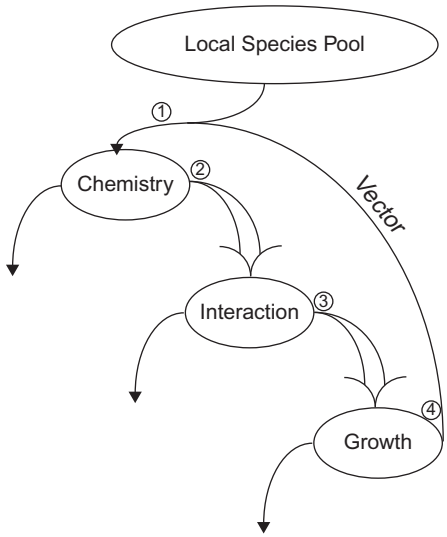


FIGURE 6.3 Dynamic cycle showing important processes that influence the composition of the yeast–cactus community.

5.1.1. Equilibrium

The idea that yeast communities persist over long periods of time has not been extensively studied. The fact that the same species are repeatedly recovered from similar habitats in surveys argues that equilibrium communities exist, but explicit comparisons of yeast community structure over long periods of time are few. Latham (1998) examined a specific cactus–yeast community in Baja California, Mexico over a span of 15 years and found that essentially the same species in the same relative proportions were living in the decaying stems of *Stenocereus gummosus*. She also confirmed that the community structure of the yeast species over a hierarchy of within-rot, between-rot, and among-localities had the same patterns in 1982 and 1997. This similarity extended to the physiological profiles of the yeast assemblages in the hierarchy studied in both years (1982 and 1997). Her comparison showed that cactophilic yeast communities do retain their identity over long periods of time. We have observed a similar stability in the yeast community of morning glory flowers and their insects, studied over a 17-year period in Kipuka Puaulu, a small forest located on a slope of the Mauna Loa volcano on the Island of Hawai'i (Lachance et al. 1988a, 2003a, 2005).

5.1.2. Dispersal

Dispersal of an ascomycetous yeast to a new habitat is generally restricted by the habits of the vector and the yeast's adaptation to active transport. By contrast, a basidiomycetous yeast can be passively transported in air currents. Ballistospore and ballistoconidal-forming yeasts have adaptations which increase their dispersal capacity by the forcible ejection of ballistospores into the air above their growth surfaces. The spores are then transported in moving air. Yeasts that form hydrophobic cell walls accumulate on the surfaces of their growth substrates. The surface films provide islets of concentrated yeast that are more likely to be encountered by flying insects that come to these surfaces to feed (Vacek et al. 1979). Ultimately the successful vectoring of the yeast will depend on many specific properties that result in attraction of the vector, survival on or within the vector, and the ability to grow in a fresh substrate.

When the vector has limitations on its activity and responds to a narrow range of habitat cues, one expects that the microbes it carries to also be limited in the habitats that they can colonize. At the extreme, if suitable vectors are absent, habitats that could be

occupied by local yeasts are not colonized and thus not occupied. For example, the smooth-leaved elm (*Ulmus carpinifolia*) forms slime fluxes that have predictable yeast communities over seasons in their North American distribution (Phaff et al. 1964a). Several flying insects visit these fluxes, and drosophilids (*Aulacigaster* sp.) are considered one of the important yeast vectors for these substrates. In Australia, where elms were introduced, a study of elm slime fluxes over several years in central New South Wales failed to detect the presence of yeasts or drosophilids in the fluxes (W. T. Starmer, unpublished observations). In this case we concluded that the appropriate yeasts, the appropriate vectors, or both were missing from the system. Likewise rotting tissues of cacti growing in isolated gardens outside of the natural distribution of the cacti usually have no yeasts or only basidiomycetous species that are likely to have arrived passively by air movement.

Rosa et al. (1994) studied the distinct yeast communities found in the flowers and fruits of the cactus *Pilosocereus arriabidae* in three restinga ecosystems (coastal plains formed during the Quaternary) in southeastern Brazil. They concluded that the most important influence on the community structure was the host-specific activity of insect vectors such as the moth *Sigelgaita* sp. This moth was associated with an increased incidence of the yeast *Clavispora opuntiae,* and had a large influence on the community composition. We have observed a similar situation with the increased incidence of *C. opuntiae* in *Opuntia* cladode necroses that have been attacked by the cactus moth *Cactoblastis cactorum* (Starmer et al. 1988c).

The role of *Drosophila* species in dispersing yeasts has been extensively studied and discussed in the literature (Barker et al. 1984, Barker and Starmer 2000, Carson et al. 1956, da Cunha et al. 1957, Dobzhansky and da Cunha 1955, Fogleman and Foster 1989, Ganter et al. 1986, Gilbert 1980, Heed et al. 1976, Lachaise et al. 1979, Lachance et al. 1989, 1995, Morais et al. 1992, 1994, 1995a, 1995b, 1996, Phaff et al. 1956, Rosa et al. 1994, Shehata et al. 1955, Starmer et al. 1982, 1988a, 1991). These studies show that varying degrees of host-specific feeding and oviposition behavior of drosophilid flies are important to the types of yeasts found in the habitats of the flies. In some cases the yeasts found in the adult flies are not the same as those found in the larval habitats. Investigators have concluded that the yeasts used by the different life stages are partitioned, i.e., adults feed on substrates that are different from those found in the places where they lay eggs. In other situations where the succession of the microbial community can be tracked, different groups of drosophilids may use the habitat at different times of the succession (Morais et al. 1995b). An analogous situation exists for the microbial populations found in Calimyrna figs, where the initial microbial community is vectored by a wasp pollinator (*Blastophaga psenes*). The community consists of *Candida carpophila* and the bacterium *Serratia plymuthica*. These organisms are considered the normal biota during the ripening of the fruit. However, drosophilids are attracted to the ripe fruit and bring with them fermentative yeasts (apiculate yeasts and *Candida stellata*) that change the yeast community composition considerably (Miller and Phaff 1962). Beetles (discussed later in this section) that use woody tissues of trees, tree fluxes, or flowers may play a similar role in the distribution of yeasts on which they rely for larval nutrition.

5.1.3. Habitat Chemistry

Host or habitat chemistry has an initial influence on which yeasts can grow in a new habitat. In the soil, strains of actinomycetes produce antibiotics. The production of cycloheximide by *Streptomyces griseus* may have a pronounced influence on the yeasts that live there (di Menna 1962, Phaff and Starmer 1987). Other bacterial activities may also affect the ability of yeasts to colonize substrates where a fermentation is in progress. Acetic acid bacteria (e.g., *Gluconobacter*) as well as some yeasts (*Brettanomyces* and *Dekkera* spp.) produce acetic acid by the oxidation of ethanol. At low pH values the undissociated form of the acid inhibits the growth of many yeasts. The pH of the substrate also influences the activity of killer toxins produced by yeasts (see section on killer yeasts) and affects the toxicity of other host chemicals.

Organ pipe cactus (*Stenocereus thurberi*) stem tissue possesses an unusual complement of medium chain-length (C_8–C_{12}) fatty acids esterified to neutral triterpenes and stero-diols (Kircher 1982). During the decay process, the fatty acids are released and become toxic at the low pH that characterizes the initial necrosis (Starmer 1982). The presence of these potentially toxic lipids has been linked to the abundance of lipolytic yeasts (e.g., *Magnusiomyces starmeri* and *Yamadazyma* (*Pichia*) *mexicana*) in *Stenocereus* substrates. The lipolytic activity protects both the other yeasts and the *Drosophila* larvae living in the tissue.

Other cactus stem tissue chemicals can have significant influences on the colonization of decaying tissue. The triterpene glycosides of *Stenocereus* species are an important example. In the North American Sonoran Desert, *Stenocereus gummosus* (pitaya agria) and *S. alamosensis* (cina) contain large amounts (20–40% of the tissue dry weight) of triterpene glycosides in their stem tissue. Of the various fractions of triterpene glycosides separated on thin-layer chromographic plates, gummosogenin (Fig. 6.4) has been identified as the most active component (V. Simons, S. Erdman and W. T. Starmer, unpublished data). The ability of yeasts to grow in the presence of the triterpene glycosides is temperature dependent, i.e., strains grown on a medium supplemented with triterpene glycosides cannot grow at intermediate temperatures, but are capable of growth at elevated temperatures. This observation, coupled with genetic studies (Starmer et al. 1980a) on the "*amethionina* complex" (*Starmera* species), and more recently using the knock-out gene collection of *S. cerevisae* have shown that the activity of the triterpene glycosides is likely to be associated with the production of membrane components such as ergosterol. Notable is the observation that the triterpene glycosides from *S. gummosus* cause ergosterol to precipitate from solution. Recently we have found that several dominant cactophilic yeasts (e.g., *Pichia cactophila* and *Sporopachydermia cereana*) show resistance to triterpene glycoside activity in strains isolated from *Stenocereus* species but not those isolated from cacti that are devoid of triterpene glycosides (e.g., *Carnegiea gigantea*, Saguaro). When we originally discovered that triterpene glycosides inhibited the growth of many yeast species, we concluded that most cactus yeasts were resistant. However, this recent evidence argues against that generalization. Now the evidence suggests that several independent lineages have diverged in response to the triterpene glycosides.

Shifrine and Phaff (1956) found that species, then classified in *Hansenula* and *Pichia*, associated with the bark beetles that attack

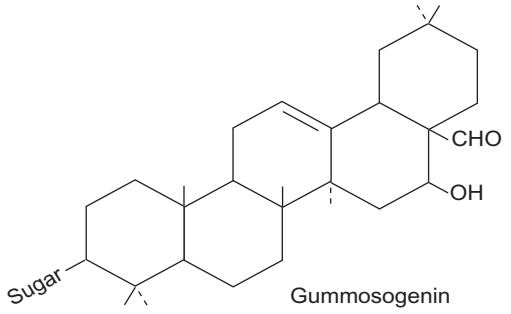


FIGURE 6.4 Chemical structure of the triterpene glycoside gummosogenin found as a major constituent of agria cactus stems.

coniferous trees such as fir and pines, are resistant to inhibitory oleoterpenes. Similarly to the cactus triterpene glycoside example, the types of oleoterpenes and their concentration in conifers can have differential effects on yeasts associated with bark beetles. For example, *Pinus jeffreyi* produces high concentrations of n-heptane, which inhibits the growth of the bark-beetle yeast, *Ogataea pini*, that can grow in other species of pine.

5.1.4. Yeast Interactions

The potential yeast–yeast interactions that could influence successful growth in a community are competition and mutualism. In particular, interference competition has been investigated because of the widespread occurrence of killer yeasts in natural communities. Another section of this chapter discusses the importance of the killer phenomenon in the ecology of yeasts. Even though many studies that report killers in natural systems suggest that killer toxin production could be one of the most important factors influencing community composition, definitive experimental studies that demonstrate that this is the case in natural communities are still lacking. Comprehensive surveys of yeast communities (Starmer et al. 1987b) show that killer species occur in most yeast communities (tree fluxes, cactus stems, fruits). With some exceptions, the killer species seem to exert their interfering effects on yeasts that belong to other communities (e.g., killer yeasts in fruit yeast communities kill yeasts in tree-flux communities more readily than they kill yeasts in their own community). This result is to be expected, given that yeasts that are often found together are more likely to be resistant to the toxins that they frequently encounter (Ganter and Starmer 1992).

In a more general perspective, killer yeasts may affect the overall composition of communities by increasing their diversity. Czárán et al. (2002) used a spatially explicit game theoretical model to evaluate the influence of antibiotic interactions (such as the killer phenomenon) on the structure of microbial communities. The study showed that this form of interference competition is a potentially effective mechanism for the maintenance of high levels of biodiversity in communities.

Other types of competition that involve the use of limiting resources (resource competition) have not been extensively studied in natural systems. Abranches et al. (2001) found that common fruit yeasts (*Hanseniaspora* and *Pichia* spp., including *Issatchenkia*), are limited by carbon when grown as monoculture in fruits such as tomato or guava. Their work demonstrated that when common fruit yeasts are simultaneously inoculated, the growth rates of the individual yeasts are reduced when compared to the rates reached in monoculture. Because there were no mycocin effects, their results suggested that the yeasts were competing for limiting resources. However, when potentially limiting resources (nitrogen, carbon, or vitamins) were added individually to cultures in stationary phase, some of the yeasts did not resume growth in the mixed culture.

Possible explanations for these results are

1. multiple limiting factors operating in mixed culture conditions,
2. accumulation of inhibitory substances produced during late growth stages, and
3. unnatural conditions caused by simultaneous inoculation in systems that are usually sequential.

The study demonstrates that the nature of yeast–yeast interactions can be complex, and that more studies using conditions closer to natural situations are desirable. The fruit–yeast community is an attractive system to use in this manner.

Mutualism is another factor that can influence the amplification phase of the yeast community habitat cycle. In the section on symbiosis we discuss the cactus–*Drosophila* yeast system where yeasts have positive influences on one another's growth rates. The mechanism responsible for the observed mutualism is not known, but is probably related to beneficial cross-feeding, multiple limited resources, detoxification of toxic chemicals, or the extreme character of the habitat that constrains the types of yeasts that can grow there. As mentioned earlier, this phenomenon was not found in similar studies of fruit yeasts, where yeast–yeast interactions were mainly competitive (Abranches et al. 2001).

When a habitat shows a transition from one type of community to another (succession) the sequential use of resources and products of earlier occupants may dictate the community organization over time. This process has been studied in the Amazonian amapa fruit (*Parahancornia amapa*). The succession has several important features (Morais 1995b). As the amapa fruits decay, simultaneous changes take place in the yeast composition, the vector community, and the physical features of the decaying substrate. Over a 2-week period, the yeast community showed a distinct pattern with two species present throughout the study period, five species dominating the middle phase (days 4–10), and four species in the later stage (days 10–14). Population sizes (cfu's) peaked at 10^8 after days 2–3, fell to 10^4 by day 8, and increased again to 10^6 by day 14. The dynamic changes in community composition were thought to be influenced by 1) the rapid use of fermentable sugars during the early phase, 2) the activity of killer yeasts during the intermediate phase, and 3) occupation by yeasts with broad physiological abilities when the pH increased from 4.0 to 6.0 and nutrients were exhausted in the later period. Even though guilds of drosophilids were implicated in the process, the authors concluded that other insect vectors were probably also important.

The yeast community associated with prickly pear (*Opuntia stricta*) cladode and fruit rots in eastern Australia provides an interesting case that has been studied extensively by J.S.F. Barker and colleagues (Barker et al. 1983, 1984, 1986a, 1986b, 1987, 1994, Barker and Starmer 2000, Vacek et al. 1985). Part of their effort has been focused on discovering the important biotic and abiotic factors involved in the maintenance of genetic diversity. The central organism was *Drosophila buzzatii*, which uses the rotting cladodes of the *Opuntia* plants as oviposition sites. The larvae ultimately derive nutrition from both the plant tissue and the yeasts that grow in it. The variation in the yeast communities of the breeding sites provides an opportunity for habitat selection by the flies, and is thus a key topic of study since habitat selection could foster the maintenance of genetic diversity in the flies. One of the many studies (Barker et al. 1987) of yeast heterogeneity explored the influence of both time (weeks) and space (separate localities) on the community structure of the yeasts. The two localities in eastern Australia were 7 km apart, and seven or eight rots were studied at each locality. Each rot was sampled sequentially for yeast species abundance over a 3-week period. Even though the yeast species were essentially the same at the two localities, the variation over space and time differed. One site showed considerable variation from rot to rot and less variation over the sampling period, whereas the other site had little variation from rot to rot but more variation over time. Several explanations were proposed, based on the age, structure, and density of the cactus population, as well as the influence of *Cactoblastis cactorum* (a moth that initiates rots in *Opuntia*) on the incidence of rots in young versus older cactus populations. One of the localities was characterized as a low density population with young, relatively homogeneous cacti that were prone to attack by the moth, whereas the other site was characterized by cacti of mixed ages that provided heterogeneous sites for yeast communities to develop. The study illustrates the importance of historical factors in the trajectory and character of yeast communities in space and time.

5.1.5. Benefits to Vector

Yeasts that directly or indirectly benefit their vectors are more likely to be transported to new habitats. Many examples of the benefits that yeasts can provide to their vectors are given in the section on yeast associations with other organisms as symbionts. The community-benefit relationship of cactophilic yeasts and their vector argues for a community-level phenomenon that contributes to community organization and persistence. Some of the potential benefits to the insect include the detoxification of medium- chain fatty acids by *Magnusiomyces starmeri,* and the elimination of harmful volatiles by *C. sonorensis*. However, analysis of larval survival and development (time to develop and size attained in the resulting adult) showed that mixed communities of yeasts in decaying cactus tissue provide better conditions for development (Moreteau et al. 1992, Starmer and Barker 1986, Starmer and Fogleman 1986). The mixed culture effect is to some degree host specific (Starmer and Aberdeen 1990).

5.2. Regional Communities

Local populations are usually thought to occupy an area within which the individuals are free to disperse and have equal likelihoods of contacting other members of their community. For yeasts which live in discrete habitats (e.g., fruit) and rely on vectors for movement to new habitats, the local community would be determined by the neighborhood size of the vector. A group of local communities (regional communities) would have more dispersal potential within each local area, but some constraints on dispersal among the local groups. Often the dispersal constraint can be the lack of suitable habitats between patches, even though the environmental conditions are similar in adjacent areas. Comparisons of groups of local communities in the same geographical area are thus comparisons of regional community structure. The biogeography thus becomes important when exploring biodiversity and the reasons for differences in local community structure as the size of the geographic area is increased. This perspective has been used to study the biodiversity of cactophilic yeasts (Lachance et al. 2000c, 2001b, Starmer et al. 1982, 1992, 2005), yeasts that occur in tree fluxes (Lachance et al. 1995, Phaff et al. 1972) and yeasts associated with ephemeral flowers (Lachance et al. 2001e).

An overall review of the biogeography of cactophilic yeasts published in 1992 (Starmer et al. 1992) used the regional distribution of host plants and indices of yeast community similarity in order to evaluate the influence of host cactus (Stenocereinae, Pachycereinae, Opuntieae, and cactus fruit) and geographic regions (Sonoran Desert, Southern Mexico, Southwestern USA, Caribbean and Venezuela) on yeast community structure. This was done with the help of a two-by-two analysis of variance that compared yeast communities from the same versus different hosts and from the same versus different regions. The definitive comparison was between yeasts from the same host but different regions (SH-DR) and those from different hosts in the same region (DH-SR). Whether cactus-stem yeast communities were compared alone or including cactus-fruit yeast communities, the host effect was significant whereas the region effect was not. The yeast communities from the same host in different regions were more similar to one another than the yeast communities from different hosts of the same regions.

A more recent review of the biogeographic diversity of cactophilic yeasts (Starmer et al. 2005b) examined data from an expanded collection of cactus stems. Two diversity indices (species richness, **S**, and species diversity, **H′**) were used to evaluate the reasons for observed patterns of diversity as the geographic scale increased along the following levels: 1) within a cactus rot, 2) between rots at a locality, 3) among localities, 4) between sub-regions, 5) across regions, and 6) between continents. We found that species richness, **S**, increases as one goes from the lowest level to the highest level but that most of the increase in richness occurs at the regional and continental levels. We concluded that the increase in **S** is due to finding different but relatively rare non-cactus specific yeast species in different regions or continents. These rare additions to the community are likely due to accidents, contamination, or unusual circumstances. They represent indeterminate factors responsible for an increase in biodiversity. In contrast, species diversity (**H′**, relative proportions of species and their uncertainty) is influenced primarily by the abundance of a small number of core cactus-specific species within a sample of rotting cactus tissue. Thus, diversity at the lowest level of information (variation within a sample) accounts for most of the information. If this diversity metric reflects salient biological factors, then local processes have a relatively strong influence on **H′** and regional processes, i.e., speciation, extinction, and immigration have a lesser role in determining **H′**. These findings do not imply a lack of community structuring at the global level. In cases where diversity among strains of globally distributed taxonomic species has been scrutinized closely (Lachance et al. 2000b, 2001a), genetic structuring at levels ranging from ecotype to subspecies or even species has been identified.

A comparison of yeast communities associated with *Drosophila* species across the USA (Lachance et al. 1995) showed that habitats had the largest effect on the yeast community composition. The phylogeny of the drosophilids had only a minor influence on community structure. An east–west gradient in yeast diversification implicated a regional effect (speciation). This observation led to the conclusion that geography was also an important influence on community structure changes. The study also demonstrated that if the physiological profiles of the communities were used instead of the names of taxa, then habitat was the major factor determining the profiles. This is consistent with the view that microbial physiotypes are universally available to fill new niches, as suggested by Beijerinck's principle that "everything is everywhere, the environment selects". However, the regional partitioning of genetically defined species shows that the ubiquity rule cannot be extended indiscriminately to the species themselves. This phenomenon is amply demonstrated by the work of Cadez et al. (2003) on the biogeographic distribution of recently described *Hanseniaspora* species (*H. meyeri, H. clermontiae, H. lachancei, and H. opuntiae*) all of which have almost identical fundamental and realized niches, but differ in the sequences of their D1/D2 region of the 26S rDNA and internal transcribed spacer (ITS) region of 5.8S rDNA.

The literal ubiquity of microbial species has been advocated vigorously, recently, by Fenchel and Finlay (2004). Strong support for the opposite view, which emphasizes the importance of geographic and historical factors as determinants of yeast biodiversity, comes from extensive collections and characterization of yeasts associated with beetles, drosophilids, and bees that visit short-lived flowers (Lachance et al. 2001a). The insect vectors appear to be the primary agents responsible for the organization of the yeast communities, but purely historical explanations for the distribution are obvious in many cases, notably the large-spored *Metschnikowia* species (Lachance et al. 2005). The ephemeral flower–yeast–insect system is a very attractive system for community ecologists to study as it has many desirable features (discrete, known participants, possible to study within and between cycles, worldwide distribution, and suitability for both laboratory and natural experimentation). These characteristics allow scientists to address questions about such things as assembly rules, the dynamics of metacommunities, or community stability and persistence.

5.3. Community Origins

The cactophilic yeast community is characterized by a set of widely distributed, commonly found yeasts (core species: *Pichia cactophila*, *Sporopachydermia cereana,* and *Candida sonorensis*; common

species: *Starmera amethionina* and relatives, *Magnusiomyces starmeri*, *Clavispora opuntiae*, and *Myxozyma mucilagina*). Given that the phylogenetic relationships (Kurtzman and Robnett, 1998a) and the habitat sources of most yeasts are known, we were able to map the habitat ancestry of the cactophilic yeast community (Starmer et al. 2003). The mapping showed that the cactophilic yeasts have independent origins, each coming from different clades, and that their habitat ancestry is diverse. For example, *P. cactophila* appears to have evolved from a lineage that occupied fruit rots, while *S. cereana* has relatives that live in tree fluxes. Because the core and common cactus yeasts are widespread and cactus-specific, they are likely to have evolved early in the radiation of cacti and thus represent an old community. The exact timing is difficult to estimate, but it could be in the order of 50–100 million years. Our relatively new ability to map characteristics on the genetic history of taxa (phylogeny) provides a strong tool for investigating determinants of community structure.

5.4. Community Organization and Phylogeny

Anderson et al. (2004) used the ascomycetous cactophilic-yeast community to study the influence of phylogeny on the abundance of species in the community. This investigation compared each species in the community to all others in terms of genetic distance (from the molecular phylogeny) and relative abundance or frequency of occurrence. Two different results were apparent for yeasts from columnar cactus stem rots and those yeasts from prickly pear cladode necroses. In the former case, abundant yeasts are usually genetically distant from one another, whereas the rare species are more likely to be closely related. In the case of *Opuntia* cladode rot yeasts, closely related and unrelated yeasts have equivalent likelihood of abundance relationships. This was an unexpected result given that the taxa from the two communities are essentially the same. The abundance patterns of the species were nevertheless different, and the authors speculated that the more restrictive environment of the columnar species was at least partially responsible for the outcome. Possible constraints associated with the columnar species included the lack of free sugars, the presence of toxic chemicals, harsh desert conditions, and strict host–vector associations.

5.5. Leaf Surface Communities

Leaf surfaces are commonly occupied by a community of microorganisms that includes bacteria, yeasts, and other fungi (Andrews and Harris 2000, Last and Price 1969). The organisms usually grow at the expense of the leaf exudates but some can use the secretions of insects such as aphids that feed on the leaf surface. In general the phylloplane yeast community includes species of *Bullera, Bensingtonia*, *Cystofilobasidium*, *Cryptococcus*, *Leucosporidium*, *Pseudozyma, Rhodotorula*, and *Sporobolomyces.* Maksimova and Chernov (2004) reported that the dominant forms on leaves in sub-boreal forests of Europe and parts of Russia are *Sporobolomyces roseus*, *Cryptococcus laurentii*, *Rhodotorula minuta*, and *Rhodotorula mucilaginosa. Leucosporidium scotii* was also frequent, but most common on moss-covered sod where *Sp. roseus* was almost never found. One of the main conclusions was that forest yeast communities are more diverse than those communities of other biomes such as tundra or desert. However, they did not consider tropical forests in their analysis. The seasonal transitions in the species present in the leaf-yeast community depends primarily on the type of leaf (e.g., deciduous, evergreen) and the ecosystem in which they occur (Glushakova and Chernov 2004). Extension of these studies to soil, to which leaves are destined, showed that some of the leaf yeasts do join the soil-yeast community as the leaves become part of the litter, although their numbers decline substantially. Di Menna (1959) also reported that phylloplane yeasts only invade the upper layers of the soil, but are not dominant and do not persist. In her study of leaves, she found that yeasts on the leaves of pasture grasses show a seasonal increase in numbers from 10^5 to 10^7 per gram (fresh weight) of foliage. The lowest numbers were observed in the winter and the highest occurred in the summer.

5.6. Bark Beetle–Yeast Associations

Beetles have long been known to engage in diverse associations with yeasts. Particularly important to forest biologists are the bark beetles and the ambrosia beetles. These beetles, in the family Scolytidae (subfamilies Scolytinae and Platypodinae), live in the woody tissue of trees. They depend on fungal communities growing on the walls of tunnels and galleries carved into the wood by adults (sometimes larvae) to feed the young (Farrell et al. 2001, Malloch and Blackwell 1993). Approximately 7,500 beetles are known to associate with ascomycetes in the order Ophiostomatales, referred to as the "ophiostomatoid fungi" (Farrell et al. 2001). The species in the genus *Ophiostoma* are mainly associated with the bark beetles that attack conifers, whereas species of *Ceratocystis*, *Ceratocystiopsis*, and their anamorphs (*Ambrosiella* and *Raffaelea*; Cassar and Blackwell 1996, Jones and Blackwell 1998) are found in association with ambrosia beetles that colonize angiosperms. The bark beetles exhibit life history patterns (primary, secondary, and saprophytic) that are characterized by whether they attack living, previously attacked (or diseased) or dead trees (Paine et al 1997). Distinctions are also made based on whether the beetles possess mycangia that are used to carry the fungi from host to host, or whether the associated fungi are carried outside mycangia.

In both bark and ambrosia beetles, the fungal communities are vectored and inoculated into the tissue by the adult beetles, and thus the symbiosis is generally thought to be mutualistic because both partners benefit from the association. In addition, the *Ophiostoma* species, which are associated mainly with conifers, facilitate use of the trees by beetles, by blocking the tree's secretory canals, which otherwise produce defensive resins and latex (Paine et al. 1997). In contrast to fungus-farming ants, the practice of fungiculture in beetles has originated many times during their evolutionary history, and it appears that there have been no reversals away from fungus farming in the seven known fungiculture lineages of beetles (Mueller and Gerardo 2002).

The literature on these organisms has been reviewed by Francke-Grosmann (1967), and a subsequent updated annotated bibliography by Barras and Perry (1975) covers the early work on many relationships. Much of this was concerned with the nutritional relationship of *Ophiostoma*/*Ceratocystis* species or blue-stain fungi. Other reviews (Paine et al. 1997, Whitney 1982) provide broader insights into the symbiotic relationship between bark beetles and the fungi they carry as they attack the wood of conifer hosts. The evolution of beetle agriculture was discussed most recently by Farrell et al. (2001). The review by Paine et al. (1997) emphasized the multiple interactions of fungi, their influence on host tree mortality, and to a limited extent their saprophytic life history strategy (i.e., use of dead trees woody tissue). Yeasts are often intimately involved in the beetle–fungus–tree system.

Relevant literature about the community ecology of yeasts associated with bark beetles includes discussions of:

1. their role in nutrition of the beetles (Baker and Norris 1968, Barras 1973, Batra 1966, 1967, 1971, Farmer 1965, Giese 1966, Gouger 1972, Norris 1966, Whitney 1971),
2. the presence in the beetles of structural adaptations (mycangia) used for growth and dissemination of microorganisms (Batra 1963a, Farris 1965),
3. the role of the yeasts in chemical communication, for example attraction of the vectors and interactions of the yeasts with other biotic and abiotic factors (Brand et al. 1977, Leufven et al. 1984,

Lu et al. 1967, Miller and Keen 1960, Shifrine and Phaff 1956, Whitney 1971), and

4. the presence of yeasts in the tunnel walls, egg galleries, pupal chambers, or the frass produced during feeding by beetle larvae (Holst 1936, Phaff and do Carmo-Sousa 1962, Phaff and Yoneyama 1961, van der Walt and Nel 1968, van der Walt and Scott 1971a, 1971b, 1971c, van der Walt et al. 1971a, 1971b).

Although there have been no comprehensive comparisons of yeast communities in the beetle–fungus–tree system, it remains an attractive biological system for the study of community ecology and biogeography of yeasts. The worldwide distribution and the diversity of the system provide the opportunity for studying host phylogeny, vector phylogeny and their relationship to yeast community structure across biomes with multiple levels of biogeographic complexity. Comparisons along latitudinal and forest diversity gradients would be especially interesting to community ecologists that seek to understand the importance of local and regional processes in the organization of communities.

6. CONCLUDING REMARKS

Most of this chapter was directed toward reviewing studies of the ecology of yeasts in their natural habitats, and the ways in which yeasts have been used to investigate ecological questions. Ever since Emil C. Hansen made the distinction between yeasts used in the fermentation industry and "wild yeasts" in 1881 (cited in Lund 1956), mycologists have been interested in discovering new taxa and understanding why they live in particular habitats. Herman J. Phaff described his interest in natural yeasts in his autobiographical account *My Life with Yeasts* (Phaff 1986). In this essay he relates the development of his early interest in natural yeasts in the mid-20th century through contacts with evolutionary biologists. Among these were scholars who used naturally occurring drosophilids to study central ideas and questions about evolution and ecology (Theodosius Dobzansky, Hampton Carson, William B. Heed, and J.S.F. Barker). Phaff's collaborations and associations with these evolutionary biologists directly influenced and inspired our interest in yeast ecology, and have to some degree directed the scope of the material presented in this chapter. Others have developed similar lines of approach using diverse biological systems and methods. We have tried to highlight those efforts in this chapter but without a doubt have overlooked some areas that deserved more attention.

If we were to point to a single objective of this review we would hope that it will have been to stimulate others to dedicate time and thought to using natural yeasts as a means of understanding many outstanding questions in Ecology and its sister science, Evolution.

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Part III

Phenotypic, Ultrastructural, Biochemical and Molecular Properties Used for Yeast Classification

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Chapter 7

Methods for Isolation, Phenotypic Characterization and Maintenance of Yeasts

Cletus P. Kurtzman, Jack W. Fell, Teun Boekhout and Vincent Robert

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1. INTRODUCTION

In this chapter, methods for the isolation of yeasts and their maintenance are discussed, as well as procedures for morphological and physiological characterization of strains. In an era of microbial strain identification by gene sequencing, some will ask why there is still a need for morphological and physiological tests, especially considering that identification by gene sequencing is faster and more accurate.

For species identification, many laboratories sequence one or two diagnostic genes. In this case, no physiological tests are done. Alternatively, some laboratories may sort isolates using morphology and physiology or RAPDs before sequencing representative strains. Some laboratories, however, have no sequencing facilities, so identification relies exclusively on standard morphological and physiological tests.

Gene sequence analysis has made the discovery of new species increasingly rapid. For new species descriptions, morphological and physiological properties should also be reported, as such information describes the general biological properties of the species. This is of interest to a wide variety of scientists: metabolic properties may help clinicians to understand the process of mycotic infections; ecologists rely on physiological data to understand ecological interactions and to selectively isolate species groups; and biotechnologists utilize the data to predict which species or strains may have novel or improved applications.

2. ISOLATION OF YEASTS

Yeasts are recovered from a wide range of aquatic, marine, atmospheric and terrestrial habitats. Many yeasts occur widely, whereas some appear to be confined to specific habitats. Yeasts seldom occur in the absence of either molds or bacteria. Consequently, selective techniques are often used for recovery of yeasts, employing media that permit the yeasts to grow, while suppressing molds and bacteria. These media exploit the fact that yeasts are generally capable of developing at pH levels and water activities that reduce or inhibit the growth of bacteria. The media may also include antibiotics or fungistatic agents for the suppression of molds. In addition to the methods discussed in this chapter, the publications of Beech and Davenport (1969, 1971), Boekhout et al. (2002), Davenport (1980b), Deak (2002) and Kurtzman et al. (2003) discuss isolation of yeasts from natural habitats, and the publications of Buckley (1971) and Staib et al. (1989) provide methods for isolating yeasts from clinical specimens.

2.1. Temperatures for Isolation and Growth

Cultures are usually incubated at 20–25°C because most yeasts are mesophilic; however, temperatures between 4 and 15°C are essential for psychrophilic taxa. Higher temperatures, in the range of 30–37°C, are often required for yeasts that are strictly associated with warm-blooded sources. Among these species are the human and animal pathogens within *Kazachstania*, *Macrorhabdus*, *Cyniclomyces*, and *Malassezia*. The latter three genera have exceptional nutritional requirements, and specific information for their isolation is provided later in this chapter or in the chapter describing each genus. These ranges show that incubation temperatures can also serve to selectively isolate particular groups of species.

2.2. Acidified Media (pH 3.5–5.0)

Acidified media provide selective isolation; hydrochloric and phosphoric acids are preferred. Organic acids, such as acetic acid, are not recommended for general isolation purposes, since they are only slightly dissociated at pH 3.5–5.0 and the high concentrations of undissociated acids have an inhibitory effect on many yeasts. Exceptions include *Zygosaccharomyces bailii*, *Z. bisporus* and some strains of *Pichia membranifaciens* (Yarrow 1998).

When yeasts are present in high numbers they may be isolated by directly plating the material, or suspensions of the material, on acidified agar media that may also contain antibiotics or have other selective formulations. Dilution plate techniques may be used for quantitative studies.

Agar in media with a low pH is hydrolyzed when autoclaved. Therefore, the sterilized molten agar is cooled to approximately 45°C and a predetermined volume of acid is added. The medium and acid are quickly but gently mixed to avoid air bubbles and immediately poured into petri plates. The addition of approximately 0.7% (v/v) 1 N hydrochloric acid to YM agar or glucose-peptone-yeast extract agar usually gives the desired pH of 3.7 to 3.8. Many yeasts can be recovered at pH 3.7, but some species, such as those of the genus *Schizosaccharomyces*, are inhibited by high acid media and moderately acidic media with a pH in the range 4.5 to 5.0 give a higher recovery.

When yeasts are present in low numbers, population size can be increased by first incubating the sample in a liquid medium at pH of 3.7 to 3.8. The use of antibiotics or high or low temperatures can provide further selection. The development of molds can be restricted by excluding air from the culture by pouring sterile pharmaceutical paraffin over the surface of the media to form a layer about 1 cm deep. This procedure favors the development of fermentative strains, but may fail to recover aerobic strains. Another method for restricting mold development was proposed by Wickerham (1951) who favored incubating flasks of isolation media on a rotary shaker. Molds are prevented from conidiating and aggregate in pellets that are outgrown by yeasts. The yeasts may be separated from the molds either by allowing the pellets of mold to settle for a few minutes and then streaking the suspension of yeasts onto agar in petri plates, or by removing suspended pellets by aseptically filtering through a loose plug of sterile glass wool. Both fermentative and non-fermentative strains are recovered by this technique, but the method favors those species that grow well under these conditions. These pre-growth methods cannot be used for quantitation assessments.

Wickerham (1969b) described a useful isolation medium, which he termed IM, for isolating yeasts from soil and insect frass. This medium contains Yeast Nitrogen Base plus glucose and six other carbon sources (cellobiose, D-xylose, L-rhamnose, erythritol, D-mannitol,

calcium 2-keto-gluconate). The pH is not adjusted, but drops after inoculation as the growing organisms utilize the ammonium sulfate that is present as a source of nitrogen.

2.3. Osmotic Media

Yeasts can often grow on media with concentrations of sugar that are high enough to inhibit the development of many bacteria. A medium such as glucose-peptone-yeast extract agar or YM agar containing glucose at a concentration of 30–50% is suitable for recovering osmophilic and osmotolerant yeasts from foodstuffs and juice concentrates of low water activity. The selective action of these media can be enhanced by lowering the pH to around 4.5. Osmotolerant yeasts recovered in this way can usually be successfully subcultured on media containing successively decreasing amounts of sugar, for example 30, 10, 4, and 2%.

Yeast populations may be enriched before plating, by cultivation in liquid media such as glucose-peptone-yeast extract broth and YM broth containing from 30 to 50% glucose. Osmotolerant molds are not inhibited at these sugar concentrations, therefore incubation on a rotary shaker is recommended. Wickerham (1969b) described another useful medium for the isolation of yeasts from soil and insect frass. This medium, which he referred to as D-20, contains Yeast Nitrogen Base, 20% glucose, 0.1% yeast extract and 0.1% malt extract.

2.4. Use of Antibiotics and Other Selective Compounds

Several media containing antibiotics have been described (Beech et al. 1980, Bills and Foster 2004, Davenport 1980b, Stone et al. 2004), which can be used to suppress co-occuring microorganisms. The most often used include tetracycline at 50 mg/l, or a combination of penicillin G and streptomycin sulfate, each at a concentration of 150–500 mg/l. Many of these antibiotics are heat labile, and must be added after the medium has been autoclaved and is cool to the touch. In contrast, chloramphenicol (100–300 mg/l) is heat stable and can be added to the medium prior to sterilization. Antifungal antibiotics, which suppress filamentous fungi, should be used with caution to avoid growth inhibiting effects on yeasts. Such antifungals include cycloheximide (100–500 mg/l), cyclosporin A (4–10 mg/l) and pimaricin (5–100 mg/l).

Selective media compounded for the isolation of a particular genus, species, or of yeasts with a particular property are often useful. For example, van der Walt and van Kerken (1961a) described isolating species of *Dekkera* using media containing cycloheximide and sorbic acid at pH 4.8. Van Dijken and Harder (1974) used a medium containing methanol as the sole carbon source, plus cycloserine and penicillin G to inhibit the growth of bacteria, for isolation of yeasts that utilize methanol. Kwon-Chung et al. (1978) described a medium containing creatinine as a nitrogen source, and diphenyl to reduce the growth of molds, to be used for the isolation of *Filobasidiella neoformans*. Another medium for the selective isolation of *F. neoformans* contains Niger seed (*Guizotia abyssinica*), which gives pigmented colonies, and penicillin, streptomycin and gentamicin for suppression of bacteria (Staib et al. 1989).

2.5. Specialized Isolation Techniques

2.5.1. Lipomycetaceae, Methods of Isolation (Provided by J.P. van der Walt and M.Th. Smith)

Various species of the Lipomycetaceae can be recovered from soil and insect frass by a procedure that depends on utilization of thymine as a nitrogen source and resistance to cycloheximide (actidione).

Liquid medium: Add 300 mg chloromycetin (chloramphenicol) to 1 liter distilled water in a 2 liter Erlenmeyer flask and steam (not autoclave) for ca. 20 minutes until the chloromycetin is completely dissolved. After cooling to around 47°C, add 11.7 g Bacto Yeast Carbon Base with vitamins, 400 mg cycloheximide dissolved in 2.5 ml acetone and 310 mg thymine. Mix well. Dispense 50 ml of the medium per 500 ml Erlenmeyer flask. The flasks should be provided with loose plugs of non-absorbant cotton. When cooled to room temperature, inoculate with half a teaspoonful of soil. Incubate on a rotary shaker at 25°C. Examine microscopically after 3 days and then daily for up to 10 days. If growth occurs, filter the culture through a loosely packed glass wool filter. Plate the filtrate onto acidified YM agar, i.e., 3 drops of 5% tartaric acid per 17 ml liquified agar in a petri dish. Mix well by gentle swirling and allow the agar to harden. Incubate at 25°C and examine regularly for the appearance of watery to mucoid yeast colonies. Check microscopically and select several single yeast colonies. Purify on malt agar or YM agar.

Solid medium: Add 15 g deionized agar together with 300 mg chloramphenicol in 1 liter of distilled water and steam until the agar is dissolved. Cool to ca. 47°C, add the Yeast Carbon Base, cycloheximide and thymine, as above, and pour the plates. The solid medium is inoculated with air-dried soil particles or with serial dilution of the soil in sterile water. Spread 0.1 ml of the suspension over the surface of the plate with a spatula. Invert plates and provide with sterile filter paper to absorb excess water. Plate counts give a rough estimate of the Lipomycetes per gram of soil.

2.5.2. Malassezia*, Isolation, Characterization and Maintenance (Provided by E. Guého)*

(*See also Chapter 148* [*Malassezia*]).

Specimens of skin, scalp, nails, hairs, mucosis, blood, catheter or any other human or animal sources should be placed on Dixon's agar (DA) or modified Dixon's agar (mDA) for growth and isolation of *Malassezia* spp. *Malassezia* spp. do not survive below 20°C for a long period of time and are susceptible to desiccation, so samples should be plated as soon as possible. Incubate isolation plates at 32–34°C for 7 days or until growth is apparent.

Catalase activity. Add a drop of commercial hydrogen peroxide to a *Malassezia* culture smeared on a glass slide and observe if there is evolution of oxygen bubbles.

Splitting of esculin. Certain *Malassezia* species possess a β-glucosidase that is able to hydrolyze esculin at the glucosidic bond, thus liberating glucose and esculetin. The phenol moiety reacts with iron to give a black color. Esculin medium in tubes is inoculated by stabbing centrally with a platinum wire covered with the yeast culture, and then incubated at 37°C. Examine daily for 5 days. Blackening is a positive reaction; absence of blackening indicates the absence of β-glucosidase. Esculin medium may be used in petri plates, but the reaction can be slower, giving unclear results.

Utilization of Tweens, Cremophor EL and oleic acid for growth of *Malassezia*. *Malassezia* spp. are lipid dependent and require complex media enriched with lipids for growth. These requirements are used to separate species. To determine this requirement use the following procedure: Two loops of a 4–5 day-old *Malassezia* culture are suspended in 2.5 ml of sterile demineralized water. Add this inoculum to 18 ml of molten Sabouraud agar cooled to 50°C, and then pour immediately into a 9 cm petri plate. After solidifying, punch 2 mm diameter wells into the agar with four devoted to Tween 20, 40, 60 and 80 and a fifth for Cremophor EL in a center well. The wells are filed with 10 µl of each product, which is not sterilized. The petri plates are incubated for 7 days at 32–34°C, and turned upside down

the second day to slow dehydration. To avoid contamination, antibiotics can be added to the Sabouraud agar. These five lipid supplements are soluble and diffuse into the agar. In contrast, oleic acid does not diffuse and must be used in a separate medium, which is glucose-peptone-oleic acid agar.

Maintenance of *Malassezia* cultures. *Malassezia* species do not survive in the refrigerator or at room temperature. Cultures must be maintained at 30–32°C with transfer onto fresh DA, mDA or Leeming and Notman (LNA) agar every 1–2 months. With the exception of the three fastidious species *M. globosa*, *M. obtusa* and *M. restricta*, the other species can be preserved by lyophilization. All species survive freezing at −80°C (Crespo et al. 2000a, E. Guého, unpublished data). Only *M. restricta* needs to be revived every year. For freezing at −80°C or lower temperatures, fresh, 4–5 day-old cells of each *Malassezia* species are suspended in liquid Dixon medium, supplemented with 15% of glycerol and aliquoted into 1–2 ml vials. The vials are cooled at 1°C per min in a progressive freezer to −80°C, and stored at −80°C or lower. To revive cultures, vials are thawed in a 37°C water bath, centrifuged to eliminate the suspending medium, and cultured by spreading the cells sparsely onto DA, mDA or LNA media. The cultures can be incubated between 30 and 35°C, but not outside this range.

2.5.3. Prototheca *Isolation Medium (PIM) (Pore 1973, Pore et al. 1986)*

The following medium has been useful for isolation of species of *Prototheca*, as well as *Auxenochlorella protothecoides* and *Reniforma strues*. To 1 liter of distilled water, add the following: 10 g potassium hydrogen phthalate, 0.9 g sodium hydroxide, 0.1 g magnesium sulfate, 0.2 g potassium phosphate (monobasic), 0.3 g ammonium chloride, 0.001 g thiamine, 10 g glucose, 15 g agar. Adjust to pH 5.1 ± 0.1 with NaOH before sterilization and then autoclave for 15 minutes at 121°C.

To increase selectivity and further suppress yeast contamination, add 5-fluorocytosine (0.25 g/l) after sterilization. To formulate a *P. wickerhamii* selective PIM isolation medium, substitute trehalose for glucose, and for selectivity of *P. zopfii* (varieties *zopfii, hydrocarbonea* and *portoricensis* only), substitute acetate for glucose, or add acetate in addition to glucose. Trace amounts of acetate (<1 μg/l) may completely inhibit the growth of *P. wickerhamii* at pH 5.1, but not at pH 7. Lindane (hexachlorocyclohexane) at 0.01 g/l may be added for mite control. Phthalate (as potassium hydrogen phthalate) is added to PIM as a non-metabolizable buffer. In addition, it also suppresses most bacterial contamination, delays fungal growth and may have uncharacterized beneficial growth-promoting effects for *Prototheca* spp. For assimilation tests of *Prototheca* spp., the preceding medium can be used by substituting carbon sources and other nutrients.

2.6. Use of Membrane Filters

Yeasts may be recovered from liquid substrates by passing the liquid through a 0.45 μm membrane filter (e.g., Mulvany 1969). Solid substrates, such as soils, can be washed to suspend the yeast cells prior to passing the wash solution through the membrane. The filters are placed face-up on the surface of a selective agar medium followed by incubation at a temperature appropriate for the target organisms. Plates should be inspected daily. This technique is particularly useful for recovering yeasts present at low concentrations, and the method can serve as a means to quantitate yeast community densities.

2.7. Purification of Yeast Cultures

Isolates are obtained in pure culture from natural materials, or from enriched cultures, by streaking on a suitable medium, such as glucose-peptone-yeast extract agar and YM agar. Persistent bacterial contamination can often be eliminated by acidifying the media or by adding antibiotics. Single, well separated colonies of each form are selected and streaked again; twice is generally sufficient to obtain pure cultures, but it may be necessary to streak colonies several times. Sometimes separating bacterial contaminants can be a problem, for instance removing lactic acid bacteria from fermentation yeasts, but their presence will be revealed by microscopic observation. It should be noted, however, that where two or more morphologically distinct colonies persistently appear after replating a single colony, they may be morphological or sexual variants of a single species. It is useful to initially save multiple colonies from isolations because some may represent mating types. Cultures must be pure for sequence analysis, growth tests and morphological examination.

3. MORPHOLOGICAL CHARACTERIZATION OF YEASTS

3.1. Description of Agar Grown Colonies

The following factors should be included in a comprehensive colony description:

Texture: whether mucoid, fluid or viscous, butyrous, friable, or membranous. Mucoid growth is frequently associated with encapsulation of cells from production of extracellular polysaccharides; membranous growth generally results from profuse formation of hyphae or pseudohyphae.

Color: any distinctive colors, such as yellow, orange and red, are recorded. The presence of red, orange or yellow non-diffusible carotenoid pigments is characteristic of certain genera, for instance, *Phaffia*, *Rhodosporidium* and *Sporidiobolus*. Other yeasts, such as *Metschnikowia pulcherrima*, certain *Kluyveromyces* species and some adenine-requiring mutants of *Saccharomyces*, produce diffusible, non-carotenoid dark red pigments. The majority of yeasts, however, produce growth which ranges in color from white through cream to tan.

Surface: whether glistening or dull, smooth, rough, sectored, folded, ridged, or hirsute. Strains that are smooth when first isolated sometimes become rough when maintained on agar. This change is, in some cases, accompanied by a change in texture from butyrous to membranous. Restreaking generally results, once again, in formation of smooth and rough colonies.

Elevation: whether the growth is flat, depressed in the center, raised and dome-like, or conical.

Margin: whether the edge of the streak or colony is entire, undulating, lobed, erose, or fringed with hyphae or pseudohyphae.

3.2. Morphology of Asexual Cells

Asexual reproduction, sometimes erroneously termed vegetative reproduction, occurs in yeasts by budding, by fission, and by the production of forcefully ejected ballistoconidia on stalks termed sterigmata. Observing how the ballisto- and blastoconidia are formed (conidiogenesis) can provide information that aids the identification of a strain. Formation of pseudohyphae and septate (true) hyphae are other forms of asexual reproduction that are discussed below.

3.2.1. Budding, Fission, Blastoconidiation

Buds may arise either on yeast cells or on hyphal cells. Budding is initiated by the formation of a small evagination or outgrowth at some point on the surface of the cell. The parent cell remains

more or less constant in size during subsequent development, while the bud (blastoconidium) increases in size to form a new cell, which, usually after some time, separates from the parent (mother) cell. Budding is termed holoblastic or enteroblastic, depending on how the fine structure of the cell wall is formed in the process of budding. All layers of the wall of the parent cell are involved in the formation of a holoblastic bud, and the bud separates, usually on a narrow base. A scar remains on the parent cell through which no further budding occurs. Von Arx and Weijman (1979) considered holoblastic budding characteristic of the Saccharomycetales and their anamorphic states. When budding is enteroblastic, the first bud arises through a rupture in the wall of the parent cell through which the innermost layer evaginates and ultimately grows out to form the outermost layer of the bud. The site of budding is eventually surrounded by a collarette due to the recurrent formation and abscission of a succession of buds arising from the inner layer of the wall of the cell. Enteroblastic budding is characteristic of basidiomycetous yeasts.

Budding is also classified in terms of the position of the site where it occurs. Budding that is restricted to one pole of the cell is termed monopolar, and budding that occurs at both poles of the cell is termed bipolar. Budding from various sites on the cell is termed multilateral or multipolar. When the buds are abstricted on a rather broad base by the formation of a cross wall, the process is referred to as "budding on a broad base" and "bud fission" (Fig. 7.1). Recurrent budding leads to the formation of multiple scars or annellations at the poles of the cell (Streiblová 1971). Bipolar budding is characteristic of the apiculate yeasts.

Budding is also described in terms of the way successive buds are produced. Sympodial budding is on a conidiophore that extends in growth by a succession of apices. A blastoconidium is produced at each apex and the growth continues to the side of the apex; the result is a zigzag appearance, e.g., *Blastobotrys*. Acropetal budding is the formation of successive buds in a chain with the youngest at the apex. Basipetal budding is the formation of successive buds with the oldest at the apex.

Reproduction by fission is the duplication of an asexual cell by means of a septum growing inward from the cell wall to bisect the long axis of the cell. The newly formed fission cells, which are termed arthroconidia (arthrospores), elongate and the process is repeated. Recurrent fission by a cell may give rise to transverse multiple scars or annellations (Streiblová 1971). This manner of reproduction is characteristic of *Schizosaccharomyces*, *Dipodascus*, *Trichosporon* and several other genera (Fig. 7.1).

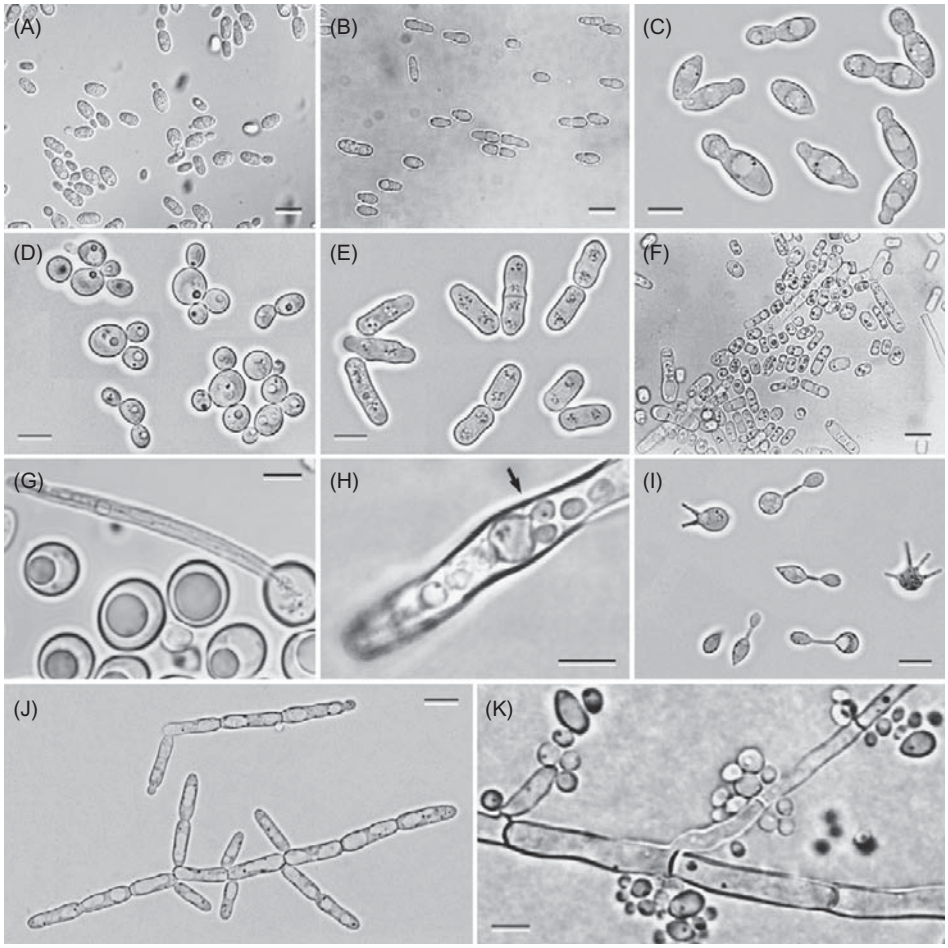


FIGURE 7.1 Various forms of asexual reproduction. (A) Polar budding on a narrow base (*Cryptococcus mycelialis*), (B) Monopolar budding on a wide base (*Malassezia pachydermatis*), (C) Bipolar budding on a wide base (*Hanseniaspora osmophila*), (D) Multilateral budding (*Pichia nakasei*), (E) Fission (*Schizosaccharomyces pombe*), (F) Arthroconidia formed by fission (*Galactomyces geotrichum*), (G) Chlamydospores, one of which has given rise to an ascus (*Metschnikowia fructicola*), (H) Endoconidia produced by budding (arrow) in a hyphal cell (*Candida ontarioensis*), (I) Blastoconidia formed on elongate conidiophores (*Fellomyces polyborus*), (J) Pseudohyphae (*Metschnikowia gruessii*), (K) True (septate) hypha with side branches bearing blastoconidia (*Candida ontarioensis*). (Fig. A, Fonseca et al., this book; Figs B, C, D, E, F, I, J, T. van Beest and T. Boekhout, CBS website; Figs G, H, K, C.P. Kurtzman).

Reproduction by the formation of blastoconidia borne on stalk-like tubular structures is uncommon among the yeasts. This type of reproduction entails the formation by a cell of one or more elongate conidiophores (erroneously termed sterigmata), each of which gives rise to a terminal conidium (Fig. 7.1). On maturation, the conidium is disjointed at a septum either in the mid-region of the conidiophore (e.g., *Sterigmatomyces*) or close to the bud (e.g., *Fellomyces*). The conidia are not forcibly discharged.

Cells can be globose, subglobose, ellipsoid, ovoid, obovoid, cylindrical, botuliform, bacilliform, elongate, apiculate, ogival, lunate, or triangular. Definitions and illustrations of the various possibilities can be found in *Ainsworth and Bisby's Dictionary of the Fungi* (Kirk et al. 2008) and in the glossary of this book. The shape of the cell may reflect the mode of reproduction and, in some cases, it is characteristic of particular genera or species. Some examples include the lemon-shaped cells of the apiculate yeasts *Hanseniaspora* and *Wickerhamia*, the bottle-shaped cells of *Malassezia*, the triangular cells of *Trigonopsis variabilis*, and the lunate cells of *Metschnikowia lunata*.

Cell morphology is examined from cultures grown in liquid media or on agar. The media most commonly used are glucose-peptone-yeast extract, malt extract, and YM broth or agar. Incubation is normally for 2–3 days at 25°C, but some strains may require other temperatures and incubation times, ranging from 4 to 42°C and 1 day to a few weeks, respectively. The culture is examined microscopically, noting the shape of the cells, their mode of reproduction, and whether they are single, in pairs, or aggregated in clusters. The length and width of at least 20 cells are measured and the extreme values should be noted. Some yeasts, notably species of *Malassezia* and *Oosporidium*, grow poorly in liquid media. The latter genus is now recognized to be a dimorphic member of the Pezizomycetes (Kurtzman and Robnett 1998a).

3.2.2. Pseudohyphae and True (Septate) Hyphae

Mature buds can either become detached as discrete cells or remain attached to the parent cell, and give rise to chains or clusters of cells. The tendency of some yeasts to form chains of cells results in the formation of pseudohyphae, defined as a filament composed of a chain of cells that has been formed by budding (Fig. 7.1).

Pseudohyphae may be either rudimentary, in which case they consist of cells of similar size and shape, or they may be differentiated into elongated cells, each of which may produce blastoconidia in a regular and more or less characteristic arrangement. The arrangement of blastoconidia was used for the differentiation of certain genera in earlier taxonomic systems (see van der Walt 1970a). The form of pseudohyphae can be markedly affected by cultural conditions (van der Walt 1970a).

An unusual type of pseudohypha is restricted to some species of *Dekkera*, called blastese. This term describes the germination of blastospores in which the germ-tube results in a slender, aseptate hypha (Langeron and Guerra 1939, 1940). This term has been broadened to include the formation of pseudohyphae consisting of a single filamentous cell which does not form septa, but which sometimes branches.

Some yeasts produce true septate branching hyphae, which elongate by continuous growth of the hyphal tip followed by the formation of septa (Fig. 7.1). Septation lags behind the growth of the hyphal tip to such a degree that the terminal cell, measured from tip to first septum, is normally longer than the preceding cell, measured from first to second septum (Wickerham 1951). The fine structure of hyphal septa varies among taxa, but light microscopy does not reveal much detail of the hyphal septa of filamentous yeasts except the presence of visible pore bodies. Hyphae may proliferate by simple branching, or they may produce blastoconidia on differentiated conidiogenous cells. The presence of blastoconidia on denticles is a characteristic of species of *Trichomonascus* (anamorph *Blastobotrys*) and *Hyphopichia*.

It may be difficult to distinguish true hyphae, pseudohyphae, and intermediate forms. Wickerham (1951) applied three criteria to recognize types of hyphae. He based these criteria on observations of the terminal cells of the filaments. First, true hyphae usually have refractive, straight septa that can generally be differentiated from the edges of vacuoles by their greater thickness and refractivity. There is little or no constriction at the septum. The terminal cells are considerably longer than the cells immediately preceding them. Secondly, pseudohyphae do not have discernible septa, and the ends of intercalary cells are curved and not refractive. There are usually marked constrictions where the cells join. The terminal cell is, as a rule, shorter than or nearly as long as the adjacent cell. It is rare to find a pseudohypha with a terminal cell that is distinctly longer than the adjacent cell. Thirdly, only a small proportion of cells are separated by septa in intermediate forms.

Hyphae of some yeasts break up or disarticulate to form one-celled arthroconidia (arthrospores) (Fig. 7.1). Arthroconidia formed in this way on solid media are frequently arranged in a characteristic zigzag fashion.

Hyphae of some basidiomycetous species form clamp connections (Fig. 7.3). Clamps arise by outgrowths on the hypha at cell division, and connect the two cells that result from the division. Their purpose is to ensure that daughter nuclei, which form during nuclear division, are both transferred to the new cell. One daughter nucleus migrates through the clamp and the other through the hypha. Some strains have incomplete clamps, i.e., the clamp does not connect to the new hyphal cell. This occurs when the nuclei fail to divide. Clamps are characteristic of the dikaryotic phase of basidiomycetous taxa. Hyphae are sometimes joined by a process in which there is the fusion of branches of the same or different hyphae, and this is called anastomosis. Anastomosing hyphae are a characteristic of *Ambrosiozyma platypodis* and certain other species.

The two most common procedures for detecting pseudohyphae and true hyphae are given below. The media most commonly used are corn meal (maize) agar, morphology agar, and potato-dextrose agar, but some clinical laboratories use rice agar, which will also allow formation of chlamydospores by *Candida albicans*. For some species, formation of hyphae and pseudohyphae may be abundant on slants of 5% malt extract agar.

Slide culture. A petri plate containing a U-shaped glass rod supporting two glass microscope slides is sterilized by dry heat at 160–180°C for 2 h. Agar is melted and poured into a second petri plate. The glass slides are quickly removed from the glass rod with a flame-sterilized pair of fine forceps and dipped into the molten agar, after which they are placed back on the glass rod. The layer of agar on the back of the slide is wiped off after it has solidified. In many laboratories the molten agar is poured onto the glass slides to form a thin layer. After the surface of the agar has dried, the yeast is lightly inoculated in either one or two lines along each slide and a sterile coverglass is placed over part of each line. A little sterile water is poured into the petri dish to prevent the agar from drying. The culture is then incubated for up to 21 days at either room temperature or other temperature suitable for the strain. The culture is examined microscopically at intervals of a few days, for formation of hyphae and pseudohyphae along the edges of the streak and under the coverglass.

Dalmau plate. Agar is poured into petri plates, which are then put aside for a day or two to allow the surface to dry. The yeast is inoculated as a single streak near one side of the plate (for example from the ten to the two o'clock positions), and as two points near the other side of the plate (for example at the four and eight o'clock

positions). A sterile coverglass is placed over the center of the streak and another over one of the point inoculations. The cultures are incubated and examined microscopically in the same way as slide cultures.

3.2.3. Asexual Endospores

Asexual endospores (endoconidia) are not commonly formed, but they have been observed in strains of the genera *Trichosporon, Candida, Cryptococcus*, *Cystofilobasidium* and *Leucosporidium*. Endospores are asexual cells that are formed within single cells and in hyphae, and seem to arise by budding (Fig. 7.1). Unlike chlamydospores and ascospores, endospores cannot be selectively stained. They are usually observed in old cultures on YM agar malt agar, potato-dextrose agar and corn meal agar kept at room temperature. No special media have been devised to stimulate the development of endospores. The publication by do Carmo-Sousa (1969b) should be consulted for a more detailed discussion of endospores.

3.2.4. Chlamydospores

The chlamydospore has been defined as a thick-walled, non-deciduous, intercalary or terminal, asexual spore formed by the rounding of a cell or cells (Ainsworth 1971). The asexual nature of the chlamydospore distinguishes it from the teliospore of the Leucosporidiales, Sporidiales and Ustilaginales from which the basidium is produced.

Chlamydospores are generally rich in lipids and well adapted to maintain viability through periods of dormancy. Mature chlamydospores have particular affinities for certain dyes and, in contrast to other asexual cells, are markedly acid-fast on staining, a characteristic shared by ascospores (van der Walt 1970a). In older cultures, chlamydospores shed their outer layers just before or during germination.

Chlamydospores are characteristic of *Candida albicans, C. dubliniensis* and *Metschnikowia* species (Fig. 7.1) but are also occasionally noticed in old agar cultures of other taxa, including some *Trichosporon* and *Cryptococcus* species. Chlamydospores fulfill a dual function in the genus *Metschnikowia* and germinate by budding or give rise to asci. The production of chlamydospores by *C. albicans* is most easily observed in slide cultures on rice agar; corn meal agar also gives good results with some strains. Some laboratories add Tween 80 (1%) to these media. Staib agar has also been reported to cause development of chlamydospores in the preceding *Candida* species (Staib and Morschhäuser 1999).

3.2.5. Ballistoconidia

The formation of forcibly discharged asexual spores, known as ballistospores or ballistoconidia, is a specialized mode of reproduction encountered in some basidiomycetous genera, such as *Sporidiobolus, Bullera*, and *Sporobolomyces*. Ballistoconidia are produced on sterigmata that protrude from asexual cells and are discharged into the air by the so-called droplet mechanism (Kluyver and van Niel 1924).

Ballistoconidia are generally detected as an opaque mirror image of the culture formed by the discharged spores on the lid of an inverted petri plate. In petri plates that are not inverted, colonies that arise from the discharge of ballistoconidia form additional colonies resulting in the migration of the culture across the agar surface. Suitable media are corn meal agar, malt agar, morphology agar, and potato-dextrose agar. Do Carmo-Sousa and Phaff (1962) described the following procedure: inoculate a petri dish containing 10 ml of corn meal agar in two lines at right angles across its diameter. The dish is then inverted over the bottom of another petri dish containing malt agar, on which a sterile slide has been placed. One of the lines is positioned over the slide and the halves of the two dishes are taped together. The culture is incubated at 18 to 20°C. Discharged spores germinate to form colonies on the agar of the bottom dish, and are also collected on the glass slide, which can be removed for examination under the microscope.

3.2.6. Germ Tube Formation by Candida albicans and Related Species

The formation of germ tubes is accepted by many medical laboratories as a reliable means of rapidly identifying *Candida albicans* (Ahearn et al. 1966, Joshi and Gavin 1974, Stenderup and Thomsen 1964), but germ tubes are also formed by the closely related *C. dubliniensis*. A germ tube is a thin filamentous outgrowth without a constriction at its point of origin on the cell. Their formation is influenced by temperature, inoculum, medium and strain. Ogletree et al. (1978) evaluated the various techniques of inducing germ tube formation. A simple method involves suspending cells from a 24-hour-old culture (10^5–10^6 cells per ml) in either normal blood serum or egg albumin. The cells are examined microscopically after incubation at 37°C for 1–3 h.

3.3. Sexual Reproduction in Ascomycetous Yeasts

Many yeasts reproduce sexually, resulting in an alternation of generations with the formation of characteristic cells in which reduction division takes place. In the ascogenous yeasts, the site of meiosis is the ascus, where the haploid generation of ascospores is formed by so-called "free-cell" formation, i.e., the process by which the cytoplasm surrounding the meiotic nuclei becomes enveloped by a wall. In the basidiomycetous yeasts, reduction division is restricted to either the teliospore, or the basidium on which the haploid basidiospores are formed externally.

Ascogenous yeasts may be homothallic or heterothallic, and the asexual phase is usually diploid or haploid, but sometimes both haploid and diploid cells are present in the same culture. Higher degrees of ploidy have also been reported for some species, such as *Saccharomyces cerevisiae* or *Lachancea* (*Saccharomyces*) *kluyveri*, and for the latter species, Wickerham (1958) reported the formation of triploids and tetraploids from conjugation of unisexual diploid cells with unisexual haploid and diploid cells of the opposite mating type.

For haploid homothallic yeasts, plasmogamy, karyogamy and meiosis occur within the zygote, which is often formed by the conjugation of two separate asexual cells or between a cell and its bud. The diplophase is usually restricted to the diploid zygote within which the ascospores are formed. This type of life cycle is termed haplontic.

One method of diploidization involves a haploid asexual cell undergoing mitosis and then forming a bud. The bud remains attached to the parent cell, which is converted into an ascus in which usually one to four ascospores are formed. Asci bearing such vestigial buds are found in *Debaryomyces*, *Torulaspora, Pichia*, and certain other genera. Kreger-van Rij and Veenhuis (1975a, 1976b) and Kreger-van Rij (1977a) maintained that the bud is abstricted, with subsequent dissolution of the cross wall that separates the two cells before the two daughter nuclei fuse. Van der Walt et al. (1977) presented the view that abstriction of the bud is not a prerequisite of the process. This mode of ascus formation is referred to as conjugation between a cell and its bud (mother–daughter cell conjugation) or bud-meiosis. As the process involves the fusion of two sister nuclei, it does not constitute heterogamy. Strains of species in which diploidization is

initiated exclusively by this process would be predominantly inbreeding, because conjugation between a cell and its bud does not involve the fusion of independent cells. A process comparable to cell–bud conjugation appears to operate in the genus *Nadsonia*, where karyogamy is initiated by the fusion of the nuclei of a bud and its parent. The contents of the zygote then move into a bud at the opposite pole. The second bud, which is abstricted by a septum, becomes the ascus.

Diploidization may also be brought about by the fusion of two independent haploid cells. The cells themselves may fuse, giving rise to amoeboid conjugated asci as in *Schizosaccharomyces*, or the cells may form elongated conjugation tubes, which fuse to give a dumbbell-shape as in *Zygosaccharomyces* or *Kodamaea* (Fig. 7.2). Occasionally, the conjugation tubes fail to fuse. Cells bearing abortive conjugation tubes sometimes convert into asci with one or two spores nevertheless (Fig. 7.2). It is presumed that the haploid nuclei of these cells undergo mitosis, and the sister nuclei fuse in a manner comparable to that seen in conjugation between a parent cell and its bud. The process constitutes somatogamous autogamy because the protuberance is not abstricted from the cell. Asci bearing either vestigial buds or abortive conjugation tubes may be formed in the same culture, as seen for *Debaryomyces* and *Torulaspora.*

In homothallic yeast strains with a diploid asexual phase, a single diploid asexual cell may undergo reduction division, and become an unconjugated ascus, as in the genus *Saccharomyces*. The diploid condition is soon restored, either by germinating ascospores conjugating within the ascus, or by daughter nuclei fusing autogamously at the conclusion of the first mitotic division within a germinating ascospore (Winge and Laustsen 1937). The latter process has been referred to as direct diploidization or autodiploidization. The haploid phase is of very short duration in such a cycle, and is restricted to the ascosporal stage. A life cycle characterized by these features is referred to as diplontic.

When some zygotes, in the case of the haplontic cycle, proceed to reproduce mitotically, or when, in the case of the diplontic cycle, diploidization of the ascospores is delayed, the result is an asexual phase consisting of both diploid and haploid cells. The mixed asexual phase can form conjugated as well as unconjugated asci.

The diploid cells of heterothallic strains are normally heterozygous for the mating-type genes and are bisexual. The existence of unisexual diploid strains has been reported (Oshima and Takano 1972, Wickerham 1958). The asci remain unconjugated and unisexual haploid ascospores of both mating types are formed if the diplophase

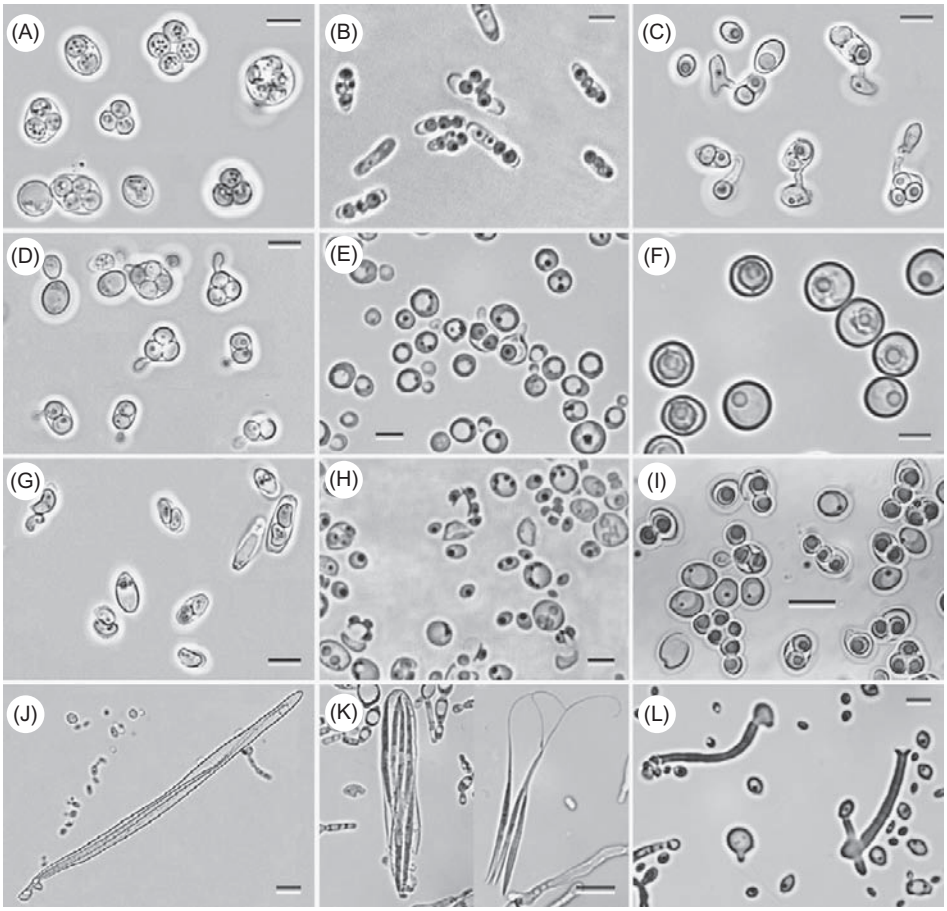


FIGURE 7.2 Various forms of ascospore formation. (A) Persistent, unconjugated asci with globose ascospores (*Saccharomyces paradoxus*), (B) Deliquescent, unconjugated asci with globose and hat-shaped ascospores (*Pichia membranifaciens*), (C) Asci with globose ascospores formed from conjugation of complementary mating types (*Kodamaea ohmeri*), (D) Persistent asci with globose ascospores formed by conjugation between cells and their buds (*Schwanniomyces pseudopolymorphus*), (E) Persistent asci with tapered bud-conjugants and globose ascospores (*Torulaspora delbrueckii*), (F) Persistent, unconjugated asci, each with a roughened, spherical ascospore (*Citeromyces siamensis*), (G) Deliquescent asci with bean-shaped ascospores (*Kluyveromyces marxianus*), (H) Hat-shaped ascospores released from deliquescent asci (*Lindnera veronae*), (I) Saturn-shaped ascospores formed in deliquescent asci (*Saturnispora ahearnii*), (J) Elongated, needle-shaped ascospores in a persistent ascus (*Metschnikowia hawaiiensis*), (K) Elongated ascospores with a whip-like tail released from a deliquescent ascus (*Eremothecium coryli*), (L) Hat-shaped ascospores released from an ascus formed at the tip of an ascophore (*Pachysolen tannophilus*). (Figs A, C, D, G, J, T. van Beest and T. Boekhout, CBS website; Figs B, E, F, H, I, K, L, C.P. Kurtzman).

is stable. Ascospores of opposite mating types either conjugate within the ascus giving rise to the diplophase, as in *Saccharomycodes*, or the ascospores germinate giving haploid asexual cells that can be of opposite mating types. Normally the diplophase can only be restored if conjugation of haploid cultures of opposite mating types occurs. Active cultures of mating types are not invariably stable, and may revert to sporulating cultures as a result of mutation of the mating-type alleles (Hawthorne 1963, Takano and Oshima 1967, 1970). Some species have both heterothallic and homothallic strains; *Pichia membranifaciens* and *Saccharomyces cerevisiae* are examples. Heterothallism may also be associated with sexual agglutination, as in *Wickerhamomyces canadensis* (*Hansenula wingei*) and *Lachancea* (*Saccharomyces*) *kluyveri* (Wickerham 1956, 1958), in which cells of opposite mating types agglutinate when mixed. Agglutination in *W. canadensis* is mediated by complementary glycoproteins present on the surface of cells of the opposite mating types (Brock 1959, Crandall and Brock 1968, Taylor 1965).

The mycelial phase of filamentous yeasts may be either haploid or diploid, and this determines how the ascus is formed. The fusion of two hyphae of opposite sex, or anastomoses of lateral branches of two such hyphae, precedes ascus formation in the case of the haploid heterothallic species *Trichomonascus* (*Stephanoascus*) *ciferrii*. The asci of yeasts with diploid hyphae are often borne either in characteristic clusters (as in *Ambrosiozyma monospora*) or in terminal chains (as in *Ambrosiozyma platypodis*), or hyphal units can be converted into intercalary asci (as in *Saccharomycopsis capsularis*).

Ascospores vary in number present in the asci, in morphology, in size, in ornamentation and in color (Fig. 7.2). The number of ascospores in an ascus can be one or many, though two to four is the most common. Asci with either one or two ascospores are typical for *Lodderomyces*, and some species of *Debaryomyces*. Asci with more than four spores are usually characteristic of *Lipomyces* and some species of *Vanderwaltozyma*, although they have occasionally been observed in strains of some species of *Pichia* and also in *Saccharomyces cerevisiae*.

The shape of ascospores varies widely and includes globose, ellipsoidal, cylindrical, reniform, crescentic, clavate, hat-shaped (galeate), cap-shaped, saturnoid, walnut-shaped, falcate, needle-shaped, and spindle-shaped with a whip-like appendage (Fig. 7.2). The surface may be smooth or rough. However, surface ornamentation, brims and ledges may be reduced to such an extent that they cannot be detected by light microscopy. The morphology of ascospores was previously regarded to have significant diagnostic value, but phylogenetic analyses have shown that ascospore shape is not necessarily useful in genus assignment, as seen for *Pichia* and the former genus *Williopsis* (Kurtzman et al. 2008). Furthermore, variation in the shape of ascospores has been observed within a species. An example is *Kodamaea ohmeri,* where both hat-shaped and globose ascospores have been found, depending on the strains paired (Wickerham and Burton 1954b).

Ascospores may be pigmented in genera such as *Lipomyces, Nadsonia, Pichia, Saccharomycopsis* and *Debaryomyces* and, as a result, sporulating cultures assume an amber, brown or reddish-brown color. Ascospores are generally acid-fast; a notable exception is the spores of *Schizosaccharomyces*. However, the spores of some species of this genus stain blue with Lugol's iodine due to the presence of amyloid substances.

Ascosporulation is generally induced under conditions which restrict asexual growth. However, it is sometimes important that cells should be well nourished and growing vigorously on a rich medium when transferred to these conditions, though some strains sporulate without any special preparation. Some genera sporulate best on a particular medium; acetate agar has been recommended for *Saccharomyces* (Adams 1949, Fowell 1952, Kleyn 1954, McClary et al. 1959), and dilute V8 agar for *Metschnikowia* (Pitt and Miller 1968). Many strains of *Pichia* sporulate on malt agar. Some strains of *Zygosaccharomyces rouxii* are reported to sporulate best on media containing 2% sodium chloride (Wickerham and Burton 1960). Sporulation of many strains of the genus *Lipomyces* is favored by dilute media at low temperatures (15–20°C). Temperature can affect ascus formation markedly, and temperatures between 20 and 25°C are suitable for most yeasts. Nevertheless, strains of *Debaryomyces hansenii* generally sporulate best at 15–20°C, and many species of the genus *Metschnikowia* require temperatures between 12 and 17°C.

Some yeasts sporulate rapidly, i.e., within 24–48 hours, especially when first isolated; others may require much longer – up to 6 weeks or more. The ability to sporulate sometimes declines when a strain is maintained in the laboratory, and may even be lost altogether. This occurs rapidly in some isolates, perhaps after two or three subcultures, whereas other strains may be kept for many years without any apparent decline in their ability to form spores. Occasionally, ascosporogenous diploid cultures will revert to a single haploid mating type following prolonged growth on agar, and it appears that one of the mating types adapts more competitively to laboratory media to the exclusion of the other mating type (Kurtzman and Smiley 1976).

Because conditions vary so greatly for inducing ascosporulation, the following represents a suggested start for ascospore detection: strains placed on slant cultures of YM, 5% malt extract, dilute V8 and RG agars should be incubated at 15 and 25°C and examined weekly for 2 months. If ascosporulation is not detected, other media, such as Gorodkowa and acetate agars, can be tried. Strains that do not form ascospores may represent mating types, and it is advisable to mix strains of the same species with the possibility that complementary mating types may be present. Conjugation often occurs within 24–48 hours, but occasionally 1–2 weeks may be required.

Ascospores can be stained with malachite green, but visualization of unstained cells with either bright field or phase contrast microscopy is favored over staining by many observers. Nonetheless, the following staining protocol is provided. A cell suspension is heat-fixed over a low flame and flooded with a solution of 0.5% malachite green and 0.05% basic fuchsin, and then heated again over a low flame to steaming for 1 min, washed thoroughly in flowing water and blotted dry. Wickerham (1951) recommended flooding a heat-fixed preparation with a 5% solution of malachite green, heating to 80°C for 3–5 min, washing for 30 seconds, and counter-staining with a 0.5% solution of safranine for 10 seconds.

3.4. Sexual Reproduction in Basidiomycetous Yeasts

Basidiomycetous yeasts occur as a budding haplophase, a dikaryotic hyphal phase, or a self-sporulating diplophase. Septate dikaryotic hyphae with clamp connections are characteristic of the sexual states for many basidiomycetous yeasts (Fig. 7.3).

Sexual reproduction in the basidiomycetous yeasts is either heterothallic or homothallic. The incompatibility system in the heterothallic species can be either bipolar or tetrapolar and dikaryotic hyphae are produced by one of the conjugants after a pair of compatible cells have mated. The dikaryotic hyphae eventually form large, inflated, frequently lipid-rich, clamped cells in which karyogamy occurs. These cells have been interpreted as probasidia because of this function. They are intercalary, lateral or terminal, and are sometimes thick-walled. Two kinds of homothallism, which are termed primary and secondary homothallism, are found in homothallic or self-fertile strains (Fell 1974b). The hyphae are uninucleate and lack clamp connections in strains with primary

homothallism, whereas they are dikaryotic and have clamps in those with secondary homothallism. The manner in which the large lipid-rich cells subsequently develop into basidial structures differs widely between taxa (Fig. 7.3).

The thick-walled cells found in the genera *Rhodosporidium* and *Leucosporidium* (Pucciniomycotina) have been referred to as teliospores, teleutospores and ustospores (Fig. 7.3). These cells are of various shapes, ranging from globose, through ovoid to angular, and are sometimes pigmented as in *Rhodosporidium toruloides*. The teliospore forms a germ tube, called a metabasidium or promycelium, after maturing and passing through a period of dormancy (see Chapter 100). For *Leucosporidium scottii,* the diploid nucleus migrates into the basidium where it undergoes reduction division and the resulting four haploid nuclei are distributed throughout the basidium. However, in *Rhodosporidium toruloides,* meiosis occurs in the teliospore and the four haploid nuclei migrate into the young basidium. The basidia then form transverse septa that separate the haploid nuclei. Each nucleus then divides mitotically and one of these nuclei migrates into a bud that usually develops laterally on each of the basidial cells. These haploid sessile buds are termed basidiospores or sporidia. The genetic factors controlling compatibility segregate during meiosis, with the result that the basidiospores give rise to yeast phases of different mating types in heterothallic strains. In some strains of *Mrakia frigida* and *Cystofilobasidium* spp. (Cystofilobasidiales, Tremellomycetes), the metabasidium does not become septate and the basidium remains a single cell on which the basidiospores develop terminally (Fell and Phaff 1970).

Both terminal and lateral basidia are formed on hyphae with clamp connections in *Filobasidium* (Filobasidiales, Tremellomycetes). Thin-walled cells, slightly broader than the hyphae bearing them, elongate to form long slender non-septate metabasidia that taper apically. The tip is inflated and bears six to eight sessile basidiospores arranged in a characteristic petal-like whorl. The basidiospores give rise to yeast phases of opposite mating types. In the genus *Filobasidiella* (Tremellales, Tremellomycetes), the basidia generally arise in groups either terminally or laterally on septate dikaryotic hyphae. The basidia are slender, non-septate elongations with swollen apices. These apices have up to 20 haploid basidiospores in acropetal chains arising from each of four sites on an apex. Karyogamy and meiosis occur in the swollen apices (Kwon-Chung 1980). The sessile basidiospores give rise to yeast phases of opposite mating types.

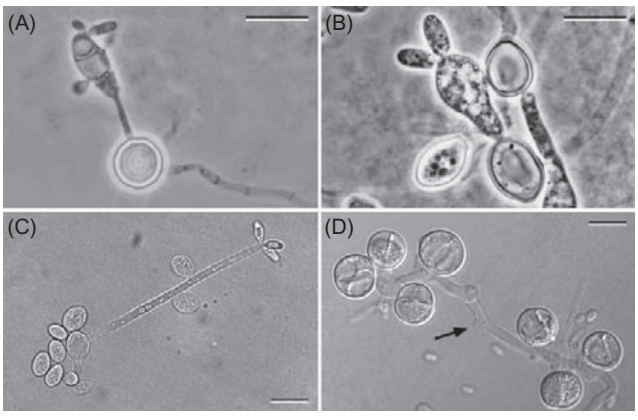


FIGURE 7.3 Sexual states of basidiomycetous yeasts. (A) Basidiospores produced on a transversely septate basidium arising from a teliospore (*Sporidiobolus ruineniae*), (B) Basidiospores formed on a non-septate metabasidium arising from a teliospore (*Mrakia frigida*), (C) Basidospores (top right) produced on an elongated basidium formed from a cell–bud mating and not a teliospore (*Xanthophylomyces dendrorhous*), (D) Clamp connections (arrow) on hyphae that have formed teliospores (*Kwoniella mangroviensis*). (Figs A, B, D, J.W. Fell; Fig. C, T. van Beest and T. Boekhout, CBS website).

Heterothallic basidiomycetous yeasts are often isolated as budding haploid yeast states rather than as the sexual states. Therefore, compatible strains need to be mated to obtain the dikaryotic clamp-bearing hyphal phase. A loopful of cells of each test strain is thoroughly mixed in a small area on an agar plate or slant. The cultures are incubated and examined at frequent intervals for clamped hyphae growing into the agar around colonies where mixing has occurred. Cultural conditions such as temperature may have an appreciable effect on the results of the mating tests. Media such as 5% malt extract agar, corn meal agar, hay infusion agar, and sucrose-yeast extract agar are used (see Banno 1967, Fell and Statzell-Tallman 1980b, Fell et al. 1969, 1973, Kwon-Chung 1976a, 1977b).

The basidia of *Filobasidium* and *Filobasidiella*, as well as the teliospores of some ustilaginomycetous species, will mature and develop on the media on which the dikaryotic mycelium is produced. The teliospores of other pucciniomycetous yeasts fail to germinate under these conditions, and special treatments have been developed for them. Usually, bits of agar containing spores are soaked in demineralized water at low temperatures, sometimes for as long as 3 months, before being put on water agar. The descriptions of the individual species should be consulted for further details.

3.5. Isolation of Mating Types

When dealing with strains whose sexual state or teleomorph is unknown, and when testing for interfertility, it is necessary to isolate mating types from heterothallic species. A strain that does not produce a sexual state might be a mating type, and should be tested to determine mating ability by mixing it with other non-sporulating strains of the same species. The more strains that are tested, the greater is the chance of detecting compatible mating types. Approximately equal amounts of young, actively growing cells of the test strains are mixed on the surface of sporulation media, either as agar slants or in petri plates. The cultures are observed microscopically for conjugation between cells, zygotes and sexual structures after 1–2 days and then at intervals of about 3 days for up to 2–3 months. If sexual activity is detected and the mixture contained more than two strains, the strains are then mixed in pairs to determine which are compatible. More details can be found in the publications of Wickerham (1952, 1960, 1965a, b, 1969a), Wickerham and Burton (1952, 1954a, b, 1962), Phaff and Yoneyama (1961) and Slooff (1964).

Mating types of diploid heterothallic species can be obtained by isolating single ascospores and basidiospores. This is most rapidly and reliably done by using a micromanipulator (e.g., Fowell 1969) when the strain produces enough sexual spores to be easily found and isolated. When the strain produces few ascospores, the heat treatment method described by Wickerham and Burton (1954a) can be used. In this latter method, a suspension of cells from a sporulating culture is heated in 1–2 ml of YM liquid medium, and samples are taken at frequent intervals and spread on agar plates. A temperature should be chosen at which asexual cells are killed within about 5 min, after which only ascospores remain viable, so the colonies arising on plates near the end of a series are derived from ascospores only. The most suitable temperature varies with species, but generally lies in the range of 52 to 65°C. Mating types ordinarily cannot be isolated from basidiomycetous yeasts using the heat treatment method, as there is little or no difference in heat tolerance between basidiospores and asexual cells.

3.6. Visualization of Cell Nuclei

3.6.1. Staining of Nuclei

Several methods have been recommended for staining the nuclei of yeast cells, but none surpass the Feulgen-Giemsa technique of Ganesan and Swaminathan (1958), as modified by Robinow (1961). This method, if followed carefully, gives good preparations and has been applied for chromosomal counts. It involves the hydrolysis of albumin-mounted cells in 1 N HCl at 60°C, followed by washing in a buffer, and the application of Giemsa stain. It should be kept in mind that not only is the time allowed for hydrolysis critical, but also this varies between yeasts. It is therefore necessary to determine the best time to allow for hydrolysis. The publications of Robinow (1961) and McCully and Robinow (1972a, b) should be consulted for further details.

3.6.2. Observing Nuclei in Living Cells

Robinow and Bakerspigel (1965) and Matile et al. (1969) reported a simple method for microscopic observation of nuclear division in living yeast cells that provides spectacular views of division of a cell and the nucleus, with migration of the daughter nucleus into the new cell, followed by separation of the cells. The procedure works well for many yeasts, but the larger cells of *Schizosaccharomyces pombe* and *Wickerhamia fluorescens* give especially good results. A microscope with an oil immersion phase contrast objective lens (ca. 95–100 × magnification) is needed along with a medium, consisting of 21 g gelatin, 0.5 g yeast extract, 2 g glucose and 100 ml distilled water. The distilled water and gelatin are warmed in hot water until the gelatin dissolves, and the other ingredients are then added. The medium is aliquoted into screw-cap microfuge tubes, 1–2 ml per tube, and autoclaved for 15 min at 121°C, followed by storage in a refrigerator. The procedure starts by cooling a microscope slide in the refrigerator followed by addition of a small drop of molten gelatin medium to the slide. Freshly grown yeast cells are gently added to the top of the gelatin droplet using a transfer needle. Few cells are needed. A coverglass is placed over the gelatin droplet and the edges of the coverglass are sealed with Vaseline to prevent drying of the preparation during observation, which can occur over a number of hours. Once placed under the phase contrast objective, cell walls appear black and the nucleus is gray-white with a gray nucleolus. Surprisingly, the nucleus moves quite a lot within the cell and nuclear division usually begins within a few minutes.

3.7. Media for Growth, Selective Isolation, Morphological Characterization, and Development of Sexual States

Acetate agar (Fowell 1952). Dissolve 5 g of sodium acetate trihydrate in 1 liter of water and adjust the pH to between 6.5 and 7.0 before adding and dissolving 20 g of agar. Sterilize by autoclaving at 121°C for 15 min.

Acetate agar (McClary et al. 1959). Dissolve 1 g of glucose, 1.8 g of potassium chloride, 8.2 g of sodium acetate trihydrate, 2.5 g of yeast extract and 15 g of agar in 1 liter of demineralized water. Sterilize by autoclaving at 121°C for 15 min.

AF agar for inducing ascosporulation in species of the Lipomycetaceae. Dissolve 2.85 g sucrose, 230 mg aspartic acid, 510 mg glutamic acid, 245 mg KH_2PO_4, 660 mg $MgSO_4 \cdot 7H_2O$, 1700 μg $FeCl_3 \cdot 6H_2O$, 510 μg $MnSO_4 \cdot 6H_2O$, 4500 μg $ZnSO_4 \cdot 7H_2O$, 410 mg KOH and 20 g agar in 1 liter of demineralized water. Sterilize by autoclaving at 121°C for 15 min.

Corn meal (maize) agar. Heat 42 g of maize in 1 liter of demineralized water at 60°C for 1 h, filter through paper then restore the volume to 1 liter by adding water. Add and dissolve 12 g of agar. Sterilize at 121°C for 15 min. Commercial products are available from various suppliers.

***Cyniclomyces* medium.** Dissolve 10 g of yeast autolysate, 40 g of glucose, 10 g of proteose peptone and 20 g of agar in 1 liter of demineralized water. Sterilize by autoclaving at 121°C for 15 min. Melt the agar just before use, cool to approximately 45°C, then adjust the pH with 1 N HCl to between 3.5 and 4.5 (approximately 4.5 ml is required for each 100 ml of medium), and pour into petri plates. Yeast infusion can be substituted for the water and yeast autolysate. Once the medium has been inoculated, the culture needs to be incubated in an atmosphere of approximately 15% CO_2 at 37°C. A simple method for adding CO_2 to the atmosphere is to place the culture in an anaerobe jar and add a small (ca. 5–8 mm diam.) pellet of dry ice. Close the lid of the jar and approximately the correct level of CO_2 will be present. If dry ice is not available, burning a small candle in the jar for a minute or so will also suffice.

***Debaryomyces hansenii* Differential Medium for selective detection of *D. hansenii*.** Dissolve 5 g yeast extract, 3 g malt extract, 3 g proteose peptone, 10 g glucose and 20 g agar in 1,000 ml deionized water. Sterilize by autoclaving at 121°C for 15 min. After autoclaving, add filter sterilized solutions of Salmon-Gluc (6Cl-3-indoxyl-β-D-glucopyranoside), O-Me-Gl c (1-O-methyl-D-glucopyranoside) and chloramphenicol, in order to make the final amounts per 1,000 ml medium as follows: 0.15 g Salmon-Gluc (6Cl-3-indoxyl-β-D-glucopyranoside, Biosynth, Switzerland), 0.1 g O-Me-β-Glc (1-O-methyl-β-D-glucopyranoside, Biosynth, Switzerland), 0.08 g XGal (5-bromo-4-chloro-3-indolyl-D-galactopyranoside, Sigma), 0.1 g IPTG (isopropyl-D-thiogalactopyranoside, Sigma) and 0.5 g chloramphenicol.

***Dekkera/Brettanomyces* Differential Medium (DBDM).** Dissolve 6.7 g Yeast Nitrogen Base (Difco), 60 ml ethanol (v/v), 0.01 g cycloheximide, 0.1 g *p*-coumaric acid, 0.022 g bromocresol green and 20 g agar in 1 liter of deionized water. All ingredients, except the agar, are sterilized by filtration, and the pH adjusted to 5.4. *Use:* Isolation and identification of *Dekkera* and *Brettanomyces*.

Dichloran 18% Glycerol (DG18) agar for selective isolation of xerotolerant yeasts. Dissolve 5 g peptone, 10 g glucose, 1 g KH_2PO_4, 0.5 g $MgSO_4 \cdot 7H_2O$, 0.002 g dichloran, 0.1 g chloramphenicol, 220 ml glycerol and 15 g agar in 1 liter of demineralized water and sterilize by autoclaving at 121°C for 15 min. All ingredients except glycerol are dissolved by heating, the volume made to 1,000 ml with water and glycerol is then added giving a final concentration of 18% (w/w). Dichloran (2,6-dichloro-4-nitroaniline) is added as 1 ml of a 0.2% solution in ethanol. DG18 agar is also available commercially.

Dichloran Rose Bengal Chloramphenicol (DRBC) agar. Dissolve 10 g glucose, 5 g peptone, 1 g KH_2PO_4, 0.5 g $MgSO_4.7H_2O$, 0.025 g Rose Bengal, 0.002 g dichloran, 0.1 g chloramphenicol and 15 g agar in 1 liter of deionized water and sterilize by autoclaving at 121°C for 15 min. Chloramphenicol can be added before autoclaving. Dichloran (2,6-dichloro-4-nitroaniline) is added in 1 ml of 0.2% solution in ethanol, and Rose Bengal as 0.5 ml of 5% solution in water. Prepared medium should be kept in the dark. *Use:* DRBC agar is one of the most commonly used general purpose media for the enumeration and isolation of yeasts from foods.

Diphenyl solution. Dissolve 1 g of diphenyl in 100 ml of 95% ethanol. Add 10 ml aseptically to 1 liter of molten medium when it has cooled to approximately 45°C. Diphenyl is used to inhibit the growth of molds.

Dixon's agar (DA), van Abbe agar (van Abbe 1964 for *Malassezia* species). Dissolve 60 g of malt extract, 20 g of dessicated ox bile, 10 ml of Tween 40, 2.5 g of glycerol monooleate, 0.5 g of chloramphenicol and 0.5 g cycloheximide in 1 liter of demineralized water, adjust the pH to 6.0–6.5 and then add 15 g of agar. Sterilize by autoclaving at 115°C for 15 min.

Dixon's agar, modified (mDA for *Malassezia* species). Dissolve 36 g of malt extract, 10 g of bacteriological peptone, 20 g of dessicated ox bile, 10 ml of Tween 40, 2 ml of glycerol, 2 g of oleic acid, 0.5 g of chloramphenicol and 0.5 g cycloheximide in 1 liter of demineralized water, adjust the pH to 6.0–6.5 and then sterilize by autoclaving at 115°C for 15 min. The two antibiotics must be doubled for isolation of *Malassezia* species from animals.

Esculin agar (EA). Dissolve 10 g bacteriological peptone, 1 g ferric ammonium citrate and 1 g esculin in 1 liter demineralized water, adjust the pH to 7.4, and then add 15 g agar. Distribute 6 ml per culture tube. Sterilize by autoclaving at 115°C for 15 min.

Esculin agar, modified, Tween 60 esculin agar (TEA) (Kaneko et al. 2005). Dissolve 10 g of bacteriological peptone, 10 g of glucose, 2 g of yeast extract, 0.5 g of ferric ammonium citrate and 1 g of esculin in 1 liter of demineralized water, adjust the pH to 7.4, and then add 15 g of agar. Distribute 8 ml per culture tube. Sterilize by autoclaving at 115°C for 15 min.

Glucose-peptone-oleic acid agar (GPOA). Dissolve 20 g glucose, 10 g bacteriological peptone and 10 ml oleic acid in 1 liter of demineralized water, adjust the pH to 6.0–6.5, and then add 15 g of agar. Sterilize by autoclaving at 121°C for 15 min.

Glucose-peptone-yeast extract agar (GPY agar). Add 40 g of glucose, 5 g of peptone, 20 g of agar and 500 ml of yeast infusion to 500 ml of demineralized water and dissolve. Alternatively, 5 g of powdered yeast extract in 500 ml of demineralized water can be substituted for the yeast infusion.

Glucose-peptone-yeast extract agar, 2% (w/v). Dissolve 20 g of glucose, 10 g of peptone and 5 g of yeast extract in 1 liter of demineralized water, and add 20 g of agar. Sterilize by autoclaving at 121°C for 15 min.

Gorodkowa agar. Dissolve 1 g of glucose, 5 g of sodium chloride, 10 g of peptone and 20 g of agar in 1 liter of tap water. Sterilize by autoclaving at 121°C for 15 min. A variant of this medium, which is used in some laboratories, contains 2.5 g glucose, and 10 g of meat extract, which is substituted for the peptone.

Grape juice pre-sporulation medium. Freshly expressed juice of any variety of grape is diluted to a density of 8–10° Balling (see Glossary). The juice is sterilized in flowing steam or by autoclaving at 110°C for 10 min.

GY agar. Mix 1% glucose, 0.01 1% yeast extract and 2% agar. Sterilize by autoclaving at 121°C for 15 min.

Gypsum blocks and wedges for inducing ascospore formation. Mix 8 parts of gypsum (calcium sulfate hemihydrate) with 3 parts of water. Cast the paste into cylindrical or wedged-shaped cylindrical forms 3–4 cm high. After they have set, the blocks are placed in suitable sterile glass dishes with lids and heated to 110–120°C for at least 2 h. Before use, either sterile water or a solution of mannitol and phosphate is added to a depth of about 1 cm. The mannitol and phosphate solution is prepared by adding 2 ml of a 5% solution of K_2HPO_4 to 18 ml of a 1% solution of mannitol. The gypsum may also be prepared in tubes. Gypsum and water are mixed to a creamy paste which is poured into test tubes through a funnel. The tubes are plugged with cotton, slanted and the gypsum allowed to harden for 24–48 h at 50°C. The slants are sterilized by autoclaving at 121°C for 15 min. The surface of the gypsum is lightly inoculated with freshly grown cells, and every few days the cells are examined microscopically for ascospore formation.

Hay infusion agar. Autoclave 50 g of decomposing hay in 1 liter of demineralized water for 30 min at 121°C and then filter. Dissolve 2 g of potassium monohydrogen phosphate and 15 g of agar in the filtrate, and adjust the pH to 6.2. Sterilize by autoclaving at 121°C for 15 min.

***Kluyveromyces* Differential Medium (KDM).** Basal medium: 5 g yeast extract, 3 g malt extract, 3 g proteose peptone, 10 g glucose, 20 g agar, 1 liter of deionized water. After autoclaving, add filter sterilized solutions of Xgal (5-bromo-4-chloro-3-indolyl-β-Dgalactopyranoside), IPTG (isopropyl-β-thiogalactopyranoside) and chloramphenicol, in order to make the final amounts per 1 liter of medium as follows: 0.08 g Xgal (5-bromo-4-chloro-3-indolyl-D-galactopyranoside, Sigma), 0.1 g IPTG (isopropyl-β-D-thiogalacto-pyranoside, Sigma) and 0.5 g chloramphenicol. The medium is poured into petri plates, and after solidification, 5–10 μl of the sample is streaked, and incubated at 28°C for 7 days. *Use:* KDM has been used with success to selectively isolate *Kluyveromyces marxianus* and *K. lactis.* Dark blue colonies are produced when β-galactosidase is induced in the presence of its chromogenic substrate.

KM-030 agar. Mix 5 g corn meal agar medium, 5 g malt extract, 1 g yeast extract, 2 g glucose, 15 g agar and 1,000 ml distilled water. Sterilize by autoclaving at 121°C for 15 min.

Leeming and Notman agar (LNA) (Leeming and Notman 1987) for *Malassezia* species. Dissolve 10 g of bacteriological peptone, 0.1 g of yeast extract, 5 g of glucose, 8 g of desiccated ox bile, 1 ml of glycerol, 0.5 g of glycerol monostearate, 0.5 ml of Tween 60, 10 ml of whole-fat cow's milk and 12 g of agar in 1 liter of demineralized water. Sterilize by autoclaving at 110°C for 15 min.

Lindegren's pre-sporulation medium. This medium contains 10 ml of beet-leaf extract (100 g per 100 ml of boiling water), 10 ml of beet-root extract (100 g per 100 ml of boiling water), 35 ml of canned apricot juice, 16.5 ml of grape juice, 2 g of dried baker's yeast, 2.5 ml of glycerol, 1 g of calcium carbonate and 3 g of agar. Water is added to give a final volume of 100 ml. The medium is sterilized by autoclaving at 121°C for 15 min.

Malt extract agar, 5% (Wickerham 1951). Dissolve 20 g of agar in 1 liter of distilled water, and then add 50 g of powdered malt extract (Difco). Sterilize by autoclaving at 121°C for 15 min. As little heat as possible should be used when melting the sterile medium.

Malt extract agar (Lodder and Kreger-van Rij 1952). Mix 1 kg of malt with 2.6 liters of tap water and heat to 45°C for 3 h with continuous stirring. Then raise the temperature to 63°C for 1 h. Next filter the mixture through cheesecloth. The filtrate is then filtered through paper and diluted to a density of 15°C Balling using a flotation meter. The pH is adjusted to 5.4, if necessary, and 2% (w/v) of agar is added. The medium is sterilized by autoclaving at 115°C for 15 min.

Malt extract agar-2% calcium carbonate. Finely powdered calcium carbonate is sterilized by dry heat (160–180°C) for 2 h, and 20 g is added to 1 liter of malt agar. It is then sterilized by autoclaving at 121°C for 15 min. When preparing slants and plates, the medium must be gently agitated until the agar is on the point of setting, otherwise most of the calcium carbonate will settle to the bottom of the tube or plate.

Morphology agar. The composition of this chemically defined medium is given in Table 7.1. This medium, marketed by Difco Laboratories as Bacto Yeast Morphology Agar, should be prepared according to the instructions on the container.

Niger seed agar for *Filobasidiella* species (Kwon-Chung et al. 1982b). Dissolve 1 g of glucose and 20 g of agar in 800 ml of demineralized water, and add 200 ml of Niger seed infusion. Chloramphenicol (40 mg/ml) may be added before sterilizing at 121°C for 15 min, and add the diphenyl solution (see above) when the medium has been cooled, just before pouring into petri plates. The Niger seed infusion is prepared by autoclaving 70 g of ground or pulverized seeds of *Guizotia abyssinica* in 350 ml of demineralized water for 10 min at 110°C and then filtering the infusion through gauze.

Niger seed agar for *Filobasidiella* species (Staib et al. 1989). Pulverize 50 g of Niger seed in a blender, boil in 1 liter of demineralized water for 30 min, filter through paper, and restore the final volume to 1 liter. Dissolve 10 g of glucose, 1 g of potassium dihydrogen phosphate, 1 g of creatinine and 15 g of agar in this solution. Sterilize

TABLE 7.1 Composition of Chemically Defined Media*

Formula Ingredients per Liter	Yeast Morphology Agar	Yeast Nitrogen Base for Carbon Assimilation Tests	Yeast Carbon Base for Nitrogen Assimilation Tests	Vitamin-free Yeast Base for Vitamin Requirement Test
Nitrogen sources				
Ammonium sulfate	3.5 g	5 g	none	5 g
Asparagine	1.5 g	none	none	none
Carbon source				
Glucose (dextrose)	10 g	none	10 g	10 g
Amino acids				
L-Histidine monohydrochloride	10 mg	10 mg	1 mg	10 mg
DL-Methionine	20 mg	20 mg	2 mg	20 mg
DL-Tryptophan	20 mg	20 mg	2 mg	20 mg
Vitamins				
Biotin	20 μg	20 μg	20 μg	none
Calcium pantothenate	2000 μg	2000 μg	2000 μg	none
Folic acid	2 μg	2 μg	2 μg	none
Inositol	10 000 μg	10 000 μg	10 000 μg	none
Niacin	400 μg	400 μg	400 μg	none
p-Aminobenzoic acid	200 μg	200 μg	200 μg	none
Pyridoxine hydrochloride	400 μg	400 μg	400 μg	none
Riboflavin	200 μg	200 μg	200 μg	none
Thiamine hydrochloride	400 μg	400 μg	400 μg	n'one
Compounds supplying trace elements				
Boric acid	500 μg	500 μg	500 μg	500 μg
Copper sulfate	40 μg	40 μg	40 μg	40 μg
Potassium iodide	100 μg	100 μg	100 μg	100 μg
Ferric chloride	200 μg	200 μg	200 μg	200 μg
Manganese sulfate	400 μg	400 μg	400 μg	400 μg
Sodium molybdate	200 μg	200 μg	200 μg	200 μg
Zinc sulfate	400 μg	400 μg	400 μg	400 μg
Salts				
Potassium phosphate, monobasic	0.85 g	0.85 g	0.85 g	0.85 g
Potassium phosphate, dibasic	0.15 g	0.15 g	0.15 g	0.15 g
Magnesium sulfate	0.5 g	0.5 g	0.5 g	0.5 g
Sodium chloride	0.1 g	0.1 g	0.1 g	0.1 g
Calcium chloride	0.1 g	0.1 g	0.1 g	0.1 g
Agar	18 g	none	none	none
Amount of final medium from 100 g of dehydrated medium (liters)	2.8	14.9	8.5	5.9
Amount of dehydrated medium per liter of finished medium	35.0 g	6.7 g	11.7 g	16.7 g

[a]These media, originally marketed by the Difco Laboratories of Detroit, Michigan, USA, in dehydrated form, are based on the formulas published by Wickerham (1951), and can be obtained from other suppliers. The commercially produced media have been fortified with greater amounts of biotin, myo*-inositol and calcium pantothenate. The pH has been raised from 5.2 to 5.6 by the phosphates listed in the table.*

by autoclaving at 110°C for 20 min. Add streptomycin (40 μg/ml), penicillin (20 μg/ml), and diphenyl solution (see above) when the medium has cooled to about 50°C. *Filobasidiella* (*Cryptococcus*) *neoformans, F. bacillispora* (*Cr. gattii*), *Cryptotrichosporon anacardii* and *Cr. podzolicus* produce brown, usually mucoid, colonies after 3–8 days at 25°C on this medium.

Oatmeal agar. Boil 40 g of oatmeal in 1 liter of water for 1 h, and then filter through cheesecloth. Add enough water to restore the volume to 1 liter and then add 15 g of agar. Sterilize by autoclaving at 121°C for 15 min.

Polyol Agar. Dissolve 6.7 g Yeast Nitrogen Base (Difco), 5 g either ribitol or glucitol, and 15 g agar in 1 liter of deionized water. Sterilize by autoclaving at 121°C for 15 min. *Use:* Basidiospore formation by *Xanthophyllomyces dendrorhous* (*Phaffia rhodozyma*).

Potato-dextrose agar. An infusion of potatoes is prepared by soaking 300 g of washed, peeled, and finely grated or homogenized potato in 900 ml of water overnight in a refrigerator. The resulting infusion is filtered through cheesecloth and autoclaved at 110°C for 1 h; 20 g of dextrose (glucose) and 20 g of agar are dissolved in 230 ml of the potato infusion and 770 ml of demineralized water. It is then sterilized by autoclaving at 121°C for 15 min. Commercial products are available from various suppliers.

Restricted growth (RG) agar (Herman 1971a). Dissolve 0.2 g of yeast extract, 0.2 g of peptone, 1.0 g of glucose and 20 g of agar in 1 liter of demineralized water. Sterilize by autoclaving at 121°C for 15 min.

Rice agar. Simmer 20 g of *unpolished* rice in 1 liter of water for 45 min, filter, and add water to restore the volume to 1 liter. Add and dissolve 20 g of agar. Sterilize by autoclaving at 121°C for 15 min. Commercial products are available but the results obtained are usually inferior to those obtained with the medium freshly prepared with rice infusion.

Rose Bengal Stain for staining *Prototheca* (Pore 1985). Dissolve 100 mg Rose Bengal in 100 ml distilled water. *Staining procedure:* mix a drop of fresh cells suspended in water with a drop of Rose Bengal

Stain, overlay a coverglass and let stand for 10 minutes. Microscopically, sporangiospores and sporangia become permeable to the red stain, while dauer cells resist staining and are colorless for 30 min. All cells stain if they are heat or alcohol fixed. Dauer cell walls are more light-refractive by phase microscopy (stained or unstained) than are other cell stages.

Sabouraud's 4% glucose agar. Dissolve 10 g of peptone and 40 g of glucose in 1 liter of demineralized water, adjust the pH to 7.0 and then add 20 g of agar. Sterilize by autoclaving at 121°C for 15 min. Commercial products in dried powder form are available from various suppliers.

Sucrose-yeast extract agar. Dissolve 1 g of potassium dihydrogen phosphate, 0.5 g of magnesium sulfate heptahydrate, 0.1 g of calcium chloride, 0.1 g of sodium chloride, 0.5 g of yeast extract, 20 g of sucrose, 5 μg of biotin, and 40 g of agar in 1 liter of demineralized water. Sterilize by autoclaving at 121°C for 15 min.

Trace Element Solution. To 100 ml 0.001 N HCl, add 8 mg $CuSO_4 \cdot 5H_2O$, 40 mg $FeCl_3 \cdot 6H_2O$, 100 mg H_3BO_3, 20 mg KI, 80 mg $MnSO_4 \cdot 4H_2O$, 40 mg $NaMoO_4 \cdot 2H_2O$, 80 mg $ZnSO_4 \cdot 7H_2O$. Add 5 ml of the stock solution to make 1,000 ml final volume.

Vegetable juice agar (Mrak et al. 1942a). Either mince or finely grate equal weights of washed unpeeled carrots, beet roots, cucumbers and potatoes, and mix with an equal weight of water. Autoclave the mixture at 115°C for 10 min and express it through cheesecloth. The extract has a pH of approximately 5.7. Add 2% (w/v) dried baker's yeast and 2% (w/v) agar to the extract. Sterilize by autoclaving at 121°C for 15 min.

V8 juice agar (Wickerham et al. 1946). Suspend 5 g of compressed baker's yeast in 10 ml of water and add to 350 ml of canned V8 juice, adjust the pH to 6.8 and heat in a boiling water bath for 10 min. The pH is again adjusted until a cooled sample has a pH of 6.8. This hot medium is then mixed with a hot solution of 14 g of agar in 340 ml of water. Sterilize by autoclaving at 121°C for 15 min. The canned vegetable juice, which contains a blend of tomatoes, carrots, celery, beet, parsley, lettuce, spinach and watercress, can be obtained at many food shops and is marketed under the name "V8 Vegetable Juice" by Campbell Soup Company, Camden, NJ, USA.

V8 juice agar, dilute (Pitt and Miller 1968). Mix a can of V8 juice with an equal volume of demineralized water and adjust the pH to 5.5 with sodium hydroxide, before filtering through Whatman No. 1 paper. The filtrate is then diluted 1:2, 1:9, 1:19 as required and solidified with 2% (w/v) agar. It is sterilized by autoclaving at 121°C for 15 min.

Vegetable wedges. Wedges of carrot, potato, beet, cucumber or turnip can be used. The vegetables are thoroughly cleaned by washing, and then long cylinders about 1 cm in diameter are cut with either a cork borer or an apple corer. The cylinders are cut obliquely to make wedges, rinsed in cold water and put into a glass tube with a little water to prevent drying. They are sterilized by autoclaving at 115°C for 10 min.

Water (aqueous) agar. Dissolve 20 g of agar in 1 liter of demineralized water. Sterilize by autoclaving at 121°C for 15 min.

***Yarrowia lipolytica* Differential Medium.** Dissolve 5 g peptone, 5 g yeast extract, 1.8 g L-tyrosine, 0.28 g $MnSO_4 \cdot 7H_2O$, 5 g lactate (90% sol) and 20 g agar in 1 liter of deionized water. Adjust pH to 6.2. Sterilize by autoclaving at 121°C for 15 min. *Use:* Isolation and identification of *Yarrowia lipolytica*. The selectivity of this medium is based on the principle that only *Y. lipolytica* produces brown pigments from tyrosine in the presence of Mn^{2+} ions. After incubation at 25°C for 24 h, colonies of *Y. lipolytica* develop a unique deep brown color.

YCBAS agar. The medium is Yeast Carbon Base supplemented with 0.01% ammonium sulfate and solidified with 1.5% agar. Sterilize by autoclaving at 121°C for 15 min.

Yeast infusion agar. Yeast infusion is prepared by mixing 1 kg of compressed baker's yeast with 5 liters of demineralized water and heating to 50°C for 24 h. Add the whites of two eggs to clarify the liquid, shake well and filter through thick paper. Dissolve 15 g of agar in 1 liter of yeast infusion. Sterilize by autoclaving at 121°C for 15 min. Alternatively, 5 g of powdered yeast extract dissolved in 1 liter of water may be used.

Yeast extract-2% glucose agar. Dissolve 5 g of yeast extract, 20 g of glucose and 20 g of agar in 1 liter of demineralized water. Sterilize by autoclaving at 121°C for 15 min.

YM agar (yeast extract-malt extract-peptone-glucose). Dissolve 3 g of yeast extract, 3 g of malt extract, 5 g of peptone and 10 g of glucose in 1 liter of water. The pH of the medium will vary between 5 and 6 across batches of ingredients. The medium is dispensed into containers and autoclaved at 121°C for 15 min. This medium is commercially available as Bacto YM agar (Difco).

YM-2% sodium chloride agar. This medium is prepared by adding 20 g of sodium chloride to 1 liter of YM agar.

***Zygosaccharomyces bailii* Medium (ZBM) for acidified foods and fruit juice concentrates.** Dissolve 20 g fructose, 2.5 g yeast extract, 0.25 g trypan blue, 5 ml acetic acid glacial, 0.1 g potassium sorbate and 30 g Sabouraud dextrose agar in 1 liter of demineralized water. Sterilize by autoclaving at 121°C for 15 min. *Use:* Detection of *Z. bailii* in acidified foods and fruit juice concentrates.

4. PHYSIOLOGICAL AND BIOCHEMICAL TESTS

The physiological tests commonly used for identification are; fermentation of seven to eight carbohydrates, growth on various carbon and nitrogen sources, determination of requirements for vitamins, growth at various temperatures, growth on media with a high content of sugar or sodium chloride, testing for hydrolysis of urea, and for resistance to antibiotics. There is no single standardized method for many of these tests, and results are sometimes dependent on the techniques employed. Some investigators use additional tests. In all cases, young vigorously growing cultures should be used as inocula. It is essential that only pure, high-grade carbohydrates are used in the preparation of the media used in these tests.

4.1. Fermentation of Carbohydrates

There appear to be no exceptions to the rule that when a yeast strain ferments a carbohydrate it is also able to grow on it. However, the reverse does not hold true; many yeasts grow aerobically on sugars they cannot ferment.

Yeasts vary in their ability to ferment sugars, as measured by the production of carbon dioxide. Species of *Kluyveromyces, Saccharomyces* and *Zygosaccharomyces*, for example, ferment glucose and some other sugars vigorously, whereas other species may ferment sugars weakly or not at all.

Various tests have been devised to detect the production of carbon dioxide from carbohydrates (van der Walt 1970a), but Durham tubes containing 2% solutions of sugars have been found to be the most useful for routine purposes (Wickerham 1951). Durham tubes are test tubes with a small inverted tube inserted to collect any gas that may be produced. The basal medium in which the sugars are dissolved must contain adequate nutrients, so that conditions are suitable for the synthesis of the enzyme systems involved in the transport and hydrolysis of the carbohydrates. The basal medium must be free of contamination with fermentable sugars, such as trehalose in yeast infusion, because this contamination may lead to falsely positive results. The fermentation of D-glucose, D-galactose, sucrose, maltose, lactose, raffinose and α-α-trehalose is generally

used for routine identification; other compounds such as inulin, starch, melibiose, cellobiose and D-xylose are less commonly used. The sugars are tested as 2% (w/v) solutions, except for raffinose where 4% is usually used, since some strains cleave and ferment only part of the molecule of this trisaccharide.

Medium. The fermentation basal medium is that of Wickerham (1951). Dissolve 4.5 g of powdered yeast extract and 7.5 g of peptone in 1 liter of demineralized water. Add bromothymol blue to give a sufficiently dark green color. Bromothymol blue stock solution is 50 mg/75 ml distilled water. Add 4 ml of the stock solution per 100 ml fermentation basal medium. Put 2 ml aliquots of basal medium into tubes 12×150 mm in size, which contain small (approximately 6×50 mm) inverted tubes. Sterilize at 121°C for 15 min. During autoclaving, the inserts fill with the liquid medium. Aseptically add 1 ml of the concentrated, filter-sterilized sugar solution to give a final sugar concentration of 2% (w/v). Some laboratories use screw-capped tubes instead of plugged tubes, because they have the advantage that they can be stored longer without drying, but the disadvantage is that screw-capped tubes are less easy to inoculate.

Procedure. Add 1 ml of sterile water to a 24–48 hour YM slant culture and suspend the cells by stirring with the pipette tip. Using this pipette, inoculate each tube of test media, including a sugar-free control, with ca. 0.1 ml of cell suspension. Gently shake the inoculated tubes to mix the cells. The tests are incubated at 25–28°C for up to 28 days. The tubes are shaken and inspected at frequent intervals for accumulation of gas in the insert, and if the sugars are consumed, the indicator changes color from green to yellow, but if the sugars are not consumed and the amino acids present are utilized as a carbon source, the medium turns blue.

The results are scored as follows, depending on the time taken to fill the insert with gas and the amount accumulating:

+, strongly positive, insert filled within 7 days;
l, delayed positive (latent), insert rapidly filled, but only after more than 7 days;
s, slowly positive, insert slowly filled after more than 7 days;
w, weakly positive, the insert is not fully filled with gas (e.g., less than one-third full is often considered weak, whereas greater than one-third full is positive);
−, negative, no accumulation of gas in the insert;
v, variable, some strains are positive, others are negative

4.2. Growth (Assimilation) on Carbon Compounds

The tests determine the ability of a yeast to grow aerobically on a particular carbon compound supplied as the sole source of energy. The tests can be done on either solid or liquid media, but the latter are believed by some taxonomists to give more reproducible results. The size of growth tubes and the amount of medium used can vary widely among laboratories, so the following examples can be modified to suit the investigator.

The method employing tubes of liquid media was described by Wickerham and Burton (1948) and Wickerham (1951). The composition of the defined media that were formulated by Wickerham (1951) are given in Table 7.1. The results are improved by agitating the tubes during incubation (Ahearn et al. 1960, Barnett and Ingram 1955, Barnett et al. 1990). Some laboratories incubate the tests for a period of 3 weeks, others for 4. These long incubations allow the yeasts to adapt to utilize some compounds.

The tests on solid media can be done in two ways. The first is the auxanographic method of Beijerinck (1889a) in which the yeast is suspended in agar in pour plates and the test sugars are spotted at intervals around the circumference. The second method incorporates the test compound into a nutrient agar basal medium in petri plates and the test yeast is inoculated as either a streak or a point on the surface. This technique was used by Shifrine et al. (1954) and Beech et al. (1955) for screening many isolates on a single plate, and can be used with replica-plating. The disadvantage of agar plates is that they tend to dry within a few days and therefore do not detect delayed growth reactions. However, petri plates have the advantage that the results can be read after 2–4 days, and that any contaminating organisms can easily be seen, which makes them very suitable for the preliminary screening of many isolates.

In the present volume, growth reactions on 36 carbon compounds are tested as part of the description for each species. In this volume, the order of the listing of compounds in species descriptions has been changed to correspond with the molecular structure of the compounds (Table 7.2). Additional compounds are often used to discriminate between species and may include 2-keto-D-gluconate, 5-keto-D-gluconate, saccharate, arbutin, D-glucuronate, xylitol and L-arabinitol.

4.2.1. Liquid Media

These tests are conducted in rimless test tubes (16×180 mm), either with cotton plugs or sliding caps. Each tube contains 5 ml of liquid yeast nitrogen base medium with one test substrate, except those for the negative controls, which have no carbon source added, and those for the positive controls, which contain glucose. It is convenient to prepare the tubes in sets of 10. Cleanliness of the tubes is a critical factor in obtaining accurate results, and tubes must be thoroughly rinsed after washing, since residual soap affects the results. Some investigators use an acid wash, such as 1 N HCl.

The tubes of inoculated test media are incubated at either 25°C or 28°C, usually for 3 weeks, though some laboratories extend this to 4. Strains of some species fail to grow, or grow only poorly at these temperatures (see descriptions of individual species), and a suitable temperature must be used; 15°C is suitable for most psychrophilic yeasts. Some laboratories keep the tubes stationary during incubation, but better aeration and mixing are obtained if the tubes are agitated, giving more reliable and quicker results. This can be achieved either by putting the tubes on a rotary shaker or a Rollordrum (New Brunswick Scientific Co.), or by rocking them. The angle of rocking should be as wide as possible without causing wetting of plugs or caps. Statzell-Tallman et al. (2007) modified the incubation procedure through the use of 2 ml microcentrifuge tubes with 1 ml of liquid media. The tubes were placed on a roller drum that had been adapted to accept them. This method reduces the amount of media and volume of glass/plasticware necessary, and increases the number of tests that can be placed on a single roller drum.

Results from growth tests are read after 1 and 3 weeks; in some laboratories also after 2 and 4 weeks. The degree of growth is assessed by eye, by placing the tubes, after they have been shaken to disperse the yeast cells, against a white file card on which lines 0.75 mm thick have been drawn approximately 5 mm apart with black ink. The result is scored as 3+ if the lines are completely obscured, as 2+ if the lines appear as diffuse bands, as 1+ if the lines are distinguishable but have blurred edges, and as negative growth reactions if the lines are distinct and sharp edged. In cases where the outcome is doubtful, growth may be checked by inoculating 0.1 mm of the culture into a tube of fresh test medium. After reading, several culture tubes are tested for a starch reaction as described in a later section.

Results are presented in the descriptions as follows:

+, positive, either a 2+ or a 3+ reading after 1 week, or 2 weeks in some laboratories;
l, delayed positive (latent), either a 2+ or 3+ reading develops rapidly, but after 2 weeks or longer;

TABLE 7.2 Carbon Compounds Commonly Used in Growth Tests

Glucose			Hexose-based carbon sources
Inulin Sucrose	ß-Fructosides		
Raffinose		α-Galactosides	
Melibiose			
Galactose			
Lactose		ß-Galactoside	
Trehalose Maltose Melezitose Methy-α-D-glucoside Soluble starch	α-Glucosides		
Cellobiose Salicin	ß-Glucoside		
L-Sorbose			
L-Rhamnose	Methyl-pentose		
D-Xylose L-Arabinose D-Arabinose D-Ribose	Pentoses		
Methanol	C1	Simple alcohols	Alcohols
Ethanol	C2		
Glycerol	C3	Polyols	
Erythritol	C4		
Ribitol Xylitol	C5		
Galactitol D-Mannitol D-Glucitol *myo*-Inositol	C6		
DL-Lactate	C3	Acids	
Succinate Citrate	C4		
D-Gluconate Gluconolactone 2-Keto-D-gluconate 5-Keto-D-gluconate	Glucose-based		
D-Glucosamine *N*-Acetyl-D-glucosamine		Amines	
Hexadecane	Alkane		

s, slow positive, a 2+ or 3+ reading develops slowly over a period exceeding 2 weeks;
w, weakly positive, a 1+ reading;
−, negative;
(+), seldom positive (if a particular result is seldom observed, it is sometimes given in parentheses);

Various combinations may be also used, such as:

v, variable: some strains are positive, others negative;
+/w, positive or weak: all strains grow, but some of them grow weakly;
w/−, weak or negative.

4.2.1.1. Media

Inoculation medium (Wickerham 1951). Dissolve 6.7 g of Bacto Yeast Nitrogen Base and 1 g of glucose in 100 ml of demineralized water. This 10-fold concentrated solution is filter sterilized and stored in a refrigerator. The final medium is prepared by aseptically pipetting 1 ml amounts of this basal medium into 9 ml of sterile demineralized water.

Growth medium for carbon assimilation tests in liquid medium using Yeast Nitrogen Base. The composition of Bacto Yeast Nitrogen Base is given in Table 7.1. A 10-fold concentrated solution of yeast nitrogen base medium is prepared by dissolving 6.7 g of Bacto Yeast Nitrogen Base in 100 ml of demineralized water and the amount of the carbon compound equivalent to 5 g of glucose (with warming if necessary). For acidic or basic compounds, adjust the pH to 5.6. Filter sterilize and store refrigerated. Tubes of test media are prepared by aseptically pipetting 0.5 ml of the concentrate into 4.5 ml of sterile water in a 16 × 180 mm test tube.

The inoculum for the carbon growth tests is starved before use. The medium used is yeast nitrogen base but with only 0.1% glucose. One or two tubes of this medium are inoculated with ca. 0.1 ml of aqueous cell suspension from a 24–48 hour YM agar slant culture, and the tubes are gently shaken for 48 hours. The growth from these tubes is diluted with carbon-free yeast nitrogen base until the cell suspension has a density of 1+ on the reading card described above. This inoculum is used to inoculate the carbon assimilation tubes with each tube receiving 0.1 ml of inoculum.

4.2.2. Assimilation Tests on Agar Medium

The ability to grow on various carbon sources in an agar medium may be tested either in tubes, or on agar plates by replica plating

or in auxanogram plates. When using agar plates, there is the possibility of cross-feeding between strains. For example, when starch is depolymerized by one strain, the glucose may diffuse to adjacent colonies.

4.2.2.1. Agar Tube Method

The tubes of test media are prepared by aseptically adding 0.5 ml of a 10-fold concentrated filter-sterilized solution of the test compound to 4.5 ml of sterile molten basal medium in 16 × 180 mm test tubes. The tubes are slanted after their contents have been carefully mixed and the agar is allowed to set. Each tube of a set containing the various carbon sources in a basal agar medium is inoculated with one drop of a suspension of cells from a young culture that has been grown on a low-glucose medium as described above. The tubes are incubated at a suitable temperature and the results assessed by inspecting the cultures after 1, 2 and 3 weeks. The amount of growth on each of the test media is compared with a negative control consisting of the basal medium without any carbon source.

4.2.2.2. Replica Plating Method

A set of plates, each containing one carbon source in basal agar medium, is inoculated by transferring cells from many young colonies simultaneously by replica plating or through use of a multipoint inoculator. The results are read by inspecting the plates and comparing the colonies of a negative control provided by a plate containing the basal medium without a carbon source.

Inoculum for the strains to be tested are spot inoculated with a needle or multipoint inoculator onto a plate of a suitable agar medium such as yeast nitrogen base with low glucose. The plates are incubated for 24–48 hours. The petri plates are marked to orientate them and the young colonies are "printed" to each of the plates in the test set. This can be done by replica plating. A sterile velveteen cloth is used, attached to the end of a wooden or metal cylinder. First it is pressed onto the master plate and then, in turn, onto each of the test plates. Alternatively, a multipoint inoculator featuring a cluster of needles or small loops may be used.

4.2.2.3. Auxanograms

Petri dishes of basal agar medium in which yeast cells are suspended in the agar are seeded with carbon sources at various points around the periphery. The basal agar medium is melted and cooled to between 40 and 45°C. A suspension of young cells in water is added to a tube of medium, mixed and then poured into a petri plate. Alternatively, the suspension is pipetted into a petri plate into which the agar medium is then poured and the plate is then gently swirled to mix the contents. Three to six carbon sources can be tested on each petri plate. The bottom of the petri plate is marked around the periphery to locate and identify the carbon sources, and a small amount of each compound is deposited as aseptically as possible on the surface of the agar. The plates are examined for growth around the carbon source every 2 days for up to a week.

4.2.2.4. Basal Agar Medium

Dissolve 6.7 g of Bacto Yeast Nitrogen Base and 20 g of high-grade agar in 1 liter of demineralized water. Dispense into tubes or bottles and sterilize at 121°C for 15 min.

4.2.3. Assimilation Tests in Microplates

The use of physiological tests in tubes or on plates for the identification of yeasts is time consuming, labor intensive, and requires experienced and highly skilled staff. An alternative to the traditional techniques is the use of microplate technology (Robert et al. 1997). Reading of these plates can be automated and linked to identification software (Robert 2003). Inoculation and reading of microplates is easier and faster than the conventional method of using tubes, but it is also more sensitive to the volume of the inoculums, and the strains have to be starved before inoculation to avoid growth on their own reserves. Consequently, this method should be used with care, since false positive results are more frequent than with testing in tubes. This is especially true for basidiomycetous yeasts, such as *Cryptococcus* species.

Details for preparation, inoculation, incubation and reading of the microplates as used at the Centraalbureau voor Schimmelculture (CBS) are provided below. The microplates can be obtained from the CBS. Other companies provide microplates (e.g., API, Biolog) for testing physiological properties of yeasts, and more information about these alternative systems is given below.

4.2.3.1. Preparation of Microplates

Microplate wells for assimilation and other growth tests (Nunc, 96 wells, flat bottom) are filled with 100 μl of the media described in Robert (2003) or available from http://www.cbs.knaw.nl/yeast. Microplates are sealed by heat using polypropylene-aluminum sealing foil, and can be stored at −18°C or lower temperatures for a year or longer. The media are sterilized by heating or filtration prior to their addition to sterile microplates. Alternatively, filled and sealed microplates can be sterilized by gamma irradiation at 4 KGRay. This latter option should be favored if a gamma radiation facility is available.

4.2.3.2. Inoculation and Incubation of Microplates

Fifty μl of inoculum (MacFarland standard # 2, diluted by a factor of 10) is introduced into each well with a multi-channel (8 or 12 channels) pipette. A loose cellophane cover (not sealed, because air should be able to circulate) is placed on the microplate to avoid desiccation of the wells. Replace the cover of the microplate. The microplate is incubated at 25°C (or other temperature if required) for 3 to 10 days. Agitation of the microplates during incubation is not required.

4.2.3.3. Test Reading

Microplates are shaken with a microplate shaker just before automatic reading with a microplate reader. Absorbance values at 405 nm are transferred by cable (RS-232 through a serial port) to the computer and transformed by software computation (Robert 2003, 2007) into negative, weak or positive growth reactions. The results of each test are independently transformed.

4.3. Growth (Assimilation) on Nitrogen Compounds

Yeasts are capable of utilizing a wide variety of nitrogen sources. Nitrate, nitrite, ethylamine hydrochloride, cadaverine dihydrochloride, L-lysine, imidazole, glucosamine, creatine, and creatinine are the compounds most commonly tested. The methods for testing growth are similar to those described for growth on sources of carbon, using liquid or solid media, with carbon base instead of nitrogen base.

Yeasts which grow with nitrate as the sole source of nitrogen are also able to grow on nitrite, but the reverse does not always apply. For instance, some strains of *Debaryomyces hansenii* utilize nitrite but not nitrate. Nitrite can be toxic to the yeast due to nitrous acid formation at pH values below 6, therefore media should be adjusted initially to pH 6.5, and nitrite should be used at low concentrations.

Because of this toxicity, auxanograms are particularly suitable for testing the utilization of nitrite and of ethylamine, which also can be inhibitory at high concentrations. The use of the auxanographic method was recommended by van der Walt (1970a) for testing the utilization of creatine and creatinine.

4.3.1. Assimilation in Liquid Medium (Wickerham 1946b, 1951)

The medium used to test the ability to utilize various nitrogen sources is prepared in much the same way as that used for growth tests on carbon compounds.

Yeast Carbon Base medium (Wickerham 1951). The stock medium is prepared at a 10-fold concentration by dissolving 11.7 g of Bacto Yeast Carbon Base, together with the required amount of the nitrogen source, in 100 ml of demineralized water. The following amounts of nitrogen sources are used: 0.78 g potassium nitrate, 0.26 g sodium nitrite, 0.64 g ethylamine hydrochloride, 0.68 g cadaverine dihydrochloride, and 0.56 g L-lysine (van der Walt and Yarrow 1984a). What is needed is 0.108 g of nitrogen. Using the following example, KNO_3 = formula weight 101.11, i.e., 39.1 (K) + 14.01 (N) + 48 (O_3). KNO_3 is 13.856% N, i.e., 101.11/14.01. Consequently, 0.108 g N/13.856% = 0.779 (or 0.78) g of KNO_3.

The stock solution is sterilized by filtration and stored in a refrigerator until required. The final medium is prepared by aseptically pipetting 0.5 ml of the concentrated medium into 4.5 ml of sterile demineralized water. Tubes for negative controls are prepared by adding filter-sterilized basal medium without a nitrogen source. Typically, the tubes are inoculated with starved cells as part of a set with the carbon assimilation tests. However, for the nitrogen tests, two tubes are made for each strain. After 1 week of growth in the first tube, a small loopful of growth is transferred to the second tube, and it is the second tube that is measured for growth with the reading card as described above.

An alternative method to test for the utilization of nitrate in liquid media is to use a chemical test for nitrate as described by Nickerson (1944a). Four tubes of assimilation medium are incubated and tested after about 3, 5, 10 and 15 days. One of the tubes will give a positive reaction for nitrite if the yeast utilizes nitrate. A few drops of reagent 1 and reagent 2, described below, are added to the culture. The development of a distinct pink or red color indicates the presence of nitrite produced as a result of the partial utilization of nitrate. However, the absence of color may indicate that the nitrate has been completely consumed. Therefore, to test for nitrate in the medium, a small pinch of zinc powder is added to the tube in which the previously described test has just been done. Any nitrate still present is reduced to nitrite in the presence of the zinc and the characteristic pink color will develop after a few minutes.

Reagent 1. Dissolve 8 g of sulfanilic acid in either 1 liter of 5 N acetic acid (1 part glacial acetic acid to 2.5 parts of water) or 1 liter of dilute sulfuric acid (1 part concentrated acid to 20 parts of water).

Reagent 2. Dissolve 5 g α-naphthylamine in 1 liter of either 5 N acetic acid or dilute sulfuric acid (1:20), or dissolve 6 ml of dimethyl-α-napthylamine in 1 liter of 5 N acetic acid.

4.3.2. Auxanographic Method (Lodder and Kreger-van Rij 1952)

A procedure similar to that described for the carbon tests is used, but the basal medium lacks a nitrogen source, and contains glucose as carbon source. Three nitrogen sources are tested on each plate by spotting them around the periphery, and either ammonium sulfate or peptone is spotted in the center and used as a positive control. Sodium nitrite and ethylamine hydrochloride should be used sparingly, and can be applied to the agar by dipping an inoculating needle into saturated solutions of the salts and then touching the surface of the seeded plate with the tip. After the nitrogen sources have been introduced, the plates are incubated at a suitable temperature and inspected after 2 and 4 days for zones of growth around the sites of the nitrogen sources.

Basal medium. Dissolve 11.7 g of Bacto Carbon Nitrogen Base and 20 g of agar in 1 liter of distilled water. Sterilize by autoclaving at 121°C for 15 min.

4.4. Other Growth Tests

4.4.1. Growth in Vitamin-Free Medium and Vitamin Requirements

The ability to grow in a glucose/mineral medium devoid of all vitamins was introduced as a diagnostic property by Wickerham (1951) and extended to include the requirements for individual vitamins by van Uden and Farinha (1958), and van Uden and do Carmo-Sousa (1959).

Vitamin-free medium. The composition of this medium is given in Table 7.1. A 10-fold concentrated stock medium is prepared by dissolving 16.7 g of Bacto Vitamin-Free Yeast Base in 100 ml of distilled water, which is warmed slightly to completely dissolve the ingredients and sterilized by filtration.

Vitamin stock solutions (van der Walt and van Kerken 1961a). The following vitamins and amounts are for 100× stock solutions. The vitamins can be prepared as individual stocks or as a stock mix, and 10 ml of the stock concentrate is added to 1 liter of final strength (1×) medium. For 100× stock solutions, the following amounts are added to 1 liter of demineralized water: biotin, 0.2 mg; calcium pantothenate, 40 mg; folic acid, 0.2 mg; *myo*-inositol, 200 mg; niacin, 40 mg; *p*-aminobenzoic acid, 20 mg; pyridoxine hydrochloride, 40 mg; riboflavin, 20 mg; thiamine, 100 mg. The stocks are sterilized by filtration and stored frozen at −20°C.

The determination of requirements for vitamins is based on whether or not a yeast can grow in a complete mineral medium devoid of either all, one, or a pair of vitamins. A tube of vitamin-free medium is inoculated with starved cells as described under the carbon assimilation tests. Generally, the yeast grows well in this tube owing to reserves being carried over within the cell. A second tube of vitamin-free medium, and a complete set of tubes lacking individual vitamins, when individual requirements are being tested, are inoculated with a small loopful of cell suspension from the first tube. The cultures are incubated and evaluated for growth as described under the procedure for carbon assimilation tests. Note that the test tubes, particularly pre-used tubes, need to be rinsed with 1 N HCl to remove any contaminating vitamins.

4.4.2. Growth in Media of High Osmotic Pressure

Yeasts from substrates with high sugar and salt contents are usually resistant to high osmotic pressures. Many yeast species grow well in glucose concentrations up to 40% by weight, whereas few species grow at sugar concentrations between 50 and 70%. The ability to grow with high concentrations of sugar is generally tested by growth on agar media containing 50% and 60% (w/w) glucose.

Culture media in cotton-plugged tubes and petri plates tend to dry quite rapidly in dry climates as the result of evaporation. The water loss can affect the results of tests and can be reduced by incubating the tubes either in plastic bags inflated with air or with

self-sealing plastic caps (Kimble P.M. Cap Closures, Kimble Inc., Toledo, Ohio, USA), which permit gaseous exchange but prevent water loss. A strip of plastic film is sometimes used to seal petri plates, but this can have an adverse effect on growth by preventing aeration. An alternative is to seal the petri plates with Parafilm (Pechiney Plastic Packaging, Menasha, Wisconsin, USA).

50% Glucose agar. First dissolve 13 g of agar and then 500 g of glucose in 500 g of either yeast infusion or a 1% solution of yeast extract. Dispense into tubes and sterilize at 110°C for 10 min before slanting. Overheating leads to a noticeable browning, because the sugar becomes caramelized; any media showing browning must be discarded.

60% Glucose agar. First dissolve 22.5 g of agar and then 600 g of glucose in 400 g of either yeast infusion or a 1% solution of yeast extract. Dispense into tubes and sterilize at 110°C for 10 min before slanting. Overheating leads to a noticeable browning, because the sugar becomes caramelized; any media showing browning must be discarded.

10% Sodium chloride plus 5% glucose medium (Wickerham 1951). Dissolve 100 g of sodium chloride, 50 g of glucose, and 6.7 g of Bacto Yeast Nitrogen Base in 1 liter of demineralized water. Dispense 5-ml amounts into tubes and sterilize at 121°C for 15 min.

The media are inoculated with a loopful of cells from a 48-hour YM slant and growth is visually assessed.

4.4.3. Growth at 37°C and at Other Temperatures

Many yeasts grow optimally at temperatures between 20 and 28°C. However, some yeasts, and particularly those from restricted and specific habitats, require higher or lower temperatures. Yeasts from polar regions often grow poorly at 20°C but grow well between 4°C and 15°C (Sinclair and Stokes 1965). In contrast, yeasts from mammals, such as *Cyniclomyces guttulatus*, require a temperature of 35–37°C to grow well, and 30–35°C is reported to be the optimum for *Malassezia furfur* by Leeming and Notman (1987). Strains belonging to *Candida*, *Lachancea, Ogataea*, *Pichia*, *Trichosporon* and a few additional genera can grow at temperatures up to 42°C, or slightly higher.

Growth at various temperatures can be assessed in liquid medium or on an agar medium. When testing in liquid medium, a tube of either glucose-nitrogen base medium (as used for assimilation tests) or glucose-peptone-yeast extract broth is inoculated in the usual way and incubated at the chosen temperature. The result is recorded after 1 and 3 weeks (Wickerham 1951). When testing on agar medium, a slant of glucose-peptone-yeast extract agar is inoculated with cells of a young culture and incubated at the chosen temperature for 4 days and then inspected for growth.

4.4.4. Splitting of Arbutin

The test for splitting of arbutin is an alternative to the growth test for determining whether or not a yeast can utilize arbutin. The aglucone moiety, hydroxyquinone, gives a brown color with any soluble ferric salts in the medium, when a yeast strain hydrolyzes arbutin.

For this test, a slant of arbutin agar is inoculated with cells from a young, actively growing culture and incubated at 25°C, or other suitable temperature. If arbutin is split, the agar develops a dark brown color, usually within 2 to 7 days.

Arbutin agar. Dissolve 0.5 g of arbutin, 1 g of powdered yeast extract, and 2 g of agar in 100 ml of demineralized water. Sterilize by autoclaving at 121°C for 15 min. After sterilization, 2 ml of a sterile 1% solution of ferric ammonium citrate is added aseptically to, and mixed with, the molten agar before it is dispensed into tubes or petri dishes. The tubes are slanted and the agar is allowed to set.

4.4.5. Acid Production from Glucose

Yeasts produce traces of volatile and non-volatile acids in culture, however, it is only when large amounts of acetic acid are produced that acid formation has diagnostic value (Custers 1940, van der Walt 1970a). Custer's chalk medium, which contains glucose (5%) and calcium carbonate (0.5%), is used for the test and the result is determined by the calcium carbonate going into solution. A characteristic of *Dekkera* and *Brettanomyces* is acid production, but it is weak in some strains.

The strains to be tested are streaked onto slants or a plate of Custer's chalk medium and incubated at 25°C. The cultures are inspected at frequent intervals for up to 2 weeks for clearing of the medium around the streaks. This results from the chalk being dissolved by any acid that may have been formed.

Custer's chalk medium. Dissolve 50 g of glucose, 5 g of finely powdered calcium carbonate, 5 g of yeast extract powder, and 20 g of agar in 1 liter of demineralized water. Sterilize by autoclaving at 121°C for 15 min. Cool tubes to around 45°C and agitate the medium gently to resuspend the chalk and then slant in a cool place so that the agar gels quickly before the chalk can settle.

4.4.6. Formation of Extracellular Amyloid Compounds (Starch Formation)

Aschner et al. (1945) and Mager and Aschner (1947) found that some yeasts form starch-like extracellular polysaccharides, which give a blue to greenish-blue color with iodine solution. One of the conditions required was that the pH of the medium be maintained below 5.0. However, some species, such as those of *Leucosporidium*, give a positive result to the starch test at pH values above 5.0.

Testing in liquid culture at pH 5.6 (Wickerham 1951, 1952). Cultures for the carbon growth tests, which contain sugars or polyhydric alcohols, are tested for the presence of amyloid compounds. Cultures giving strong growth are tested after incubation for 7 days and, if these give a negative result, other strongly growing cultures are tested after the next reading. The test is done by adding one or two drops of dilute Lugol's iodine and mixing it with the culture by shaking the tube. A positive result is indicated by the development of a color varying from dark blue to green. The strain may be retested by cultivating it in yeast nitrogen base medium with 3% glucose if the result is doubtful.

The relatively large amount of glycogen synthesized by some yeasts interfers with the test, especially if iodine solutions stronger than 0.02 N are used. The brown color typical of glycogen may mask a weak starch reaction. The tubes should be allowed to stand at room temperature for several hours when this occurs, after which time the brown color of the glycogen reaction will have disappeared and the blue color of the starch reaction remains.

Testing on solid media. One or more strains are inoculated onto agar medium in petri plates. The cultures are incubated for 1–2 weeks, then flooded with dilute Lugol's iodine, and inspected for formation of a blue to green color.

Lugol's iodine solution (Gram's modification). Dissolve 1 g of iodine and 2 g of potassium iodide in 300 ml of demineralized water.

4.4.7. Hydrolysis of Urea

Seeliger (1956) tested the hydrolysis of urea by yeasts on Christensen's urea agar. Hydrolysis is generally absent in ascogenous species, whereas it is present for basidiomycetous genera such as

Cryptococcus and *Rhodotorula* (Abadie 1967a, Hagler and Ahearn 1981). The ascogenous yeasts *Schizosaccharomyces pombe* and *Lipomyces* species are exceptions. Booth and Vishniac (1987) established the presence of urease and, probably, its role as the major enzyme concerned in the utilization of urea by yeasts. Urease catalyzes the hydrolysis of urea, giving ammonia and carbamate which, itself hydrolyzes to form carbonic acid and another molecule of ammonia (Andrews et al. 1984). The overall reaction leads to an increase in pH. The test can be done on solid (Seeliger 1956) or liquid media (Barnett et al. 1990).

Testing on solid media. Cells from a young culture are inoculated onto a slant of Christensen's urea agar (Christensen 1946), and a control tube of the basal medium without urea, and incubated at 25°C. The cultures are inspected daily for up to 4 days, and the result is recorded as positive when a deep pink color develops in the tube of test medium but not the control.

Christensen's urea agar. Dissolve 1 g peptone, 5 g sodium chloride, 2 g dihydrogen phosphate and 12 μg phenol red in 1 liter of demineralized water and adjust the pH to 6.8. Add and dissolve 20 g of agar and dispense 4.5 ml amounts into 16 mm diameter plugged glass tubes. Autoclave at 121°C for 15 min, then add 0.5 ml of a filter-sterilized 20% solution of urea. After mixing, slant the tubes and allow the agar to set. This medium is commercially available in powdered form.

Testing in liquid media. Difco Bacto Urea R Broth is dissolved in sterile demineralized water and amounts of 0.5 ml are dispensed into tubes aseptically. A loopful of cells from a 1–2 day-old culture is suspended in the broth and incubated at 37°C (regardless of whether the yeast can grow at this temperature). The tubes are examined every half hour for a change of color to red, which indicates hydrolysis of urea. Many yeasts giving a positive result produce the color change within half an hour, most do so within 2 hours and all within 4 hours.

4.4.8. Lipase Activity

Lipase activity has been reported in several species, including *Yarrowia lipolytica, Candida rugosa* and *Zygoascus hellenicus*. Several methods have been proposed, and these methods use substrates such as tributyrin, olive oil, tallow, Tween 40, 60, and 80, as well as partial glyceryl esters of higher fatty acids (Bulder 1955, Sierra 1957, Tuynenburg-Muys and Willemse 1965). Tuynenburg-Muys and Willemse (1965) recommended the use of partial glycerol esters of higher fatty acids, which have a higher melting point than beef tallow.

Method: Melt and filter fresh beef suet, then sterilize the tallow by autoclaving it at 121°C for 15 min. Pipette approximately 0.5 ml of molten fat into a slightly warmed sterile petri plate and then tilt it from side to side so that the fat spreads evenly over the bottom. Remove surplus fat with a pipette. Put the dish in a refrigerator for an hour or two to solidify the fat. Melt 18–20 ml of either YM agar or Gorodkowa agar and let it cool to about 40°C, pour over the fat and allow to set. The plates are inoculated by streaking the test strains across the plate, cutting slightly into the agar medium with the needle, and incubating at 25°C. The plates are inspected daily for the formation of an opaque zone, formed by calcium salts of the liberated fatty acids, which is usually apparent along the streak within a week.

4.4.9. Cycloheximide Resistance

Whiffen (1948) was the first to report that yeasts varied in their sensitivity to the antibiotic cycloheximide (Acti-dione). Her results indicated that yeasts could be divided into three categories: 1) markedly sensitive, inhibited by 1 μg/ml, e.g., *Saccharomyces cerevisiae*; 2) moderately sensitive, inhibited by 25 μg/ml, e.g., *Schizosaccharomyces pombe*; 3) tolerant, not inhibited by concentrations as high as 1000 μg/ml, e.g., *Kluyveromyces lactis*.

The test is done in liquid Bacto Yeast Nitrogen Base with D-glucose, as for the assimilation tests, with cycloheximide added to give a final concentration (w/v) of either 0.1% (1000 μg/ml, 1000 ppm) or 0.01% (100 μg/ml, 100 ppm). The results are read and scored in the same way as the carbon assimilation tests.

4.4.10. Tolerance of 1% of Acetic Acid

Sand (1973) and Pitt (1974) showed that yeasts could be distinguished on the basis of their resistance to benzoic and acetic acids. A test was described by Yarrow (1984d) for growth on a medium containing 1% acetic acid to discriminate *Zygosaccharomyces rouxii* from *Z. bailii* and *Z. bisporus*.

A 4-mm loopful of the same cell suspension used to inoculate assimilation tests is either spotted onto or streaked across an agar plate of test medium. The plates are incubated at 25°C and examined after 3 and 6 days for the development of colonies.

Acetic-acid (1%) agar. Dissolve 10 g glucose, 1 g tryptone, 1 g powdered yeast extract and 2 g agar in 100 ml of demineralized water and autoclave at 121°C for 15 min. Cool the sterilized medium to between 45°C and 50°C, add 1 ml of glacial acetic acid, mix rapidly and pour into petri plates.

4.4.11. Gelatin Liquefaction

The ability to liquefy gelatin is of limited diagnostic value since few yeasts are strongly proteolytic. This property is used as a confirmatory test for species which liquefy gelatin rapidly and completely within about a week.

Stelling-Dekker (1931), Lodder (1934) and Lodder and Kreger-van Rij (1952) used a medium containing malt extract and 20% gelatin, whereas Wickerham (1951) used a synthetic medium containing 10% gelatin, which was preferred for standardization. Inoculate tubes of test medium with the same amount of inoculum as each tube of assimilation medium. When done on plates, the surface of the medium is inoculated with a needle or a multi-point inoculator. The cultures are examined regularly for up to 3 weeks for signs of liquefaction.

Medium. Dissolve 100 g gelatin, 5 g glucose and 6.7 g Bacto Yeast Nitrogen Base in 1 liter of demineralized water, dispense into either tubes or bottles. Sterilize by autoclaving at 121°C for 15 min. The medium in tubes is allowed to gel with the tubes in a vertical position.

4.4.12. Diazonium Blue B Color Reaction

Van der Walt and Hopsu-Havu (1976) reported that basidiomycetous yeasts gave a dark red color reaction when a buffered solution of Diazonium Blue B (DBB) was applied to the cultures, whereas ascogenous yeasts did not give this reaction. The mechanism of the reaction has not been elucidated, but the test can be used to determine whether an asexual yeast is basidiomycetous or ascomycetous. The synonymy in the chemical nomenclature of the reagent and related compounds has been discussed by Barnett et al. (1990).

Reaction on solid media. Strains are cultivated on YM agar. Van der Walt and Hopsu-Havu (1976) incubated the cultures for 3 weeks, however, Hagler and Ahearn (1981) reduced this period to 5–7 days, followed by 16 hours at 55–60°C. Hagler and Mendonça-Hagler (1991) reduced the time needed for this test even further by incubating the cultures on carbon base-urea agar at 25°C for 3 days, followed by incubation overnight at 55°C. Culture plates are cooled to

room temperature before the cultures are tested. One or two drops of freshly prepared chilled DBB reagent are applied to the surface of each colony. The result is recorded as positive if a dark to violet red color develops within 1–2 min at room temperature.

Reaction in liquid media. Strains are cultivated in 5 ml of yeast nitrogen base with 0.5% glucose (pH 7.0) for 3 days with agitation, but slow-growing strains may have to be cultivated for longer. The cells are collected by centrifugation and the supernatant is discarded. The cells are then suspended in 0.5 ml of 0.05 N KOH and the tube is placed in boiling water for 10 min. The suspension is cooled to ambient temperature and mixed with 2.5 ml of 95% ethanol. The cells are sedimented by briefly centrifuging, and the supernatant is discarded. The cells are suspended in 0.3 ml of DBB reagent. The test is scored positive if a violet color develops within a few seconds. The color is retained by the cells for several hours if 0.1 ml of 95% ethanol is added immediately after the color has formed.

DBB reagent. The DBB reagent is prepared by dissolving 15 mg Diazonium Blue B salt (Brentamine Blue B, ICI plc; Fast Blue Salt B, Farbwerke Hoechst AG) in 15 ml of chilled 0.25 M tris(hydroxymethyl)aminomethane (Tris) buffer, pH 7.0. The salt is unstable under warm and damp conditions, but 15-mg portions of the dye can be stored in sealed tubes at 4°C. The freshly prepared reagent is kept in an ice bath, and used before it turns dark yellow, which is within about 30 min.

4.4.13. Canavanine-Glycine-Bromothymol Blue (CGB) Agar for Identifying Filobasidiella neoformans (Cryptococcus neoformans) and Sister Species

Filobasidiella neoformans can be distinguished from *F. bacillispora* within 2–5 days by incubating cultures on CGB agar at 25°C. Isolates of *F. bacillispora* hydrolyze glycine and are resistant to L-canavanine. The pH of the medium rises and the color of the bromothymol blue indicator turns to blue when glycine is hydrolyzed. Most isolates of *F. neoformans* do not hydrolyze glycine, and the few that do are sensitive to the canavanine, so the medium remains greenish-yellow in color (Kwon-Chung et al. 1982b, Min and Kwon-Chung 1986).

A loopful of cells from a young culture is streaked onto CGB agar in either a tube or a petri plate and incubated at 25°C for up to 5 days. The color of the medium does not change if the strain is *F. neoformans* (*Cr. neoformans*), but turns blue if the strain is *F. bacillispora* (*Cr. gattii*).

Canavanine-glycine-bromothymol blue (CGB) agar. The complete medium is prepared by cooling 900 ml of bromothymol agar (below) to about 55°C and adding 100 ml of stock solution A (below).

Stock solution A. Dissolve 300 mg L-canavanine sulfate, 100 g glycine, 10 g potassium dihydrogen phosphate, 10 g of magnesium sulfate heptahydrate, and either 10 drops of Bejectal with vitamin C (Abbott Laboratories, Chicago, IL, USA) or 10 mg thiamine hydrochloride in 1 liter of demineralized water, adjust the pH to 5.6 and filter sterilize.

Bromothymol blue solution. Dissolve 0.4 g sodium bromothymol blue in 100 ml of demineralized water and filter sterilize.

Bromothymol blue agar. Dissolve 20 g agar in 880 ml of demineralized water and add 20 ml bromothymol blue solution. Sterilize by autoclaving at 121°C.

4.4.14. Melanin Synthesis on L-DOPA Medium

The formation of melanin-like pigments from various *ortho*- and *para*-diphenols is a rapid presumptive test for *Filobasidiella neoformans* and *F. bacillispora*. Note that *Cryptococcus podzolicus* and *Cryptotrichosporon anacardii* are also able to form melanin (Okoli et al. 2007, Petter et al. 2001). A variety of substrates may be used: extracts of the seeds of *Guizotia abyssinica* (Niger seed), catechol, chlorogenic acid, protocatechuic acid, norepinephrine, dopamine, hydroxymetanilamine, dihydroxymetanilamide and dihydroxyphenylalanine (DOPA) (Chaskes and Tyndall 1975, 1978, Nurudeen and Ahearn 1979, Staib 1962).

Cells from a young culture are streaked onto L-DOPA agar in either a tube or a petri plate and incubated at a temperature of 20–30°C for up to 72 hours. Colonies of *F. neoformans* are black on this medium.

L-DOPA solution. Dissolve 0.04 g dihydroxyphenylalanine (DOPA), 1 g asparagine, 1 g L-glutamine and 1 g glycine in 200 ml of demineralized water. Adjust the pH to 5.5 with 1 M potassium hydrogen phosphate (about 2.5 ml is needed) and filter sterilize the solution.

Basal medium. Dissolve 4 g potassium dihydrogen phosphate, 2.5 g magnesium sulfate heptahydrate, 10 mg thiamine hydrochloride, 20 μg biotin, 0.5 g glucose and 25 g agar in 800 ml of demineralized water. Adjust the pH to 5.5 with approximately 7 ml of 1 M potassium hydrogen phosphate and sterilize by autoclaving at 121°C for 15 min. Cool the agar medium to 55°C and mix with the L-DOPA solution before pouring into petri plates or test tubes. The complete medium should be stored at 4°C and used within 1 week of preparation.

4.4.15. Tetrazolium Indicator Medium (TTC Medium)

Media containing tetrazolium salts are used as an aid in isolating and presumptively identifying some species (Mendel et al. 1960, Pagano et al. 1957, Yamane and Saitoh 1985). *Candida tropicalis* produces dark red to maroon colonies from reduction of the tetrazolium salt, whereas yeasts that are incapable of reducing the tetrazolium salt, such as *Candida albicans*, produce pale pink to whitish colonies.

Cells are either streaked or spotted onto the agar. The plate is incubated for 24–48 h and then inspected for colored colonies.

TTC stock solution. Dissolve 1 g of 2,3,5-triphenyltetrazolium chloride in 10 ml of demineralized water. Sterilize by filtration and store at 4°C in a dark glass bottle.

Basal medium. Dissolve 10 g mycological peptone, 10 g glucose, and 15 g agar in 1 liter of demineralized water. Sterilize by autoclaving at 121°C for 15 min. Melt the agar just before use and cool to 45–50°C, then add 0.1 ml of the stock TTC solution, to give a final concentration of 100 μg per ml, and pour into petri plates. The final pH of the medium is 7.0.

5. RAPID IDENTIFICATION SYSTEMS BASED ON GROWTH REACTIONS

As is apparent from the foregoing protocols for using diagnostic media, considerable time and labor are involved. There are a number of diagnostic systems that include prepared media, which have met with varying degrees of success for yeast identification. Some of the better known of these systems are listed below. A detailed analysis has been prepared by Robert (2003), and this should be consulted before considering the above systems for general yeast taxonomic studies. Also, see section 4.2.3, which describes an additional system using microtiter plates.

5.1. Automated Systems for Identification of Yeasts

API System. The API System (API 20C or API/ATB ID 32C) is the most commonly used system for identification of yeasts. API kits consist of plastic strips in which 20 or 32 growth tests are done in small wells. Results can be read manually or automatically. Reading is done at 18–24 hours, or after 4 hours for the Rapid ID 32. Identification is performed using a coding system and by comparing the results to a database of 42–63 species. The system, which has been well received, is directed primarily to clinical species and will not distinguish a broad range of yeasts.

Biolog. The MicroLog YT Station from Biolog can identify 267 yeast species using a panel of 94 tests in a microplate. Microplates can be read manually or automatically, and results are compared to the databases and a probablistic identifcation is provided.

Vitek. Vitek 2 ID-YST, developed by BioMérieux, has 47 biochemical tests. The database contains 51 species that can be identified within 15 hours. The emphasis of this system is on clinical yeasts.

5.2. Chromogenic Media

CHROMagar Candida. Commercially available CHROMagar Candida is a chromogenic differential culture medium that is used to isolate yeasts from clinical specimens. Moreover, it allows a first presumptive identification of a number of clinically important yeast species, e.g., *C. albicans, C. glabrata, C. tropicalis, C. krusei* and *S. cerevisiae* (Bouchara et al. 1996, Odds and Bernaerts 1994, Pfaller et al. 1996). Importantly, due to morphological differences between the colonies of these yeast species, it is also useful in assessing the extent of single species or multispecies infections (Murray et al. 2005). However, when additional species are being tested it is not always possible to distinguish between them. For instance, *C. glabrata* and *C. rugosa* could not be differentiated, and *C. krusei* could be confused with *C. firmetaria* and *C. inconspicua* (Hospenthal et al. 2006). Some researchers have explored the usefulness of CHROMagar Candida for the differentiation of food-related yeasts. Tornai-Lehoczki and coworkers (2003) studied yeast isolates from salads using this medium, and concluded that it is a practical method for the differentiation and rapid preliminary identification of yeast isolates from food sources. Deak (2003) provided detailed information on the colony morphology of 12 yeast species, including *C. zeylanoides, Debaryomyces polymorphus, Saccharomyces cerevisiae, S. exiguus, Kluyveromyces lactis, K. marxianus, Torulaspora delbrueckii, Zygosaccharomyces rouxii* and *Z. bailii*. Both species of *Kluyveromyces* and the two *Zygosaccharomyces* species could be differentiated. *Candida glabrata* and *Pichia kudriavzevii* (*Issatchenkia orientalis*) could not be easily differentiated, nor could *Debaryomyces hansenii* and *Torulaspora delbrueckii* (see e.g., Fig. 2.6–1 in Deak 2003). However, *C. pintolopesii, C. saitoana* and *S. cerevisiae*, isolated from feed, could be differentiated (Bovill et al. 2001). *Prototheca* species have also been studied, but it was found that the morphology of their colonies was indistinguishable from those of *C. parapsilosis* (Casal et al. 1997).

6. MAINTENANCE OF YEAST CULTURES

Maintenance of yeast cultures on a medium that contains glucose as the only carbon source reduces the risk of changes in growth and fermentative patterns due to the selection of mutants (Scheda 1966). The properties of a strain can change within a few days due to selection when an unstable strain is cultivated on media containing malt extract. Many basidiomycetous yeasts do not survive during prolonged storage on a glucose-peptone medium, although they grow well on it. Potato-dextrose agar is more suitable if cultures of these yeasts are to be kept on agar for a long period. The majority of yeasts may be stored at temperatures between 4 and 12°C and subcultured at intervals of 6–8 months. Some yeasts, for instance *Kazachstania* spp. and *Malassezia* spp., need to be subcultured every month. Strains of species of *Dekkera* and *Brettanomyces* produce excessive amounts of acetic acid, and inclusion of 1–2% calcium carbonate in the medium prolongs their viability. Nevertheless, these yeasts still need to be subcultured every 2 months, or sometimes more frequently.

Some ascogenous and basidiosporous yeasts lose their ability to reproduce sexually when maintained by serial cultivation on laboratory media, whereas other isolates still sporulate after 50 or more years in cultivation. However, for many strains, ability to sporulate is either impaired or lost within a timescale varying from a few weeks to several years. For heterothallic species, one mating type may selectively predominate in laboratory culture, which results in the loss of the sexual state. For these reasons, it is important to preserve nomenclatural types and reference strains with one of the more permanent conservation techniques as soon as possible after acquisition. Suitable techniques are lyophilization (Kirsop and Kurtzman 1988), L-drying (Mikata and Banno 1989), or freezing in either liquid nitrogen or a mechanical freezer at temperatures between −60 and −135°C, although liquid nitrogen is preferred.

6.1. Lyophilization

The procedure of lyophilization freeze-dries cultures to an inactive, low moisture state. The process starts by suspending actively growing cultures in a cryoprotectant such as sterile bovine serum or skim milk. The volume of cryoprotectant depends on the size of the ampoule used. Ampoules used in the ARS Culture Collection (NRRL) are made from 6 mm outside diameter pyrex glass tubing, which is cut in lengths of 100 mm. One end is fire-polished in a gas–oxygen flame to remove sharp edges and the other end is sealed by flame. In the ARS process, ca. 0.1 ml of suspension containing cells and bovine serum is added aseptically to the sterile, labeled lyophil tubes, which have a small cotton plug. After filling, the cotton plug is pushed a short distance into the tube and the excess cotton is burned off in a gas flame. The tube is then inserted into a rubber connector on the manifold of the lyophil machine. After all of the tubes are inserted, the manifold is lowered so that the ends of the tubes are immersed in a 50% ethylene glycol bath cooled to ca. −30°C with dry ice. Once the contents of the tubes are frozen, the bath temperature is raised to ca. −20 to −25°C with fresh ethylene glycol and the vacuum pump is started. Drying takes ca. 2 hours and is finalized by raising the manifold and allowing further drying at room temperature. Each ampoule is sealed with a gas–oxygen torch and measures about 50 mm in length after sealing (Fig. 7.4).

Some lyophil machines use larger ampoules that may contain 1 ml of cell suspension. These larger tubes may be initially frozen, but do not need immersion in a freezing bath because evaporation of this larger volume is adequate to keep the preparations frozen. Depending on design, the larger ampoules may be sealed with a gas–oxygen torch or by inserting a rubber stopper into the ampoule while it is still under vacuum.

An ampoule of each strain lyophilized should be tested for viability within a few days of processing. This is done by suspending the lyophilized pellet in liquid growth medium and determining if growth occurs. Rough quantitation of viability can be made by streaking a loopful of the suspension onto an agar plate. Many microorganisms lyophilize well, but only a few percent of the original cell population survives the process. Nonetheless, there is little

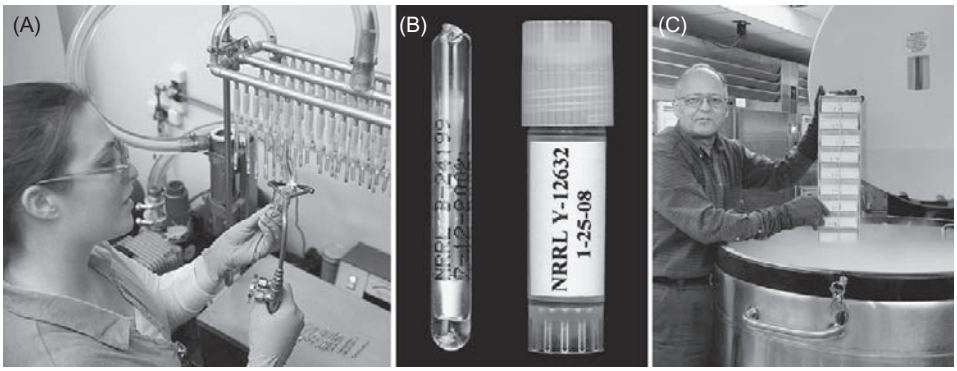


FIGURE 7.4 Preservaton of cultures. (A) Lyophilization of cultures. Ampoules containing yeast cells and a cryoprotectant were placed on the manifold of the lyophil apparatus and have been freeze-dried. The ampoules are being sealed with a gas–oxygen torch. A dry ice-ethylene glycol bath (covered) for freezing the ampoules is at the base of the manifold. A vacuum pump is at the left. The vertical metal tube behind the manifold on the left is a dry ice moisture trap to prevent contamination of the vacuum pump with water from drying cultures. A vacuum gauge is immediately behind the manifold base. (B) Lyophilized culture (left). Note the pellet of dried cells in the bottom of the tube. Cryovial (right) for storing cultures in liquid nitrogen. (C) Liquid nitrogen storage of cultures. Ampoules of cultures are arranged in numbered boxes and stored in the vapor phase of liquid nitrogen, which is pooled under a platform in the bottom of the freezer . (Photographs by Don Fraser, National Center for Agricultural Utilization Research).

evidence that certain nuclear genotypes preferentially survive, although plasmids may sometimes be lost. Lyophilized strains generally survive for many decades, though there are exceptions and the cultures should be checked periodically for viability. Lyophilized cultures are usually stored in a refrigerator at 4–5°C, because frozen storage seems unnecessary.

6.2. L-Drying

A process termed L-drying has been successfully used by several large culture collections in Japan (Mikata and Banno 1989). The process is similar to lyophilization with the exception that cells and cryoprotectant are dried more slowly under vacuum and do not freeze. L-Dried ampoules are sealed in the same manner as lyophilized preparations.

6.3. Liquid Nitrogen Preservation

Some microorganisms do not survive lyophilization or L-drying. The most common alternative, which is generally the most effective, is frozen storage at low temperatures. While storage in −80°C and −125°C mechanical freezers is often satisfactory, storage at still lower temperatures is preferable. The choice is the vapor phase of liquid nitrogen, which is ca. −180°C. Liquid nitrogen at atmospheric pressure has a slightly lower temperature of −196°C (−320°F), but a concern with immersion storage is that ampoules might leak and when thawed, the trapped liquid nitrogen will expand to gas so rapidly that the ampoule explodes, potentially causing serious injury to the person thawing the sample.

The general procedure for preparing microorganisms for liquid nitrogen storage is to suspend cells from an actively growing culture in a cryoprotectant such as 10% glycerol. Usually 1 ml of suspension is placed in a 2 ml cryoampoule (Fig. 7.4). Ordinarily, the ampoules are transferred to a storage box in the liquid nitrogen freezer and allowed to undergo uncontrolled freezing (Fig. 7.4). Occasionally, the freeze rate needs to be controlled in order to ensure high cell viability, which is often greater than 90%. Controlled freezing can be easily accomplished by putting the ampoule in a plastic foam box, which is then placed in the liquid nitrogen freezer. If this process is not adequate, freezing may be controlled by using commercially available devices that have a programmable freezing rate. To save space, some laboratories use short sections of plastic soda straws as cryoampoules. Straws are cut into sections about 2 cm long, the bottom is heat sealed with flamed forceps, and the straws are then sterilized

TABLE 7.3 Some Large International Culture Collections that Maintain a Diversity of Yeast Cultures[a]

Agricultural Research Service Culture Collection (NRRL) Peoria, Illinois USA http://nrrl.ncaur.usda.gov
All-Russian Culture Collection (VKM) Moscow Region, Pushchino, Russia http://www.vkm.ru
American Type Culture Collection (ATCC) Manassas, Virginia USA http://www.atcc.org
Belgian Coordinated Collections of Micro-Organisms (BCCM) Various cities, Belgium http://bccm.belspo.be/index/php
Centraalbureau voor Schimmelcultures (CBS) Utrecht, The Netherlands http://www.cbs.knaw.nl
Japan Collection of Microorganisms (JCM) Saitama, Japan http://www.jcm.riken.jp
National Collection of Yeast Cultures (NCYC) Norwich, United Kingdom http://www.NCYC.co.uk
National Institute of Technology Evaluation – Biological Resource Center (NBRC) Chiba, Japan http://www.nbrc.nite.go.jp
Phaff Yeast Culture Collection, University of California, Davis, California USA http://www.phaffcollection.org
Portuguese Yeast Culture Collection (PYCC) Caparica, Portugal http://www.sec-biot@fct.unl.pt

[a]*Many other culture collections can be located at the website of the World Federation for Culture Collections (WFCC) (http://www.wfcc.info/datacenters.html).*

by autoclaving. After filling with a cell suspension, the open end of the straw is then heat sealed with flamed forceps. Microorganisms that are stored in liquid nitrogen vapor usually remain viable for many decades, and perhaps longer.

6.4. Distribution of Cultures

Shipment of cultures is governed by a variety of national and international laws and regulations, some of which have developed due to the threat of global bio-terrorism. Within the US, shipment of plant and animal pathogens requires a permit from the USDA Animal and Plant Health Inspection Service (APHIS) (APHIS 523 for plant pathogens, APHIS VS 16-3 for animal pathogens). A permit is required from the US Public Health Service when a pathogen is imported into the US, or when a foreign pathogen is redistributed within the US. Other countries often have their own specific regulations, and shipment of plant and animal pathogens between countries often requires special permits. These requirements should be taken seriously, as failure to comply can result in closure of laboratories, large fines or even incarceration. Shipment of cultures can also be governed by the Convention on Biodiversity, also known as the Rio Treaty. Here the concern is that part of a country's national heritage, i.e., unique microbial germplasm, will be exploited by outside parties without due compensation. Consequently, before novel or other strains are shipped between countries, the requirements of the Rio Treaty must be known. Culture collections that maintain a wide diversity of yeasts are listed in Table 7.3.

Chapter 8

Cytology, Cell Walls and Septa: A Summary of Yeast Cell Biology from a Phylogenetic Perspective

Ida van der Klei, Marten Veenhuis, Stanley Brul, Frans M. Klis, Piet W.J. De Groot, Wally H. Müller, Kenneth G.A. van Driel and Teun Boekhout

1. INTRODUCTION

Yeast cells have been studied since the onset of microbial and biochemical research in the nineteenth century, when Pasteur (1822–1895) showed that alcoholic fermentation in wine was dependent on the presence of yeast cells. In the 20th century, important metabolic pathways were resolved using yeasts. Furthermore, yeast species are extensively used as model organisms in a wide range of disciplines in the life sciences, and they are the organisms of choice for genomics studies and also for live cell imaging to study the fundamental functional processes of eukaryote cells. Compared to higher eukaryotes, yeasts have the advantage of cultivation on simple, defined media at short generation times and easy amenability towards molecular and classical genetic approaches. Yeast genomes are relatively small compared to other eukaryotes, which was one of the reasons why the genome of baker's yeast (*Saccharomyces cerevisiae*) was the first eukaryotic genome to be completely sequenced; a major milestone in molecular yeast research (Goffeau et al. 1996).

Yeast cellular architecture parallels to some extent their phylogenetic diversity, as evidenced by the observed variety in the biochemical composition of the cell walls, ultrastructural organization and morphology of the septa (see below) (e.g., Boekhout et al. 1993, Celio et al. 2006, Fell et al. 2001, Kreger-van Rij and Veenhuis 1971a, McLaughlin et al. 1995, Moore 1987, Prillinger et al. 1990a, 1990b, 1991a, 1991b, 1993a). The aim of this chapter is: 1) to present an overview of yeast cell biology; 2) to provide an overview of the biochemical structure and composition of cell walls in various yeast species; 3) to give an overview on septal pore ultrastructure and other subcellular characteristics; and 4) to provide a phylogenetic framework to these observations.

2. YEAST CYTOLOGY

Yeast cells have ultrastructural features typical of other eukaryotic cells, which includes the presence of membrane-bound organelles. Through the use of microscopic techniques, yeast cells have been the topic of detailed structural research for many decades. Because of their relatively small size, electron microscopy is an essential tool for the study of cellular ultrastructure of the cell. Due to the presence of thick cell walls, special care has to be taken to ensure proper penetration of fixatives, dehydration and impregnation of embedding resins, which are essential steps for most electron microscopy studies. Recent advances in microscopy have allowed the imaging of whole hydrated *S. cerevisiae* cells without chemical fixation, using cryo X-ray tomography, which is an imaging technique that generates three-dimensional ultrastructural information of whole cells. Using this technique, unique images of *S. cerevisiae* cells were obtained at 60 nm resolution in three dimensions (Larabell and Le Gros 2004). A hallmark of yeast cells is the cytosol, which is densely packed with ribosomes (Fig. 8.1).

Yeast cells contain all subcellular structures typical of eukaryotes. These structures include the cytoskeleton, a nucleus and various subcellular organelles such as the endoplasmic reticulum (ER), the Golgi apparatus, mitochondria and microbodies. Like plants, yeast cells contain a vacuole, and the plasma membrane is surrounded by a rigid cell wall. However, chloroplasts are absent in all fungi, which includes the yeasts. Fluorescence microscopy methods have become an attractive tool for studying living yeast cells due to the availability of novel fluorescent dyes and the introduction of genes that encode fluorescent proteins. Upon introduction of hybrid genes encoding a fluorescent protein (e.g., green fluorescent protein, DsRed) fused to a yeast protein any subcellular structure can be specifically marked and its kinetics analyzed in real time in living yeast cells (Kohlwein 2000).

The structural and functional aspects of the various organelles contained in yeast cells are described below.

2.1. The Nucleus

Yeast cells generally contain one nucleus, which is approximately 1 μm in diameter. The nucleus harbors the genetic material of the cell, which is bound by a double membrane, the nuclear envelope (Figs 8.2, 8.9).

The nuclear envelope contains numerous nuclear pore complexes (NPCs) that allow passage of small solutes, proteins and RNA molecules across the nuclear envelope. Spectacular three-dimensional models based on electron microscopy studies of NPCs have been presented (Patel et al. 2007, for review see Rout and Aitchison 2001). NPCs are octagonally symmetric around a cylindrical axis, and each has a cylindrical core containing eight interconnected spokes, which surround a central channel. NPCs contain filaments that protrude into both the cytoplasm and the nucleus. The filaments form a basket-like structure. Using proteomics, the protein composition of the NPC of *S. cerevisiae* has been analyzed in detail. This analysis revealed that a single NPC consists of multiple copies of ~30 different proteins (nucleoporins) (Patel et al. 2007). A three-dimensional model, in which these nucleoporins are positioned, is also available (Devos et al. 2006, Rout et al.

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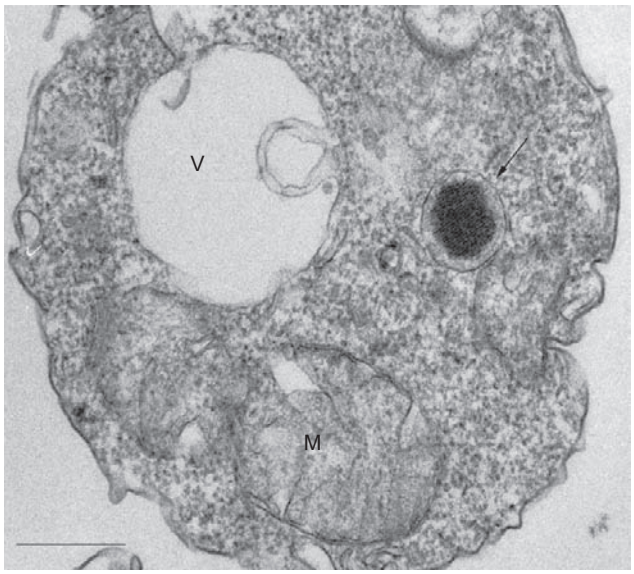


FIGURE 8.1 Electron micrograph of a thin section from a cell of *Ogataea* (*Hansenula*) *polymorpha*. The micrograph shows a part of a protoplast prepared from *O. polymorpha* cells incubated in methanol-containing media for 5 hours. The cytosol is densely packed with ribosomes. The arrow indicates a developing peroxisome, which contains the typical alcohol oxidase crystalloid. M – mitochondrial profile, V – vacuole. Bar = 500 nm.

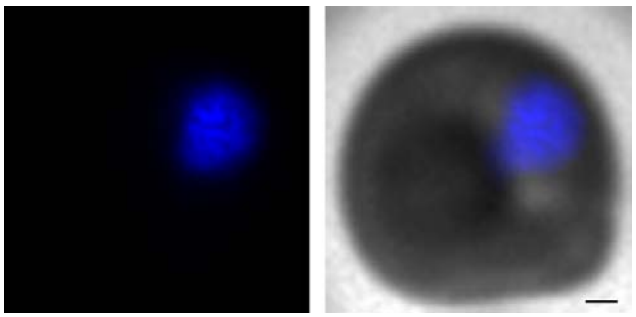


FIGURE 8.2 Fluorescence micrograph of the nucleus in *Ogataea* (*Hansenula*) *polymorpha*. The nucleus is visualized by a fluorescent DNA stain (Hoechst). Picture at the left: fluorescence image. Picture at the right: overlay of bright field and fluorescence image. Bar = 500 nm.

2000). The yeast nuclear envelope contains a unique microtubule organizing center (MTOC), also called a spindle pole body (SPB) (see also section 6.1 of this chapter). The yeast SPB, which is the functional equivalent of the centrosome, forms the two poles of the mitotic spindle. The structure and dynamics of *S. cerevisiae* SPBs have been extensively studied. They consist of three disk-like layers: an outer plaque and an inner plaque at the inside and outside of the nuclear envelope, respectively, and a central plaque that spans the nuclear envelope (Fig. 8.3). During mitosis, the SPB divides, but remains embedded in the nuclear envelope (for a review see Jaspersen and Winey 2004, see also section 6.1 of this chapter).

2.2. The Cytoskeleton

The yeast cytoskeleton is important for morphogenesis, cell polarity and intracellular transport, for instance of cell organelles (Fig. 8.4).

The two major components of the yeast cytoskeleton are actin and tubulin filaments. Both types of filaments are composed of proteins (the subunits) that associate non-covalently. Actin filaments are

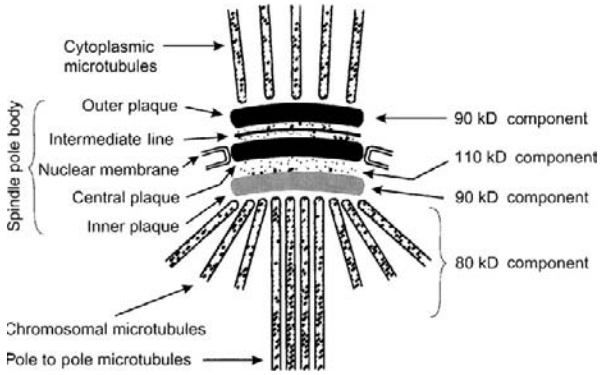


FIGURE 8.3 Spindle pole body (SPB). SPB localizations and spindle components (from Rout and Kilmartin 1990).

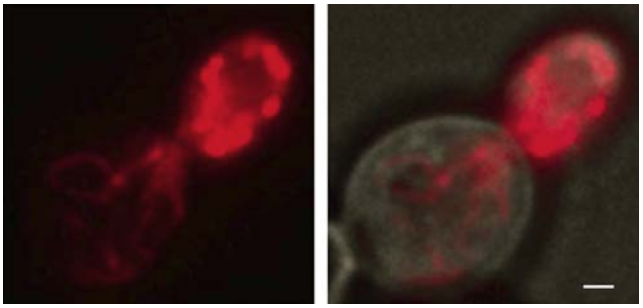


FIGURE 8.4 Fluorescence micrograph of actin filaments in a budding cell of *Saccharomyces cerevisiae*. The actin is specifically stained using Alexa Fluor phalloidin. Photograph at the left: fluorescence image. Photograph at the right: overlay of bright field and fluorescence image. Bar = 500 nm.

flexible, unbranched polymers of globular actin subunits that form two-stranded helical structures (for a review on yeast actin see Moseley and Goode 2006). Microtubules are hollow, unbranched fibers formed by tubulin subunits. Both types of filaments are dynamic and continuously formed and dissociated in response to functional needs.

A large number of proteins interact with actin and tubulin fibers, and a wealth of actin-binding proteins exists, which modulate their function (e.g., connection to other filaments, membranes or organelles). Myosins are a special class of actin-binding proteins which act as molecular motors, driving the transport of intracellular structures along actin filaments. Myosins are large, dimeric protein complexes, consisting of a globular motor head and a filament-binding domain. The motor head is capable of hydrolyzing ATP, thereby converting chemical energy into movement. In addition to myosins, eukaryotes contain two other classes of motor proteins: kinesins and dyneins. These motor proteins function in transport processes along microtubules (Steinberg 2000). The genome of *S. cerevisiae* contains five myosin genes, six genes encoding kinesins and one gene that codes for dynein. These motor proteins are important for growth, cell division, secretion, endocytosis, nuclear division, organelle transport and positioning (including proper segregation/inheritance during cell division) and RNA transport. The SPB is an important cytoskeletal element as it acts as a microtubule-organizing center (MTOC). During mitosis, microtubules, kinesins and dynein motors mediate chromosome movement. Kinesins are also involved in SPB separation. The fission yeast *Schizosaccharomyces pombe* is an extensively used model for studying cell polarity. In this yeast, cell growth is restricted to the poles and involves accurate localization of the cell's asexual reproduction machinery, a process that requires the actin cytoskeleton (for a review see La Carbona et al. 2006). For images see http://www.upstate.edu/biochem/amberg/DelatVision/actin_images.html.

2.3. The Vacuole

Like lysosomes in mammalian cells, the yeast vacuole plays a role in degradation of cellular content via autophagy (Figs 8.5 and 8.9). The vacuole also has an important function in pH and osmoregulation and in storage of amino acids, ions and polyphosphate. The size and number of vacuoles per cell is highly variable. The yeast vacuole consists of a lumen surrounded by a single membrane. It is acidic (in *S. cerevisiae,* approximately pH 6.0), and the enzymes (hydrolases) that function within it have a low optimum pH. Because the cytosol is neutral, a pH gradient exists across the vacuolar membrane. The vacuolar membrane contains a proton translocating ATPase; the V-type ATPase. This V-ATPase is composed of 13 subunits consisting of a catalytic V1 domain of peripherally associated proteins, and a proton-translocating V0 domain of integral membrane proteins (Graham et al. 2003).

The vacuole is the major site for recycling of damaged or redundant cellular content by a process termed autophagy (for a review see Huang and Klionsky 2002). During macroautophagy, double membrane structures, the autophagosomes, are formed, which engulf a portion of the cytoplasm. After completion of sequestration, the outer autophagosomal membrane fuses with the vacuole, releasing its content into the vacuole lumen for subsequent degradation by vacuolar hydrolases. An alternative mode of autophagy is microautophagy. In this process, extensions of the vacuolar membrane enclose a portion of the cytoplasm, which is directly incorporated into the vacuole.

The process of autophagy is important in human health and disease (Cuervo 2004). It has for instance been implicated in ageing, cancer, and defense against pathogens. Autophagy may protect cells against disease, but may also contribute to cell damage (Baerecke 2005, B. Levine 2005, Shintani and Klionsky 2004). Yeasts are suitable model organisms to study the molecular mechanisms involved in autophagy. Several genes involved in autophagy have been identified upon complementation of yeast mutants that are defective in autophagy. These genes, designated *ATG*, are highly conserved (Meijer et al. 2007). Hence, data obtained in yeasts contribute to understanding autophagy in higher eukaryotes, including man. In addition to non-selective autophagy, which is induced during nitrogen starvation, selective modes of degradation have also been described in yeasts, the most detailed studies being those of the selective degradation of peroxisomes. This process, also designated pexophagy, is induced when peroxisomes become redundant for growth. It was described for *Candida boidinii* and *Ogataea* (*Hansenula*) *polymorpha,* and occurs when methanol-grown cells are shifted to media containing glucose or ethanol (Bormann and Sahm 1978, Zwart et al. 1979). During growth of methylotrophic yeasts on methanol, peroxisomes harbor key enzymes of methanol metabolism (reviewed by Van der Klei et al. 2006), which become redundant for growth when glucose or ethanol is present in the growth medium.

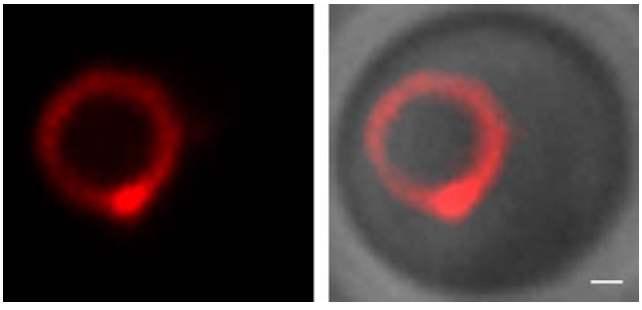


FIGURE 8.5 Fluorescence micrograph of the vacuole in *Ogataea* (*Hansenula*) *polymorpha*. The vacuole membrane is visualized by FM4-65. Photograph at the left: fluorescence image. Photograph at the right is an overlay of bright field and fluorescence images. Bar = 500 nm.

Two different modes of pexophagy have been described in yeasts, namely micro- and macropexophagy. These processes share morphological characteristics with micro- and macroautophagy respectively (for a review see Sakai et al. 2006). More recently, the process of selective degradation of mitochondria (mitophagy) has also been described in yeasts (reviewed by Abeliovich 2007). Interestingly, portions of the yeast nucleus can be degraded by selective microautophagy. This process, termed piecemeal autophagy, has been described for *S. cerevisiae* (Roberts et al. 2003). During this process teardrop-like blebs are pinched from the nucleus and incorporated in the vacuole lumen, where degradation occurs.

2.4. The ER and Golgi Apparatus

The endoplasmic reticulum (ER) is a complex network of membrane structures, part of which is continuous with the nuclear envelope. The remaining ER is localized at the cell periphery, and thus designated peripheral ER (Figs 8.6 and 8.9).

The ER is involved in lipid biosynthesis, and is also the entry point for proteins that are secreted by the cells via the secretory pathway. The ER network is continuously remodeled, a process that involves the formation of new tubules and homotypic fusion events. During budding of yeast cells, the ER is carefully partitioned over cells and their buds (Du et al. 2004). Upon translocation of secretory proteins into the ER lumen, these proteins are transported in transport vesicles to the Golgi apparatus, a cell organelle that may consist of stapled stacks of membranes, the cisternae. Different types of Golgi cisternae exist, namely the early (cis, medial) and late (trans) cisternae, which differ biochemically. Vesicles that are formed at the trans Golgi finally fuse with the cell membrane, which results in the release of the secretory proteins into the growth medium. There is a considerable debate on how the different Golgi cisternae are formed. One model predicts that each is a long-lived structure that retains a characteristic set of Golgi-resident proteins. According to this model, secretory proteins are transported by vesicles from one cisterna to the next. An alternative model predicts that each cisterna is a transient structure that matures from early to late by acquiring and then losing specific Golgi-resident proteins. Recent, detailed, live cell imaging studies in *S. cerevisiae* supported the latter model (Losev et al. 2006).

2.5. Mitochondria

Mitochondria are organelles surrounded by a double membrane and consist of four distinct sub-compartments: the outer membrane, the inner membrane, the intermembrane space and the matrix (Figs 8.7, 8.9).

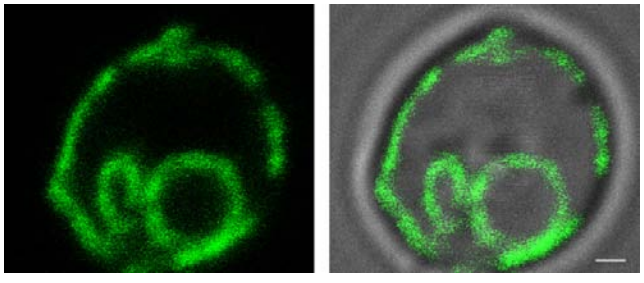


FIGURE 8.6 Fluorescence micrograph of the ER in *Saccharomyces cerevisiae.* The ER membrane was marked with a fusion protein consisting of the ER protein HMG1 fused to GFP (Du et al. 2001). In the bottom part of the figure the nuclear envelope can be seen. Photograph at the left: fluorescence image. Photograph at the right, overlay of bright field and fluorescence image. Bar = 500 nm.

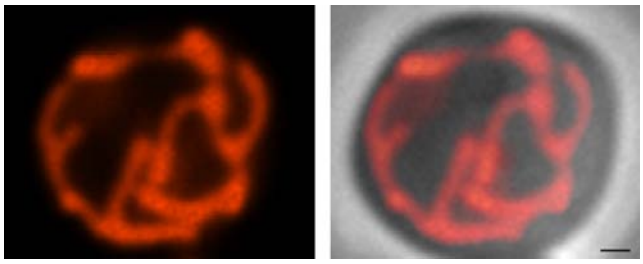


FIGURE 8.7 Mitochondria in a cell of *Ogataea* (*Hansenula*) *polymorpha* visualized by Mitotracker Orange. Note that the mitochondrion is a branched, continuous structure. Photograph at the left: fluorescence image. Photograph at the right, overlay of bright field and fluorescence image. Bar = 500 nm.

The surface of the inner membrane is much enlarged by the formation of invaginations, the so-called cristae. The outer membrane contains porins that render the membrane permeable to molecules with a mass of up to 10 kDa. The inner membrane is semipermeable, allowing the generation of a pH gradient and a membrane potential. The most important proteins of the mitochondrial inner membrane are components of the electron transport chain and the F0F1-ATP-synthase.

Generally, mitochondria are responsible for the bulk of ATP production in aerobically growing eukaryotic cells. ATP synthesis results from oxidation of carbon sources such as fatty acids and sugars. The final steps of this oxidation take place in the mitochondrial matrix, catalyzed by the enzymes of the citric acid cycle. The reducing equivalents produced (NADH and FADH2) are responsible for the generation of a membrane potential across the inner membrane, which is used to generate ATP via oxidative phosphorylation. However, when *S. cerevisiae* cells are grown in batch cultures at high glucose concentrations, the cells initially ferment the carbon source independently of mitochondria. When glucose concentrations decrease, mitochondrial oxidative phosphorylation becomes more and more important for ATP generation, and an accompanying increase in mitochondrial abundance is observed.

Other important functions of mitochondria include biosynthesis of heme and Fe/S clusters. The entire proteome of yeast mitochondria has been analyzed, revealing that *S. cerevisiae* mitochondria contain approximately 700 different proteins (Reichert and Neupert 2004). In yeast cells, mitochondria form dynamic tubular networks that change their shape and move throughout the cell. The organelles continuously divide and fuse to regulate their number. A large number of proteins involved in mitochondrial dynamics have been discovered (for a review see Okamoto and Shaw 2005). Cristae may display strong morphological varieties, dependent on the metabolic activity of the cell. Sometimes mitochondria contain very few cristae (e.g., in anaerobically grown *S. cerevisiae* cells). Unlike other yeast cell organelles, mitochondria contain their own genome, which encodes part of the mitochondrial proteins. The remainder are encoded by nuclear genes, synthesized in the cytosol and then imported into the organelle. Since mitochondrial DNA (mtDNA) encodes for a few proteins of the respiratory chain, it is essential in most eukaryotes. An important exception is *S. cerevisiae,* because this yeast is able to anaerobically ferment glucose; viable *S. cerevisiae* mutants exist that have completely lost their mtDNA (so called rho^0 mutants). When *S. cerevisiae* is grown anaerobically on glucose the mitochondria are relatively small and difficult to recognize by microscopy.

2.6. Microbodies

Microbodies (peroxisomes, glyoxysomes) consist of a proteinaceous matrix surrounded by a single membrane (Figs 8.8, 8.9).

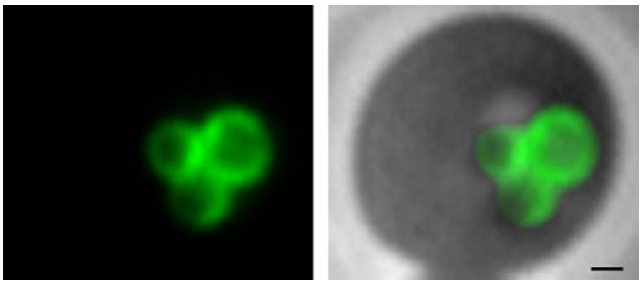


FIGURE 8.8 Fluorescence micrograph of a cluster of three peroxisomes in *Ogataea* (*Hansenula*) *polymorpha*. Peroxisomes are visualized using GFP fused the peroxisomal targeting signal 1 (PTS1), -SKL. The fluorescent rim is caused by the accumulation of GFP in the space between the alcohol oxidase crystal and the surrounding membrane. Photograph at the left: fluorescence image. Photograph at the right is an overlay of bright field and fluorescence images. Bar = 500 nm.

The matrix contains enzymes that are involved in a variety of metabolic pathways. Yeast microbodies are predominantly involved in the primary metabolism of various carbon and organic nitrogen sources, such as n-alkanes, fatty acids (oleic acid), ethanol, methanol, D-amino acids, primary amines and urate. Microbodies have been extensively studied in *S. cerevisiae, O. (Hansenula) polymorpha, Komagataella* (*Pichia*) *pastoris* and *Yarrowia lipolytica* (for a recent review see Van der Klei and Veenhuis 2006). Yeasts are a highly attractive choice for studying microbody formation because, unlike higher eukaryotes, microbody malfunction or deficiency is not lethal. This feature has allowed the isolation of mutants in which peroxisome biogenesis is affected, and cloning of the corresponding genes (*PEX* genes) by functional complementation. At present 32 different *PEX* genes are known, most of which are conserved among higher and lower eukaryotes (Kiel et al. 2006). Of all yeast species studied so far, the highest microbody (peroxisome) abundance has been encountered in yeast species that use methanol as their sole source of carbon and energy (e.g., *Candida boidinii, O.* (*Hansenula*) *polymorpha, K.* (*Pichia*) *pastoris*). In cells of these yeast species, peroxisomes develop massively during growth on methanol (Van der Klei et al. 2006). The high microbody abundance in these cells is related to the excessive levels of alcohol oxidase (AO), the first enzyme in methanol metabolism. The high intra-organellar AO concentration results in crystallization of this enzyme, which is reflected in the typical cuboid shape of the organelles. Methanol-grown cells are crowded with peroxisomes, whereas glucose-grown yeast cells generally contain only one or, infrequently, few small peroxisome(s) per cell.

3. MICROSCOPY OF YEAST CELLS

Yeast cells are readily visualized by conventional light microscopy, albeit without much resolution. The success of analyzing yeast cells by electron microscopy is strongly dependent on how the cells are cultivated. Cells containing thick cell walls or abundant storage materials (e.g., lipid, glycogen) are difficult to fix and embed in conventional resins. The best results are obtained with cells that are grown at maximum growth rates (until the mid-exponential growth phase) and have been extensively pre-cultivated. Good results are obtained when cells are fixed with potassium permanganate, post-fixed with uranyl acetate and embedded in Epon (for protocols see van der Klei and Veenhuis 2007). This method especially allows the visualization of membranes (Fig. 8.9).

Alternatively, cryo-methods can be used, which may include a combination of high-pressure freezing, freeze substitution and resin embedding, and for labeling purposes cryo-ultramicrotomy (Müller

et al. 2002). For the localization of proteins by immunocytochemistry, yeast cells are generally fixed by aldehydes, as they crosslink proteins (van der Klei and Veenhuis 2007). Glutaraldehyde, formaldehyde, or a mixture of the two, are commonly used for this purpose. For immunolabeling experiments, various special resins exist, e.g., unicryl (Fig. 8.10).

For fluorescence microscopy, several dyes exist that stain specific structures/compounds in yeasts. These dyes include FM4-64 to stain vacuole membranes, DAPI for DNA (nucleus) and dyes for mitochondria (e.g., Mitotracker). Each of the different cellular compartments can also be visualized by tagging the relevant structures with fluorescent proteins (e.g., Green Fluorescent Protein, DsRed, van der Klei and Veenhuis 2007). Peroxisomes can, for instance, be fluorescently marked by introducing a gene encoding GFP containing a peroxisomal targeting signal (e.g., the C-terminal tripeptide -SKL). Similar approaches, using other sorting signals, have been used to mark mitochondria, nuclei, the ER and Golgi with fluorescent proteins. Several protein localization databases exist, which contain microscopy data of protein localization patterns in *S. cerevisiae*. Kumar et al. (2002) epitope tagged approximately 60% of the *S. cerevisiae* proteins, and localized them by immunofluorescence (see http://ygac.med.yale.edu). Similar approaches have been followed using GFP-tags, which has the advantage that the proteins can be vizualized directly (Kals et al. 2005; *S. cerevisiae* http://YPL.uni-graz.at, Ding et al. 2000, *Schiz. pombe*). Protein localization data for *S. cerevisiae* are available at http://www.proteome.com/YPDhome.html.

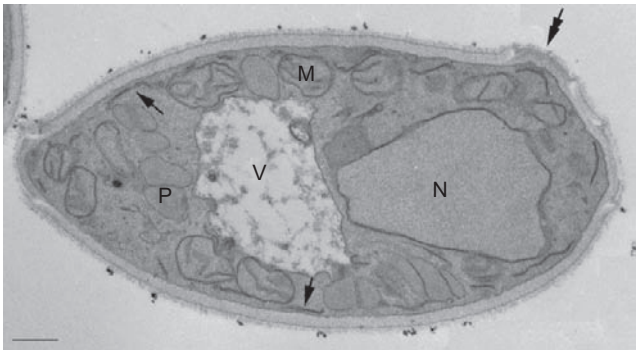


FIGURE 8.9 Electron micrograph of a thin section of a *Candida boidinii* cell grown on oleic acid. The cell is fixed with $KMnO_4$ and embedded in Epon resin. The cell contains all the normal cell organelles. M – mitochondrion, N – nucleus, P – peroxisome, V – vacuole. The single arrows indicate peripheral ER, the double arrow indicates a bud scar where the bud separated from the parent cell. Bar = 500 nm.

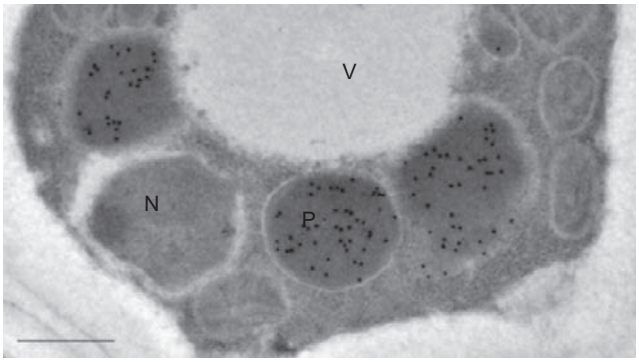


FIGURE 8.10 Immunocytochemical staining of alcohol oxidase protein in a methanol-grown cell of *Ogataea* (*Hansenula*) *polymorpha*. Sections of aldehyde fixed cells were incubated with anti-alcohol oxidase antibodies and goat-anti-rabbit secondary antibodies conjugated to gold. Bar = 500 nm.

4. MOLECULAR ARCHITECTURE OF THE CELL WALL OF YEASTS

The fungal cell wall plays a crucial role in maintaining turgor pressure, in preserving cell shape, and in morphogenesis. The cell wall protects the cell against physical damage, degradation by foreign proteins and dehydration. It also plays a crucial role in adhesion, cell–cell recognition, biofilm formation, and virulence (de Groot et al. 2005). The cell wall is not a static entity. For example, thickness, composition and structure of the wall in *S. cerevisiae* depend on environmental conditions such as pH, temperature, oxygen levels, carbon source, nutrient availability and the presence of pheromones (Aguilar-Uscanga and Francois 2003, Klis et al. 2006). Moreover, when the cell wall gets damaged, a salvage mechanism is activated to reinforce it (Levin 2005, Magnelli et al. 2002, Miyata et al. 1985, Popolo et al. 1997, Ram et al. 1998). This is reflected in the tight control that the cell exerts on the synthesis of the cell wall components. Their synthesis is rate-controlled, and subject to spatial and temporal control. In baker's yeast it has been estimated that about 1,200 of its 6,000 genes directly or indirectly affect cell wall formation (de Groot et al. 2001).

4.1. Composition and Molecular Structure of the Cell Wall of Ascomycetous Yeasts

Electron microscopic studies of the cell walls of ascomycetous yeasts usually reveal two layers: a largely transparent, inner layer, and an outer layer, which, depending on the technique used, consists of long fibrils emanating into the medium, or the cell wall is thin and dark-stained as a result of the collapse of the fibrous layer during fixation (Fig. 8.11) (Garrison 1981, Humbel et al. 2001, Osumi 1998, Travassos 1986, Yamaguchi et al. 2002).

The inner layer corresponds to the skeletal layer, and largely consists of load-bearing polysaccharides, whereas the outer layer mainly

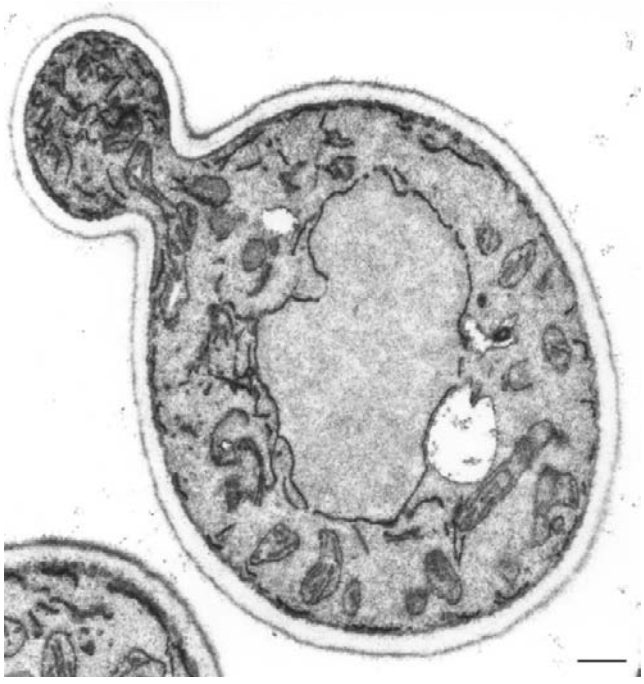


FIGURE 8.11 Ultrastructure of the cell wall of *Saccharomyces cerevisiae* showing holoblastic budding and a two-layered cell wall after potassium permanganate fixation. Bar = 500 nm.

consists of glycoproteins that are covalently linked to the skeletal inner layer. Depending on growth conditions, an additional dark layer can be observed between the plasma membrane and the transparent, inner cell wall layer. For this reason, the wall of ascomycetous fungi is sometimes described as a three-layered structure. However, in *S. cerevisiae* the dark layer adjacent to the plasma membrane consists of soluble, secreted proteins such as invertase and acid phosphatase that are too large to pass through the cell wall, but are lost during cell wall isolation and thus do not belong to the cell wall proper (de Nobel et al. 1989). Mass spectrometric analysis of the external glycoprotein layer has revealed that this layer can consist of approximately 20 different cell wall proteins, and that the glycoprotein composition of the wall tends to vary strongly depending on growth conditions (Yin et al. 2008). Chemical analysis of the walls of ascomycetous yeasts indicates that various polysaccharides and combinations of polysaccharides are used as skeletal elements. For example, in *S. cerevisiae* and similar yeasts β-1,3-glucan is the major load-bearing polysaccharide; in addition, some chitin is present (section 4.1.1). In *Schizosaccharomyces pombe*, however, α-1,3-glucan and β-1,3-glucan are the major structural polysaccharides and chitin is absent (section 4.1.2). A third category is exemplified by the yeast form of *Blastomyces dermatitidis*, in which chitin and α-1,3-glucan are the predominant structural polysaccharides, and β-1,3-glucan is a minor component (section 4.1.3). As the cell wall of baker's yeast has been extensively studied, we shall begin our discussion with this organism.

4.1.1. *The Budding Yeast* Saccharomyces cerevisiae

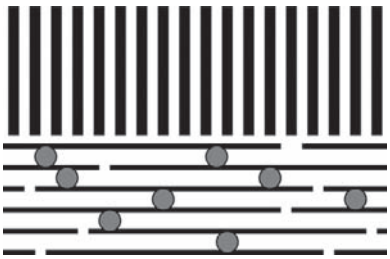
The cell wall of the budding yeast *S. cerevisiae*, which belongs to the Saccharomycotina, represents10−25% of its total biomass, depending on growth conditions (Aguilar-Uscango and Francois 2003). The molecular architecture has been extensively studied (Klis et al. 2006, Kollar et al. 1995, 1997, Lesage et al. 2006, Lipke and Ovalle 1998, Orlean 1997) (Fig. 8.12).

The major load-bearing polysaccharide of the skeletal inner layer is a moderately branched β-1,3-glucan, which forms a continuous, elastic network. This network is held together by hydrogen bonds between laterally associated β-1,3-glucan chains and by Pir cell wall proteins (Pir; *p*roteins with *i*nternal *r*epeats), which are believed to crosslink neighboring β-1,3-glucan chains (Tables 8.1, 8.2, Fig. 8.12). Under normal osmotic conditions this network is considerably expanded, which explains why the cells significantly shrink when they die. The β-1,3-glucan network is extended at its outside with highly branched and thus water-soluble β-1,6-glucan chains, which in turn may be connected to a glycosylphosphatidylinositol anchor (GPI)-dependent mannoprotein. Most cell wall proteins (CWPs) are GPI-CWPs, and thus indirectly linked to the β-1,3-glucan network (Table 8.2). The proteins can be specifically released from the cell wall by using HF-pyridine, which cleaves the phosphodiester bond in the GPI remnant (Table 8.2) (de Groot et al. 2004). In addition, some proteins such as the Pir-CWPs are directly linked to the β-1,3-glucan network through an ester linkage between specific glutamine residues and a glucosyl hydroxyl group – a linkage that is highly sensitive to alkali (Ecker et al. 2006). These proteins are called ASL (alkali-sensitive linkage)-CWPs (de Groot et al. 2005). Consistent with their direct connection to β-1,3-glucan molecules, the ASL-CWPs seem to be uniformly distributed throughout the inner skeletal layer, whereas GPI-CWPs are mainly found in the outer layer of the wall (de Groot et al. 2005, Kapteyn et al. 1999). The cell wall contains a considerable number of covalently linked cell wall proteins, including adhesins, a considerable number of carbohydrate-processing enzymes, and iron acquisition proteins (Yin et al. 2005, 2007, 2008). Intriguingly, at subsequent phases of the cell cycle different proteins are incorporated in the cell wall (Caro et al. 1998, Klis et al. 2006, Rodríguez-Peña et al. 2000, Smits et al. 2006). In addition, the composition of the protein population in the cell wall depends highly on environmental conditions (reviewed in Klis et al. 2006). These observations indicate that the incorporation of cell wall proteins is tightly controlled and that specific cell wall proteins may help the cell to cope with various forms of stress, including cell wall stress.

Chitin levels in the cell wall are normally low. Some chitin is found in the lateral walls, but only in the walls of parent cells and not in the wall of the bud. Most of the chitin is present either as a chitin ring in the neck of budding cells or in the primary septum, and in bud scars (Shaw et al. 1991). Chitin may become glycosidically linked to non-reducing ends of both β-1,3-glucan and β-1,6-glucan chains (Table 8.2) (Cabib and Duran 2005, Kollar et al. 1995, 1997). Cell wall stress activates the so-called cell wall integrity pathway (Levin 2005). This results in a strong increase in the deposition of chitin in the lateral wall, which is accompanied by increased formation of the CWP-polysaccharide complex GPI-CWP→1,6-β-glucan←chitin and increased resistance of intact cells to β-1,3-glucanase (Table 8.2) (de Nobel et al. 2000, Kapteyn et al. 1997, Lagorce et al. 2002). Further, a characteristic set of cell wall-related genes is upregulated (Boorsma et al. 2004, Garcia et al 2004, Jung and Levin 1999, Lagorce et al. 2003).

4.1.2. *The Fission Yeast* Schizosaccharomyces pombe

Electron micrographs of the cell wall of *Schiz. pombe*, which belongs to the Taphrinomycotina (formerly known as Archiascomycetes), show an electron-dense outer layer and a relatively electron-translucent inner layer, the latter representing the skeletal layer (Humbel et al. 2001, Osumi 1998). Sometimes, an additional electron-dense layer is observed adjacent to the plasma membrane (Humbel et al. 2001). As discussed above, the latter probably represents soluble, secreted proteins, which accumulate in the periplasmic region, as observed in *S. cerevisiae*. Lectin-gold labeling with β-galactoside-specific *Ricinus communis* lectin points to the presence of galactomannoproteins at the cell surface (Horisberger and Rouvet-Vauthey 1985). In contrast to *S. cerevisiae* and *Candida albicans*, the cell wall of *Schiz. pombe* contains a relatively small amount of glycoprotein (Table 8.3). However,



Dense coat of fibrillar glycoproteins and/or glycoprotein complexes extending from the cell surface into the medium and covalently linked to the stress-bearing polysaccharides that form the inner skeletal layer.

The inner layer is an elastic and porous network of helical β-1, 3-glucan chains running parallel to the cell membrane and cross-linked by a special class of cell wall proteins (filled circles). This layer can become reinforced by chitin chains.

FIGURE 8.12 Diagram of the cell wall architecture of *Saccharomyces cerevisiae*.

TABLE 8.1 Macromolecular Composition of the Cell Wall of *Saccharomyces cerevisiae*

Macromolecule	% of Wall Mass[a]	Mean Mr (DP[b]) kDa
Mannoproteins[c]	30–50	30–500 kDa[d]
β-1,6-Glucan	5–10	24 (150)
β-1,3-Glucan	30–45	240 (1500)
Chitin	1.5–6	25 (120)

The macromolecules are presented in the order in which they are found in the wall from the outside to the inside. When the cells are confronted with cell wall stress, the chitin content may increase considerably.
[a]*Aguilar-Uscanga and Francois (2003).*
[b]*DP, degree of polymerization.*
[c]*The actual protein content is a few percent; the remaining mass is from mannose-containing carbohydrate side-chains.*
[d]*M_r range of CWPs.*

TABLE 8.2 Main CWP–Polysaccharide Complexes of *Saccharomyces cerevisiae*

CWP-GPI_t–β1,6-glucan–β1,3-glucan
CWP-GPI_t–β1,6-glucan–chitin
β1,3-Glucan–Pir-CWP–β1,3-glucan
$-AA_\omega$–EtN–$Man_{4/5}$–β1,6-glucan–β1,3-glucan

CWP, cell wall protein; GPI_t, a trimmed form of the original GPI anchor. Row 4. Molecular structure of the trimmed GPI anchor of cell wall proteins. AA_ω, the omega amino acid or carboxyterminal amino acid of the mature GPI protein to which a GPI anchor becomes attached in the endoplasmic reticulum; EtN, ethanolamine.

TABLE 8.3 Cell Wall Composition of Exponentially Growing *Schizosaccharomyces pombe* Cells

Macromolecule	% of Wall mass[a]	Mean Mr (DP[b]) kDa
Galactomannoproteins[c]	13	unknown
β-1,6-1,3-Glucan	15	30 (186)[b]
β-1,3-Glucan	39	130 (800)[b]
α-1,3-Glucan	28	42 (260)[d]

[a]*Magnelli et al. (2005).*
[b]*Manners and Meyer (1977).*
[c]*The peptide portion represents ~3% of the wall dry weight.*
[d]*Grün et al. (2005).*

the peptide content of its wall is similar to that found in those yeasts, which indicates that hyperglycosylation in cell wall proteins of *Schiz. pombe* is rare. Interestingly, genomic analysis revealed only a limited number of GPI-proteins compared to *S. cerevisiae*, *C. albicans* or *C. glabrata* (de Groot et al. 2003, Weig et al. 2004), which is consistent with the observation that HF-pyridine releases only a handful of GPI-dependent proteins from isolated walls (de Groot et al. 2007). There are also no Pir-CWPs in the cell wall (Toh-e et al. 1993, BLAST search using the *Saccharomyces* Genome Database at <http://www.yeastgenome.org/>). The skeletal layer contains two types of fibrils, which probably represent α-1,3-glucan and β-1,3-glucan (Kopecka et al. 1995). In addition, a highly branched, water-soluble β-1,6-glucan has been described (Magnelli et al. 2005). This polysaccharide is probably covalently linked to the skeletal polysaccharide β-1,3-glucan (Manners and Meyer 1977), and seems to be preferentially located directly below the external glycoprotein layer (Humbel et al. 2001), which is consistent with the notion that GPI-dependent cell wall proteins may interconnect to β-1,3-glucan. Finally, the cell wall of *Schiz. pombe* does not contain chitin, but it does contain a considerable amount of another load-bearing polysaccharide, α-1,3-glucan, which is probably not covalently linked to other cell wall components (Table 8.3) (Grün et al. 2005, Hochstenbach et al. 1998, Magnelli et al. 2005, Manners and Meyer 1977, Sugawara et al. 2004). No chitin has been found either in the lateral walls or in the primary septum, which in *Schiz. pombe* consists of linear β-1,3-glucan instead of chitin (Humbel et al. 2001, Horisberger and Rouvet-Vauthey 1985). Because there is no evidence for a possible linkage between cell wall proteins and α-1,3-glucan (Grün et al. 2005), the available data are in agreement with the presence of a GPI-CWP→β-1,6-glucan→1,3-β-glucan complex in the walls. As in *S. cerevisiae*, cell wall stress seems to activate a cell wall salvage mechanism. When the synthesis of β-1,3-glucan is inhibited with aculeacin or Papulacandin B, the deposition of the other skeletal component, α-1,3-glucan, is stimulated (Miyata et al. 1985, Varona et al. 1983). It is tempting to generalize this observation to other yeasts that incorporate α-1,3-glucan in their walls.

4.1.3. The Cell Wall of Other Ascomycetous Yeasts

The cell wall organization of many other ascomycetous yeasts, including dimorphic species, is similar to that of *S. cerevisiae*. Although the cell wall model of *S. cerevisiae* has strong predictive value for other ascomycetous yeasts, it will not be fully correct for all species. One of the reasons is that its cell wall does not contain α-glucan in contrast to, for example, *Schiz. pombe*. However, since the α-1,3-glucan of *Schiz. pombe* is an independent, skeletal element unlinked to any other cell wall component, and this is also true of other fungi capable of its synthesis (Grün et al. 2005), the cell wall model of *S. cerevisiae* may well be an accurate model for most or all ascomycetous yeasts, particularly those that lack α-1,3-glucan in their walls.

The dimorphic, clinical fungus *C. albicans* is a typical example of this category. In the walls of both the yeast and the hyphal growth form of *C. albicans*, the same CWP–polysaccharide complexes have been identified as in *S. cerevisiae*, which supports the notion that the walls of both species are similarly organized (de Groot et al. 2004, Kapteyn et al. 2000, Klis et al. 2006). This also seems to be the case for the *S. cerevisiae* related species *C. glabrata* (Frieman et al. 2002, Weig et al. 2004). The cell walls of the yeast form of *Exophiala dermatitidis* (Herpotrichiellaceae, Chaetothyriales, Chaetothyriomycetidae, Ascomycota) also contain CWPs covalently linked to β-1,6-glucan, indicating that its cell wall has a similar molecular architecture to *S. cerevisiae* (Montijn et al. 1997). This view is consistent with an electron-microscopic study of rapidly frozen yeast phase cells of *E. dermatitidis*, which clearly reveals a fibrillar outer layer, with the fibrils emanating into the medium (Yamaguchi et al. 2002).

In the dimorphic yeast *Yarrowia lipolytica* (Saccharomycotina) both a Pir-CWP and a putative GPI-CWP have been identified. The GPI-CWP shows homology to the GPI-CWP Cwp1p in *S. cerevisiae*, suggesting that the molecular organization of its wall is also similar to that of bakers' yeast (Jaafar and Zueco 2004, Jaafar et al. 2003).

In other species the evidence is more indirect. For example, chemical fractionation studies based on the use of alkali on the walls of *Candida boidinii, Debaryomyces hansenii, Kloeckera apiculata*, *Kluyveromyces marxianus* and *Zygosaccharomyces bailii* (Manners et al. 1974, Nguyen et al. 1998, Santos et al. 2000) resulted in similar cell wall fractions to those obtained with *S. cerevisiae* (Fleet 1991), consistent with the view that they too have a comparable molecular architecture.

Computer-assisted genomic analysis is rapidly developing. With the number of fully sequenced fungal genomes growing rapidly, it becomes increasingly clear that phylogenetically distinct fungi share many cell wall genes, including those that code for cell wall assembly

enzymes, cell wall proteins, glycosyl transferases involved in *N*- and *O*-glycosylation of secretory proteins, proteins involved in the synthesis of chitin, α-1,3-glucan, or β-1,3-glucan and cell wall regulatory proteins. A convenient tool for this type of analysis is provided by the *Saccharomyces* Genome Database (SGD), through the function COMPARISON RESOURCES in each gene entry (Balakrishnan et al. 2005). For example, the *S. cerevisiae* gene *FKS1* encodes a multispanning membrane protein that is catalytically active in the synthesis of β-1,3-glucan, and the gene *GAS1* encodes a plasma membrane-bound transglucosylase, which is able to elongate β-1,3-glucan and may be involved in connecting chains that emerge from the plasma membrane to the existing β-1,3-glucan network (Carotti et al. 2004, Klis et al. 2006, Popolo and Vai 1999). A BLAST search carried out through SGD shows that ascomycetous yeasts such as *Candida* species, *D. hansenii, K. lactis* and *Y. lipolytica*, the dimorphic ascomycetes *Coccidioides posadasii* and *Paracoccidioides brasiliensis*, the fission yeast *Schiz. pombe*, and basidiomycetous yeasts such as *Ustilago maydis* and *Cryptococcus neoformans* all contain proteins homologous to Fks1p and Gas1p. This strongly suggests that the walls of ascomycetous and basidiomycetous fungi contain a similar β-1,3-glucan.

4.1.4. *The Cell Wall of Dimorphic* Pezizomycotina *with a Known Yeast State*

Blastomyces dermatitidis, *Histoplasma capsulatum* and *Paracoccidioides brasiliensis* are clinical fungi that belong to the family Onygenaceae (see also Chapter 2 on Clinically Important Yeasts). These fungi are dimorphic and grow in the yeast form only at 37°C, both in the laboratory and when infecting mammalian hosts. Interestingly, the cell walls of the yeast form contain more α-1,3-glucan than those of the mycelial form. Chitin and α-1,3-glucan are the major load-bearing polysaccharides of the yeast cell wall, with usually only a limited role for β-1,3-glucan. As an example, *B. dermatitidis* has yeast cell walls which contain about equal amounts of chitin (37%) and α-1,3-glucan (33%), and a minor amount of β-1,3-glucan and protein (8%) (Kanetsuna and Carbonell 1971). The cell wall compositions of the yeast forms of *P. brasiliensis* (Kanetsuna and Carbonell 1970, Kanetsuna et al. 1969, 1972) and *H. capsulatum* (Domer 1971, Kanetsuna et al. 1974) are similar. Their walls also contain some galactose and mannose, probably in the form of protein-linked galactomannan side-chains (Ahrazem et al. 2003). How the cell wall of this group of fungi is organized, and how the various cell wall components are interconnected, is largely unknown. As most β-1,3-glucan is found in the alkali-insoluble cell wall fraction together with chitin, it seems likely that β-1,3-glucan and chitin form a covalently linked complex in the form of chitin→β-1,3-glucan (Hartland et al. 1994, Mol and Wessels 1987). *P. brasiliensis* yeast cells respond in a similar way to cell wall stress as *Schiz. pombe*, by depositing more α-1,3-glucan in their walls when treated with Papulacandin B, an inhibitor of β-1,3-glucan synthesis (Davila et al. 1986).

As noted earlier, cell walls of the yeast form, which is the infectious form, contain more α-1,3-glucan than mycelial walls. Interestingly, mutants with lower levels of α-1,3-glucan tend to be less virulent, suggesting that α-1,3-glucan might protect the yeast cell against the defensive mechanisms of the host (Hogan and Klein 1994, Klimpel and Goldman 1988, San-Blas et al. 1976).

4.2. The Cell Wall of Basidiomycetous Yeasts

Knowledge of the cell wall structure of basidiomycetous yeasts is as yet too fragmentary to allow general conclusions to be drawn. However, one striking difference has been observed; the walls of basidiomycetous yeasts are often, but not always, multilayered, and when viewed by TEM show alternating regions of electron-dense and electron-translucent material (Fig. 8.13) (Depree et al. 1993, Garrison 1981, Kreger-van Rij and Veenhuis 1971a). Possibly these regions may correspond to high and low protein levels, respectively. Alternatively, electron-dense regions may be enriched with melanin. Budding of basidiomycetous yeasts is enteroblastic, leaving distinct scars when the newly formed bud cells rupture the cell wall of the parent cell (Fig. 8.13).

4.2.1. *The Cell Wall of* Ustilago maydis

Ustilgo maydis is a dimorphic fungus which is a member of the Ustilaginales (Ustilaginomycotina, Ustilaginomycetes) and causes corn smut. Anamorphs of Ustilaginales are classified in the genus *Pseudozyma* (see Chapter 153). The yeast walls are bi-layered with a dark-staining outer layer and a transparent inner layer (Ruiz-Herrera et al. 1996). Isolated yeast cell walls contain 14% chitin. When yeast cells are metabolically labeled with radioactive amino acids, labeled proteins are found in the walls that resist extraction by hot detergent, but can be liberated by digesting the walls with β-1,3-glucanase or chitinase (Ruiz-Herrera et al. 1996). These observations suggest that the dark-staining outer layer may consist of glycoproteins covalently linked to an inner skeletal layer, perhaps in a similar way to that established for *S. cerevisiae*.

4.2.2. *The Cell Wall of* Trichosporon

The genus *Trichosporon* (Trichosporonales, Tremellomycetes, Agaricomycotina) contains 37 species from diverse habitats and includes a number of clinically important yeasts (see Chapter 161). *Trichosporon cutaneum* is a dimorphic fungus initially isolated from a dairy factory and, not unexpectedly, can use lactose as a carbon source. It may grow in either the yeast or hyphal form (Depree et al.

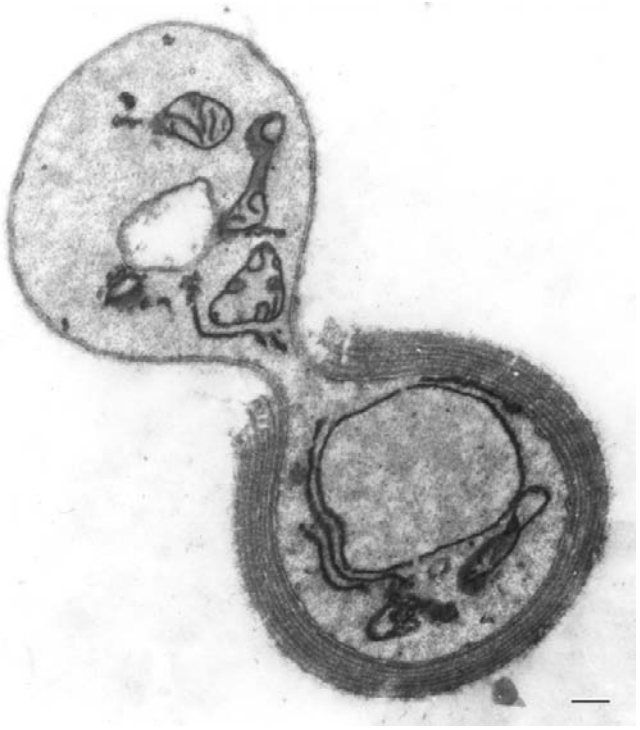


FIGURE 8.13 Electron micrograph showing enteroblastic budding and electron-dense layered cell wall of parent cell of *Rhodotorula auriculariae* after permanganate fixation. Bar = 500 nm.

1993). Electron microscopy of the cell wall reveals a multilamellar structure (Depree et al. 1993), and chemical analysis reveals the presence of 9% chitin and an alkali-insoluble β-1,3-glucan, suggesting that the latter might be associated with chitin in the form of chitin→β-1,3-glucan (Hartland et al. 1994, Mol and Wessels 1987). The alkali-soluble fraction of the wall contains not only α-1,3-glucan, but also a high-molecular-weight, acidic xylomannan, with a 1,3-mannan backbone having glucuronic acid residues attached (GXMan, glucuronoxylomannan). A similar polysaccharide could be extracted from the walls by autoclaving intact cells in neutral buffer. After purification by ion-exchange chromatography and gel filtration, this polysaccharide still contained about 7% protein. Interestingly, the outer mannoprotein layer of the cell walls of *S. cerevisiae* can also be liberated by autoclaving intact cells (Ballou 1970). This raises the possibility that *Trichosporon* might also possess an external layer of glycoproteins, linked to an underlying skeletal network, but carrying GXMan side-chains instead of mannan side-chains. Autoclaving of intact cells of *T. domesticum* and *T. asahii* released similar GXMans (Ichikawa et al. 2001a, b), and NMR spectroscopy showed that the residues of the 1,3-mannan backbone were α-linked. Importantly, the fine structure of GXMans may contribute to the serological properties of *Trichosporon* species (Ichikawa et al. 2001a, b, Ikeda et al. 1996).

4.2.3. *The Cell Wall of* Cryptococcus neoformans

Cryptococcus neoformans (Tremellales, Tremellomycetes, Agaricomycotina) is a human and animal pathogenic yeast (see Chapter 114 on *Filobasidiella*). The cells have a triple-layered wall surrounded by a capsule. Electron microscopic analysis of exponentially growing cells reveals an unusual ultrastructure of the actual cell wall: an electron-dense middle layer between electron-transparent inner and outer layers (Yamaguchi et al. 2002). The capsule forms a porous network, and may be wider than the cell wall itself (Pierini et al. 2001, Yamaguchi et al. 2002). Isolated cell walls of an acapsular mutant contain 7% chitin, 30% α-1,3-glucan, a substantial amount of β-1,6-glucan, but, surprisingly, no β-1,3-glucan (James et al. 1990). This absence is consistent with the lack of staining by the fluorescent β-1,3-glucan-binding dye aniline blue (Nicholas et al. 1994). In contrast, staining with the chitin-binding dye Calcofluor white results in uniformly fluorescing cells, indicating that the cell wall is accessible to dyes and that chitin is evenly distributed over it. The following two observations are, however, difficult to reconcile with the presumed absence of β-1,3-glucan in the walls. First, *Cryptococcus* lysates contain β-1,3-glucan synthase activity (Maligie and Seletrennikoff 2005) and secondly, the *Cryptococcus* genome contains a single copy of an *FKS1* homolog, the putative catalytic subunit of β-1,3-glucan synthase, and this gene is essential for growth (Thompson et al. 1999). This latter observation raises the question of whether the cell wall composition and structure of the acapsular mutant may differ from those of wild-type cells. Isolated walls also contain a significant amount of protein, but mannose and galactose have not been found (James et al. 1990). Finally, cell walls of *C. neoformans* may also contain melanin (Eisenman et al. 2005).

The capsule seems to be anchored to the actual wall with α-1,3-glucan, and consists of two polysaccharides (reviewed in Bose et al. 2003, Reese and Doering 2003). The major component is a glucuronoxylomannan or GXMan, consisting of an α-1,3-mannan backbone decorated with glucuronyl and xylosyl residues. The minor component polysaccharide is an α-1,6-galactan with side-chains consisting of mannose, galactose and xylose residues (MXGal). The precise molecular organization of the capsule is unknown. Various serotypes reflecting its composition have been described (Enache-Angoulvant et al. 2007, Janbon 2004).

4.3. The Cell Wall of Yeast States of Zygomycetous Yeasts (Glomeromycota)

Some species of the Glomeromycota (i.e., zygomycetes), one of the basal lineages within the fungal kingdom, are able to grow as a yeast state under certain conditions (e.g., when grown at 37°C). Our knowledge of the cell wall of zygomycetous yeasts is limited. In the discussion below, we describe cell walls of the yeast form of the dimorphic fungi *Benjaminiella poitrasii* and *Mucor rouxii*. Although the walls of both fungi contain chitin and chitosan, a glucosamine polymer obtained by deacetylation of chitin, their wall compositions also show important differences.

4.3.1. *The Cell Wall of* Benjaminiella poitrasii

Benjaminilla poitrasii is a nonpathogenic, thermally dimorphic fungus growing in the yeast form at 37°C. The walls of the yeast form contain 3% chitin and 8–9% glucose, both resistant to extraction with alkali, indicating that they are covalently linked to each other, possibly as a chitin→β-1,3-glucan complex (Hartland et al. 1994, Khale and Deshpande 1992, Mol and Wessels 1987). The walls also contain about 30% protein and 40% mannose, suggesting that they may possess mannoproteins. In addition, a substantial amount of chitosan (17%) is present. However, in contrast to species of *Mucor,* uronic acids are not detectable. The ultrastructure of the cell wall is unknown.

4.3.2. *The Cell Wall of* Mucor rouxii

Mucor rouxii is also a dimorphic fungus, with large, spherical, multinucleate yeast cells that grow isotropically (reviewed in Orlowski 1991). The yeast cell wall contains about 8% chitin, but, surprisingly, no glucose. Glucose is also absent from the hyphal walls, but it is found in the sporangiospore walls (Orlowski 1991). The cell wall of the yeast state also contains about 10% protein and some mannose, fucose and galactose. Chitosan accounts for 28% of the wall. As noted above, *B. poitrasii* yeast walls do not contain detectable amounts of glucuronic acids, but those of the yeast state of *Mucor rouxii* do contain about 12% glucuronic acid, in the form of two types of polyuronides (Dow et al. 1983). The acidic polymers presumably form an ionic complex with chitosan, which is positively charged at neutral and acidic pHs. Electron micrographs of the cell walls of the yeast state of *M. racemosus* reveal two distinct layers: a dark-staining outer layer and a lighter dark-staining inner layer (Orlowski 1991). The molecular organization of the wall of species of *Mucor* is as yet unknown.

5. SEPTAL PORE ULTRASTRUCTURE

In contrast to the yeasts, filamentous and dimorphic fungi grow by means of hyphae that extend at their apices while branching subapically. This mode of growth, together with hyphal fusion (anastomosis), results in an interconnected network of hyphae; the mycelium. Hyphae or pseudohyphae do, however, occur in many dimorphic yeasts belonging to both the Saccharomycotina (Ascomycota) and various lineages of the Basidiomycota.

Septa in almost all fungi studied so far have one or more pores (see below). The continuity of the cytoplasm discriminates the fungi from plants and animals (Müller et al. 1999). In these latter two kingdoms, intercellular cytoplasmic connections do occur, but they are much smaller. Gap junctions in animals have pores of about 1.6–3 nm in diameter, and allow streaming of inorganic ions and small water-soluble organic molecules (Perkins et al. 1997, Veenstra 1996). Plasmodesmata in plants are narrow microchannels around 1.5–2 nm wide, which restrict the intercellular flow to small molecules (reviewed by Ghoshroy et al. 1997). It should be noted that the

channels in plasmodesmata are dynamic, and can be closed or increased in diameter to 5–9 nm. General reviews on plasmodesmata can be found in Van Bel and van Kesteren (1999).

Hyphae of the lower fungi, i.e., the Glomeromycota (zygomycetes) and Chytridiomycota (Bauer et al. 2006, Schüßler et al. 2001), are sparsely, if at all, septate (James et al. 2006). Developing zygospores of the zygomycetous species *Rhizopus sexualis* and *Gilbertella persicaria*, however, were found to contain transcellular strands in septa which separate young gametangia from the suspensors. These simple, unbranched strands occur at intervals in the gametangial wall, resemble plasmodesmata, and were found to be connected with the endoplasmic reticulum (Hawker et al. 1966).

Hyphae and pseudohyphae of filamentous and dimorphic Ascomycota and Basidiomycota are regularly septate. Their septa contain pores of 50 to 500 nm width, which are covered with a continuous plasma membrane and allow streaming of cytoplasm, including organelles such as mitochondria (Bracker and Butler 1964, Gull 1978). The mycelium may be considered a functional coenocytium due to this presence of septal pores. Early observations by transmission electron microscopy (TEM) revealed the presence of morphologically diverse septal pore structures and, in many cases, septal pore associated structures, such as Woronin bodies or septal pore caps (SPCs or parenthesomes). These septum-associated structures contain useful phylogenetic information (Celio et al. 2006, McLaughlin 1995, 2006, Moore 1998b), and many studies have demonstrated that septal ultrastructure is a robust indicator for higher-level taxonomic relationships (Bauer et al. 2006, Fell et al. 2001, McLaughlin et al. 1995, Moore 1985, 1987b, 1988b, 1996a, 1998b). Extensive overviews of fungal ultrastructure have been presented by, e.g., Becket et al. (1974), Moore (1998b) and McLaughlin et al. (1995). Recently, an attempt was made to capture several of these ultrastructural characters in a comprehensive database (Celio et al. 2006). Despite the many ultrastructural studies of fungal septa and septum-associated structures, attempts to unravel their function started only recently (Jedd and Chua 2000, van Driel 2007, van Driel et al. 2007a, b, 2008b, K. van Driel, W.H. Müller, T. Boekhout, unpublished data).

5.1. Septa in Ascomycetes

The ultrastructure of the septum of Ascomycota differs between species in the Saccharomycotina or the Pezizomycotina. Although the number of species investigated remains small, the data indicate the presence of one or multiple narrow micropores or plasmodesmata-like (i.e., closure lines) structures in the septa of Saccharomycotina species. Notable exceptions are the dolipore-like septa in species of the genus *Ambroziozyma* (see below). Species of filamentous Ascomycetes (Pezizomycotina) have septa with a wider central pore, a tapering septal wall, and the presence of Woronin bodies (Fig. 8.14).

5.1.1. Septa in the Pezizomycotina

The hyphal septa of filamentous ascomycetes, viz., Pezizomycotina, are usually homogeneous and electron transparent (Fig. 8.14).

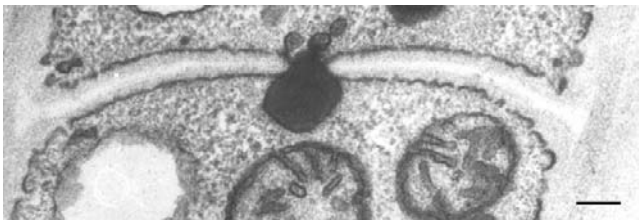


FIGURE 8.14 Hyphal septum of *Retroconis fusiformis* CBS 540.88 with central pore and tapering septum wall and Woronin bodies typical of Pezizomycotina. Bar = 500 nm.

Although the septa are extensions of the lateral cell wall, the chemical composition of the septa and lateral walls differs (Gull 1978). The septal plate is built up by chitin microfibrils and β-glucans, but α-glucans, which are a component of the lateral wall, are not found (Griffin 1994). Older septa may be covered with an amorphous protein layer (Gull 1978).

The septa in the species that have been studied are of uniform thickness or taper slightly towards the septal pore. Pores allow passage of nuclei and other organelles (Gull 1978, Moore and McAlear 1962). They have rounded rims, and are frequently accompanied on either side by Woronin bodies (Buller 1993a, Kimbrough 1994, Markham 1994, Markham and Collinge 1987, Woronin 1864). These bodies are peroxisomes of 150 to 500 nm diameter that contain paracrystalline material (Jedd and Chua 2000, Markham and Collinge 1987, Tenney et al. 2000), which also seem to occur in the hyphal tip (Momany 2002). Woronin bodies rapidly plug septal pores when hyphae are damaged, to prevent loss of cell content (Trinci and Collinge 1974). Hex1 is the main protein and forms the crystalline core of these organelles in hyphae of *Neurospora crassa* (Yuan et al. 2003). Phosphorylation of Hex1 is important for multimerization of the protein and proper formation of the Woronin bodies (Juvvadi et al. 2007). The Hex1 protein has a C-terminal peroxisome targeting signal (PTS1), and therefore it has been suggested that Woronin bodies are in fact peroxisomes (Jedd and Chua 2000, Tenney et al. 2000). Hex1 homologues have been found in several other filamentous ascomycetes, like *Aspergillus nidulans* and *Magnaporthe grisea* (Jedd and Chua 2000, Soundararajan et al. 2004), but not in members of the Saccharomycotina and Basidiomycetes (Jedd and Chua 2000, K. van Driel, unpublished observations).

5.1.2. Septa of Saccharomycotina

Pores observed in species belonging to the Saccharomycotina are either micropores that form a minuscule membranous cylinder in the center of the septum, or a closure line that looks like a punctum in surface view (Figs 8.15 and 8.17) (Markham 1994).

Micropores or closure lines are not the same as plasmodesmata, because in the former the plasma membrane is continuous between the two adjacent cells. Micropores or closure lines can occur singly or in multiples, and in the latter case the arrangement may be either random or circular.

A single and central micropore or closure line occurs in septa of several ascomycetous yeast species, such as *Ascoidea africana*, *Blastobotrys proliferans*, *Candida albicans*, *Dipodascus uninucleatus*, *Geotrichum candidum*, *Geotrichum terrestre*, *Hyphopichia burtonii*, *Saccharomycopsis (Arthroascus) javanensis*, *Saccharomycopsis (Endomycopsis) fibuligera*, *Sporothrix fungorum*, *Trichomonascus (Stephanoascus) farinosus*, *Wickerhamomyces bispora* (cited as *Hansenula beckii*), and *Yarrowia lipolytica* (Gow et al. 1980, 1983, Kirk and Sinclair 1966, Kreger-van Rij and Veenhuis 1974b, Moore 1987b, Takada et al. 1965). As these taxa are phylogenetically diverse, it seems that the micropore forms the default type of septal pore among Saccharomycotina. Hyphae of *Ambrosiozyma* spp. have centrally thickened septa around a central narrow pore (Fig. 8.16) (van der Walt and von Arx 1985), which morphologically resemble the dolipores in the Agaricomycotina.

In the genus *Cephaloascus,* the two species studied show some heterogeneity in septal structure (Kurtzman 1977, Kurtzman and Robnett 1998a). *Ceph. fragrans* has a tapering septal wall with a large pore, whereas *Ceph. albidus* has a narrow, central micropore. This example indicates that morphological variations of the septal structure may occur among phylogenetically closely related taxa.

Septa of *Galactomyces geotrichum* exhibit unbranched plasmodesmata-like structures, which extend through the cell wall. The width

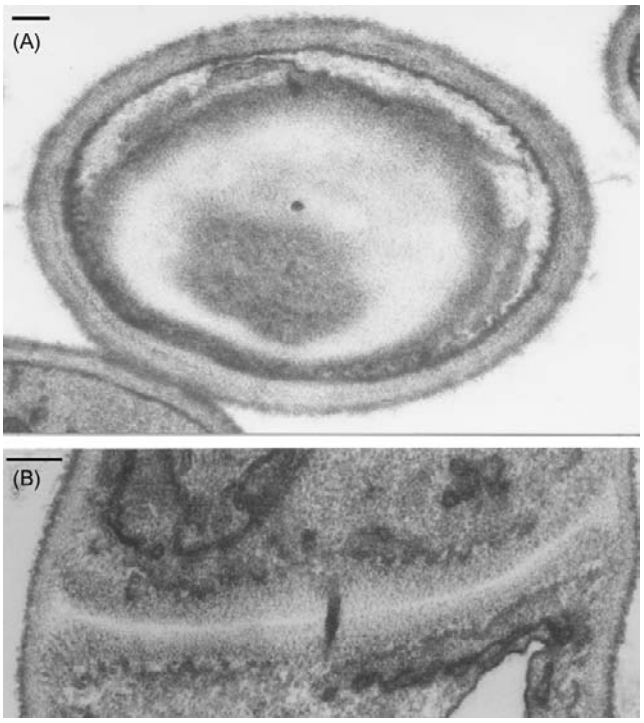


FIGURE 8.15 Single and central micropore in septum of *Blastobotrys proliferans*. (A) Top view on septum of *B. proliferans* CBS 522.75 showing the central micropore. (B) Section through septum of *Blastobotrys* species CBS 181.75 showing the narrow width of the micropore. Reprinted with permission from *Antonie van Leeuwenhoek* 51, 121–128 (1985). Bar = 500 nm.

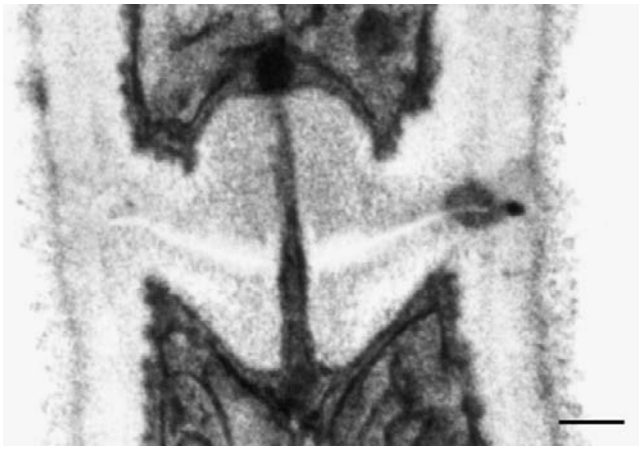


FIGURE 8.16 Electron micrograph of septum of *Ambrosiozyma platypodis* CBS 7108. Note the thickening of the septum towards the central pore. Electron dense material occurs on both sides of the pore. This septum is morphologically similar to the dolipore which occurs in many basidiomycetous fungi. Bar = 500 nm.

of these channels is 40 to 60 nm, with a desmotubule of 10 nm diameter which connects endoplasmic reticulum on either side of the septum (Marchant 1976). Van der Walt et al. (1991) considered that the presence of a closure line (referred to as plasmodesmatal canals) in *Lipomyces* (cited as *Zygozyma*) indicated a taxonomic relationship between Lipomycetaceae and Dipodascaceae. This, however, is not sustained by more recent rRNA gene sequence analysis (Kurtzman and Robnett 1998a, Kurtzman et al. 2007).

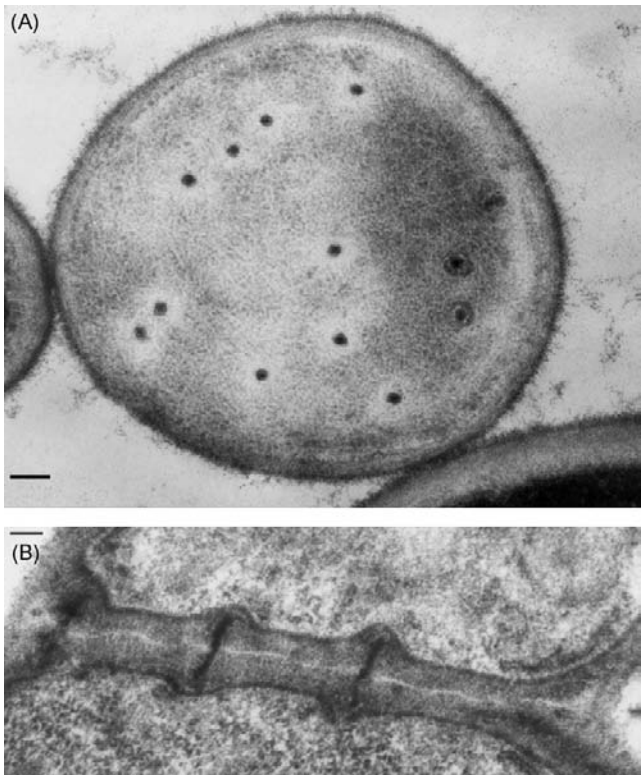


FIGURE 8.17 Multiple micropores in septum of *Trichomonascus* (*Stephanoascus*) *ciferrii* CBS 6699. (A) Top view showing the random distribution of the micropores across the septum. (B) Section through septum showng the narrow width of two micropores. Note that the plasma membrane seems to be continuous over the pores. Reprinted with permission from *Antonie van Leeuwenhoek* 51, 121–128 (1985). Bar = 500 nm.

Multiple micropores occurring in a random array (Fig. 8.17) have been observed in species that are not phylogenetically close (Kurtzman and Robnett 1998a), such as *Ascoidea africana, Endomyces decipiens, Geotrichum terrestre, Galactomyces reessii, Galactomyces geotrichum, Saccharomycopsis* (*Guilliermondella*) *selenospora*, *Saccharomycopsis capsularis, Saccharomycopsis crataegensis, Saccharomycopsis fibuligera, Saccharomycopsis synnaedendra, Saccharomycopsis vini*, and *Trichomonascus* (*Stephanoascus*) *ciferrii*, *Sporothrix guttuliformis*, *Dipodascus aggregatus* and *Lipomyces* (*Zygozyma*) *smithiae* (Kreger-van Rij and Veenhuis 1973a, 1974b, Moore 1987b, Smith and Batenburg-van der Vegte 1985, van der Walt et al. 1991). In species of *Magnusiomyces*, e.g., *M. magnusii, M. ovetensis* and *M. tetrasperma,* the pores occur in a circular arrangement (Moore 1987b). Note that in two phylogenetically closely related species, *Endomyces decipiens* and *Dipodascus armillaria* (of which *D. ovetensis* is a synonym), the micropores may occur randomly or in a circular fashion, respectively. Thus the arrangement of the micropores over the septum seems to be of low phylogenetic importance.

5.2. Septa in Basidiomycota

Basidiomycota, including the dimorphic basidiomycetous yeasts, are characterized by electron-dense and layered cell walls (Fig. 8.13) (Kreger-van Rij and Veenhuis 1971a; Simmons and Ahearn 1987) and show a more diverse septal morphology (Markham 1994, Moore 1985). Within the basidiomycetes, the three major phylogenetic lineages Pucciniomycotina (Urediniomycetes *sensu* Swann and Taylor 1995), Ustilaginomycotina (Ustilaginomycetes *sensu* Swann and Taylor 1995), and Agaricomycotina (Hymenomycetes *sensu* Swann and Taylor 1995)

are rather well supported by the ultrastructure of their septum (Bauer et al. 2006, McLaughlin et al. 1995). All three subphyla contain dimorphic species, including species with a yeast state (Boekhout et al. 1993, 1998, Fell et al. 2001). Septal ultrastructure, which is considered an important phylogenetic character complex among these fungi (see, e.g., Bauer et al. 1989, Boekhout et al. 1992b, Guého et al. 1992, Johnson-Reid and Moore 1972, Khan and Kimbrough 1980, Kreger-van Rij and Veenhuis 1971b, Kwon-Chung and Popkin 1976, Moore 1980, 1987, Moore and Kreger-van Rij 1972, Sampaio et al. 2002), correlates well with molecular studies of 5S, SSU and D1/D2 LSU ribosomal RNA gene sequences (Bauer et al. 2006, Celio et al. 2006, Fell et al. 1995, 2000, 2001, Gottschalk and Blanz 1985, McLaughlin et al. 1995, Sugiyama and Suh 1993, Suh and Sugiyama 1993, Swann and Taylor 1993, 1995a, b, Templeton 1983, Walker 1984, Walker and Doolittle 1982).

Interestingly, the biochemical composition of the cell wall sustains this pattern, and can be summarized as follows: species belonging to the Pucciniomycotina usually have septa with a single pore and attenuating septa (i.e., morphologically similar to the septa of Pezizomycotina and referred to as "simple" septa) (Fig. 8.18), but without Woronin bodies. Their cell wall composition is dominated by mannose, with glucose and some fucose and rhamnose present, but xylose is absent. Note the presence of xylose in whole cell hydrolysates of *Rhodotorula yarrowii* (Boekhout et al. 2000).

Species belonging to the Ustilaginomycotina have central pores with or without a slightly flaired margin or a dolipore (see below), and the cell walls contain glucose as the dominant monomer, with some galactose and mannose present, but xylose is absent. The third lineage, the Agaricomycotina, is characterized by a dolipore septum, which is flared towards the pore, forming a barrel-shaped structure (i.e., the dolipore) (Figs 8.19–8.26), and with glucose, mannose and



FIGURE 8.18 Electron micrograph showing the septum of *Leucosporidium scottii* CBS 4347 on V8 medium after potassium permanganate fixation. Note the central pore with the tapering electron-dense septal wall, which is a "simple" pore. Woronin bodies are absent, but a small vesicle is present. Bar = 100 nm.



FIGURE 8.19 Dolipore septum of *Bulleromyces albus* CBS 500 × CBS 7440 with a cupulate septal pore cap. Note the electron-dense bands on each side of the pore channel and the transverse band inside. Fixation was by glutaraldehyde and tannic acid. Reprinted with permission from *Antonie van Leeuwenhoek* 59, 81–93 (1991). Bar = 350 nm.

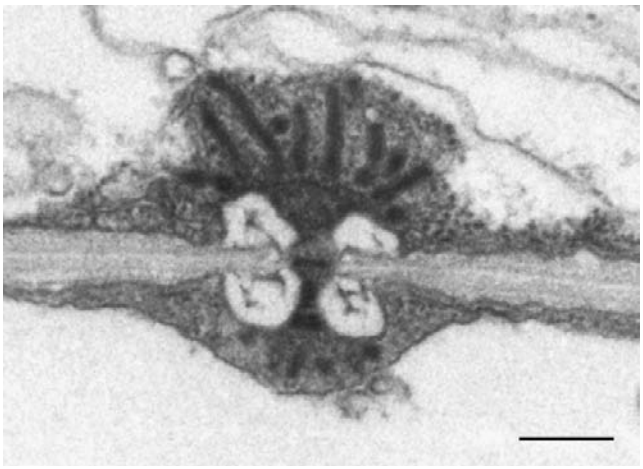


FIGURE 8.20 Dolipore septum of *Trichosporon coremiiforme* CBS 2482. Note the tubular septal pores cap. Fixation with glutaraldehyde and osmium tetroxide. Reprinted with permission from *Antonie van Leeuwenhoek* 61, 289–316 (1992). Bar = 350 nm.

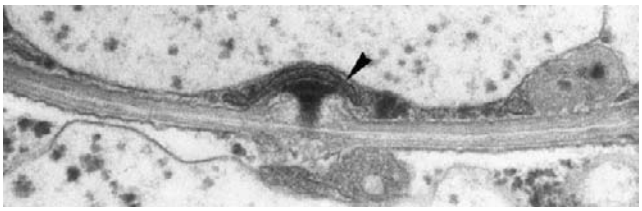


FIGURE 8.21 Dolipore septum of *Itersonilia perplexans* PD 85.1013. Note the absence of a septal pore cap, but a strand of endoplasmatic reticulum (ER) is present on the top side of the pore channel. Note the electron-dense bands present between this strand of ER and the pore channel. Reprinted with permission from *Mycol. Res.* 95, 135–146 (1991).

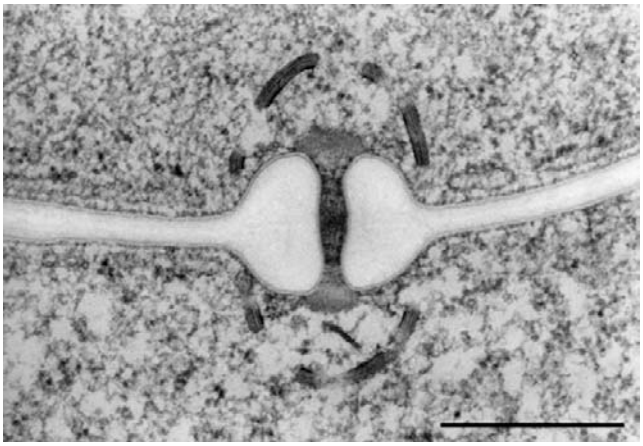


FIGURE 8.22 Perforate septal pore cap of *Schizophyllum commune* CBS 340.81 prepared for transmission electron microscopy by a combination of high-pressure freezing, freeze-substitution and Spurr's resin embedding. Bar = 500 nm.

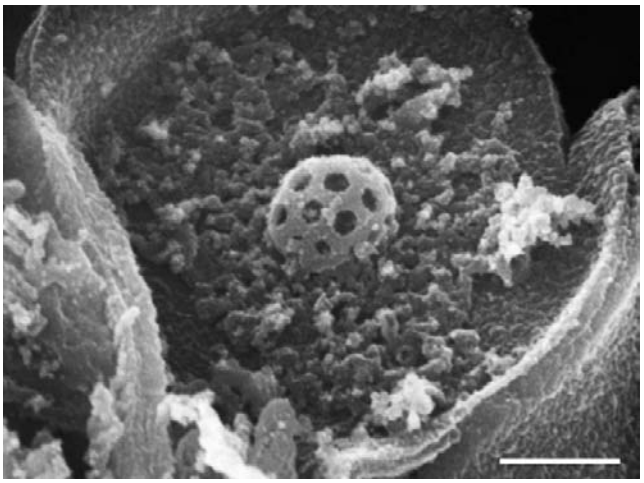


FIGURE 8.23 Perforated septal pore cap (SPC) of *Schizophyllum commune* CBS 340.81 after conventional scanning electron microscopy. The SPC measures about 600 nm across. Bar = 500 nm.

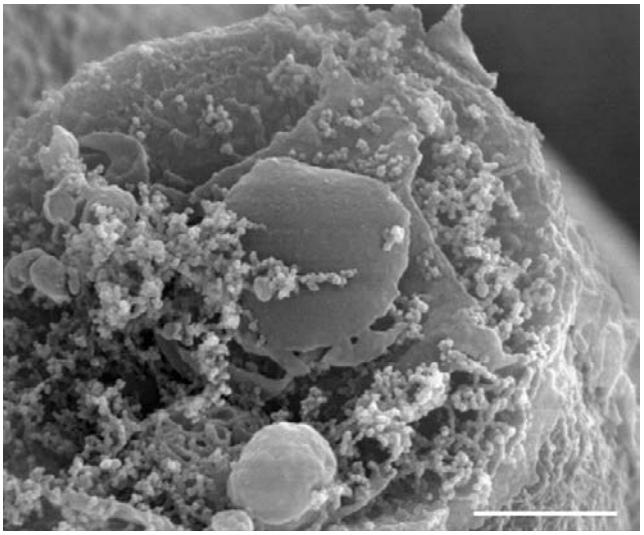


FIGURE 8.24 Non-perforate septal pore cap (SPC) of *Cyclomyces fuscus* IFO 9789 after conventional scanning electron microscopy. The SPC measures about 750 nm across. Bar = 500 nm.

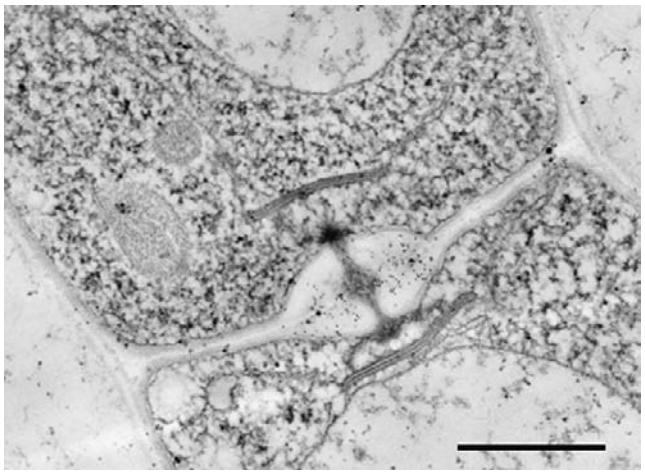


FIGURE 8.25 Non-perforate septal pore cap (SPC) of *Cyclomyces fuscus* IFO 9789 prepared for transmission electron microscopy by a combination of high-pressure freezing, freeze-substitution and Spurr's resin embedding. Bar = 500 nm.

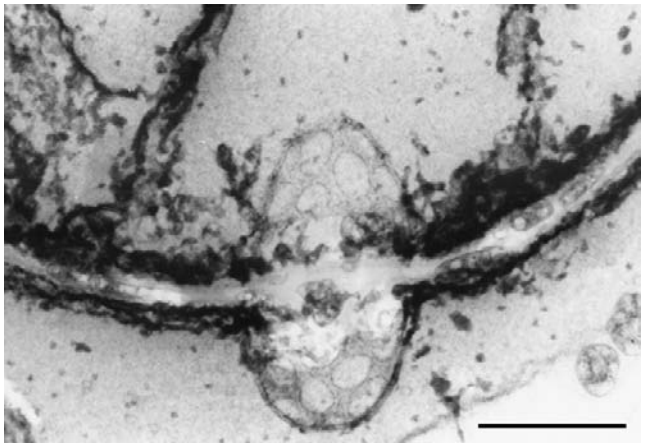


FIGURE 8.26 Perforate septal pore cap (SPC) of *Schizophyllum commune* CBS 340.81 after zinc-iodide-osmium (ZIO) staining and further prepared for transmission electron microscopy. Note the heavily stained endoplasmic reticulum compared to the SPC. Bar = 500 nm.

xylose predominant in the cell walls (Prillinger et al. 1990a, b, 1991a, b, 1993, Swann and Taylor 1995a, b, Weijman and Golubev 1987b).

5.2.1. Septa of Species with Yeast States in the Pucciniomycotina

The Pucciniomycotina accommodate a diverse array of fungi, ranging from plant pathogenic rust fungi (Uredinales) to insect associated fungi (e.g., Septobasidiales), fungi formerly classified in the smuts (e.g., *Microbotryum* spp. presently classified in the Microbotryales), mycoparasitic fungi (e.g., Heterogastridiales), and dimorphic yeast species (e.g., Leucosporidiales and Sporidiobolales). This subphylum forms a strongly supported monophyletic clade, supported by SSU and LSU rRNA gene sequences (Bauer et al. 2006, Fell et al. 2000, 2001, Swann and Taylor, 1995a, b), a type A5 rRNA secondary structure, and cell wall composition (Prillinger et al. 1991a, Swann et al. 2001).

In the most recent taxonomic scheme, the Pucciniomycotina are divided into eight classes: Agaricostilbomycetes, Atractiellomycetes, Classiculomycetes, Cryptomycocolamycetes, Cystobasidiomycetes, Microbotryomycetes (i.e., the anther smuts and relatives), Mixiomycetes, and Pucciniomycetes (i.e., rust fungi and their allies) (Hibbett et al. 2007). Species with yeast states occur scattered throughout the subphylum (see Chapter 100). All species investigated so far have septa with a central pore, with the septum gradually attenuating toward it, which is also referred to as "simple" pore. They are similar morphologically to those found in the Pezizomycotina (Bauer et al. 2006, Oberwinkler and Bandoni 1982c, Swann et al. 2001), but, notably, Woronin bodies have not been observed, and the cell wall is of medium electron density (Fig. 8.18). Examples of species with this type of septum are *Leucosporidium scottii, Bensingtonia phyllada, B. yamatoana, Rhodosporidium sphaerocarpum, R. toruloides, Sporidiobolus johnsonii* and *S. ruineniae* (Bauer et al. 2006, Boekhout et al. 1992b, Johnson-Reid and Moore 1972). Similar septa were observed in *Agaricostilbum pulcherrimum, Helicobasidium mompum* and *Heterogastridium pycnidioideum* (McLaughlin et al. 1995, Oberwinkler et al. 1990a, b). *Kriegeria eriophori*, which has a yeast anamorph, *Zymoxenogloea eriophori* (Doublés and McLaughlin 1991, 1992), however, has morphologically

similar pores, but occurring in multiples in the septa (McLaughlin et al. 1995 and references therein, Bauer et al. 2006). Microbodies, small membrane bound vesicles with unknown composition and function, may be present near the septal pore in some lineages (i.e., Pucciniomycetes and Cryptomycocolamycetes), and the pores can also be plugged by "pulley-like" electron-dense plugging material (Bauer et al. 2006, Swann et al. 2001). Species of the Cystobasidiomycetes (e.g., *Occultifur* spp.) have septal pores with so-called cystosomes, which are poorly characterized organelles that cover the pore channel, extend into the cytoplasm and have a reticulate surface (Bauer et al. 2006).

Five of the eight classes of Pucciniomycotina have dimorphic species with a yeast state and a documented septal ultrastructure (Aime et al. 2006, Bauer et al. 2006, Hibbett et al. 2007). The septal pores of *Agaricostilbum hyphaenes* and *Ag. palmicolum* (Agaricostilbales, Agaricostilbomycetes) have no associated structures or lenticular bodies (colacosomes), but fucose may be present (Oberwinkler and Bandoni 1982b, Oberwinkler and Bauer 1989). *Chionosphaera apobasidialis*, *Chion. cuniculicola* and *Kondoa malvinella* (Kirschner et al. 2001a, Oberwinkler and Bandoni 1982b, Oberwinkler and Bauer 1989, Suh et al. 1993a), all with " simple" pores, belong to this class as well. Septal pores in representatives of Atractiellomycetes, *Atractogloea stillata* and *Atractiella* spp., have symplechosomes, and microbodies or atractosomes may occur close to the septal pore (Bauer et al. 2006, Oberwinkler and Bandoni 1982c, Oberwinkler and Bauer 1989). Septal pores of species of Cystobasidiomycetes may have cystosomes, but fucose seems to be absent from the cell walls (e.g., *Occultifur* spp. classified in Cystobasidiales [Bauer et al. 2006]). The septa of *Erythrobasidium hasegawianum* (Erythrobasidiales), however, lack cystosomes and the species contains coenzyme Q-10H_2 (Bauer et al. 2006, Suh et al. 1993a). Note that Suh et al. (1993a) report the presence of electron-dense microbody-like structures near the septal pore. *Sakaguchia* (*Rhodosporidium*) *dacryoideum* and *Bannoa* spp., which are not assigned to any order, have an occluded pore channel (Aime et al. 2006, Suh et al. 1993a).

Septal pores of species of Microbotryomycetes lack microbodies, but lenticular bodies (also named colacosomes, see below) are present. Species with these characteristics are *Leucosporidium scottii* (Moore 1972), *Leucosporidium fellii* (Suh et al. 1993a) (Leucosporidiales), *Sporidiobolus johnsonii* (Moore 1972), *Sporidiobolus ruinenii* (Boekhout et al. 1992b), *Rhodosporidium toruloides* (Boekhout et al. 1992b, Johnson-Reid and Moore 1972), *Rhodosporidium sphaerocarpum* (Moore 1972) (all Sporidiobolales); and *Bensingtonia yamatoana* (Aime et al. 2006, Boekhout et al. 1992b), which is not yet assigned to any order. *Kriegeria eriophori* (Microbotryomycetes) has multiperforate septa (Doublés and McLaughlin 1991).

Species of Mixiomycetes have no clear ultrastructural characteristics. *Mixia osmundae*, a fern parasite (Mixiales) (see Chapter 122) has "simple" septa (Aime et al. 2006, Bauer et al. 2006). Septal pores in species of Pucciniomycetes usually have microbodies. *Platygloea* spp. (Platygloeales) have septa with so-called "simple" pores (Bauer et al. 2006). Note that in *P. disciformis,* microbodies may be absent, but non-membrane bound electron-dense structures have been observed (Bauer et al. 2006).

In brief, species of Pucciniomycotina have "simple" septa, but several variations may occur (e.g., the multiple septa in *Kriegeria*), and furthermore, different, but not well characterized, organelles occur in the various lineages. It is important to note that the number of species thoroughly investigated is small, thus hampering the inference of solid phylogenetic relationships.

5.2.2. Septa of Ustilaginomycotina

Ustilaginomycotina comprises two classes, Ustilaginomycetes and Exobasidiomycetes (Hibbett et al. 2007), which are largely supported by rRNA gene sequence analysis (Begerow et al. 1997, 2000, 2006, Boekhout et al. 2003, 2006, James et al. 2006, Swann and Taylor, 1993, 1995b) and composition of the cell wall (Bauer et al. 2001, Prillinger et al. 1990b, 1993a). Some investigators regard the Entorrhizomycetes as a separate class (Begerow et al. 2006), but others consider these fungi as nonclassified among Basidiomycota (Hibbett et al. 2007). Species of *Entorrhiza* (Entorrhizales/Entorrhizomycetes), have a dolipore (see below) without a septal pore cap (Bauer et al. 1997, Begerow et al. 2006).

Members of Ustilaginomycotina are mainly plant pathogens, but asexual states have been reported as saprobic yeasts (i.e., *Pseudozyma* and *Tilletiopsis* species, Boekhout 1991a, Boekhout et al. 1996 (see Chapters 153 and 160), human and animal pathogens (i.e., *Malassezia* spp., see Chapters 2 and 148), biocontrol fungi (e.g., *Pseudozyma flocculosa*, see Chapter 153), and mite-inhabiting fungi (*Meira* and *Acaromyces* spp., see Chapters 149, 135) (Batra et al. 2006, Begerow et al. 2000, Boekhout 1991a, 1992b, Boekhout et al. 1995a, 2003, 2006).

The septal hyphae of many representatives of Exobasidiomycetes and Ustilaginomycetes have a central pore, which usually has membrane caps extending somewhat into the cytoplasm (Bauer et al. 1997, 2001, Begerow et al. 2006, Celio et al. 2006). Species of *Neovossia, Conidiosporomyces, Ingoldiomyces, Oberwinkleria*, *Tilletia* and *Entyloma vignae* (Tilletiales), however, have a dolipore (see below) without a septal pore cap (Bauer et al. 1997, Begerow et al. 2006, Roberson and Luttrell 1987b). Representatives of other species show somewhat irregularly thickened septa with pore-like structures, which may not represent a real pore structure (Bauer et al. 1997, 2005). These structures, which were referred to as "amorphous" (Moore 1998b), have been observed mainly in the Georgefischerales (Exobasidiomycetes), e.g., *Eballistra* (*Melanotaenium*) *brachariae, Georgefischeria rivae, Jamesdicksonia* (*Entyloma*) *dactylidis, Jamesdicksonia* (*Entyloma*) *irregulare, Tilletiopsis fulvescens, Tilletiopsis minor,* in separate lineages (e.g. *Tilletiopsis pallescens*), but also in representatives of Ustilaginomycetes (Ustilaginales), e.g., *Anthracoidea intercedens, Moesziomyces bullatus, Trichocintractia utriculicola* and *Ustilago avenae* (Bauer et al. 1989, Boekhout et al. 1992b, O'Donnell and McLaughlin 1984b). Interestingly, young septa of *Gjaerumia ossifragi* (Gjaerumiaceaea, Georgefischerales) have a dolipore septum (Bauer et al. 1997, 2005), and the hyphal pores of *Tilletiaria anomala* (Tilletiariaceae, Georgefischerales) (Boekhout et al. 1992b) are dolipore-like as well.

Microstroma juglandis and *Sympodiomycopsis paphiopedili*, (Microstromatales, Exobasidiomycetes), which also have a yeast state, have septal pores similar to those occurring in Pezizomycotina and Pucciniomycotina (Bauer et al. 1997, Suh et al. 1993a). In contrast, another species that belongs to this order, the yeast-like species *Quambalaria* (*Cerinosterus* = *Fugomyces* = *Sporothrix*) *cyanescens* (de Beer et al. 2006, Middelhoven et al. 2000c, Sigler and Verweij 2003), has a dolipore-like pore without a SPC, but with clusters of electron-dense material present close to the pore channel (Smith and Batenburg-van der Vegte 1985, 1986b). Again, these examples indicate that care has to be taken in interpreting septal ultrastructural data in a phylogenetic context without taking other data into account, such as those based on rRNA gene sequencing.

The ultrastructure of yeast cells and septa of the human and animal pathogen *Malassezia furfur* (Malasseziales, Exobasidiomycetes) have been investigated to some extent (David et al. 2007a, Guillot et al. 1995b). No septal pores were observed in the hyphal filaments, which have electron-dense cell walls. Endogenous formation of new cells (i.e., endosporulation) occurred in filaments, and probably the yeast cells. Spindle formation during mitosis occurs in the bud, according to the pattern that occurs most widely among the basidiomycetes (David at al. 2007a). The cell wall of *Malassezia* yeasts, approximately 0.3–0.45 μm thick, exhibits a complex pattern of three layers: 1) a thin electron-dense outermost layer composed of

diffuse microfibrilles; 2) a medial layer of medium electron density, and 3) a rather thick internal layer with helicoidally oriented electron-dense structures embedded in a matrix of medium electron density (see also Chapter 148). The plasma membrane shows distinct helicoidal invaginations (David et al. 2007a, Guillot et al. 1995b). The same cell wall structure was also observed in *M. pachydermatis* and *M. sympodialis* (Gabal and Fagerland 1979, Simmons and Guého 1990, Swift and Dunbar 1965). As stated by Guillot et al. (1995b):

> *"This feature represents a characteristic of the genus* Malassezia *that seems unique in the world of fungi".*

Unfortunately, as far as we know, not a single biochemical study has been made of these unique cell walls, thus rendering the biochemical base unknown.

5.2.3. Septa in Agaricomycotina

The Agaricomycotina accommodate a diverse array of fungi, in size, life style (e.g., unicellular yeasts to mushroom-forming fungi) and ecology (e.g., saprotrophes, ectomycorrhiza symbionts and plant pathogens). The subphylum is divided into three classes; Tremellomycetes, Dacrymycetes and Agaricomycetes, with yeast states occurring in Tremellomycetes only. All species investigated have septa with a barrel-shaped swelling around the pore – a so-called dolipore – which may, or may not, be associated with a septal pore cap (SPC) (Bracker and Butler 1963). The latter is also known as a Verschlussband (Girbardt 1958) or parenthesome (Moore and McAlear 1962), and is considered as a specialized subdomain of the ER (van Driel 2007, van Driel et al. 2008b). Dolipore septa possess three basic structures (Figs 8.19–8.26): 1) a barrel-shaped dolipore; 2) occlusions within the pore channel; and 3) SPCs or parenthesomes on either side that delimit the pore domain. Different reports have been published of the diameter of the dolipore channel, which may vary from approximately 100 to 500 nm, depending on the species studied, and most likely the physiological state of the hyphal cells (Bracker and Butler 1964, Patton and Marchant 1978, Setliff et al. 1972). Within the pore structure, various electron-dense banding patterns have been observed (Müller et al. 2000, van Driel 2007), and both sides of the pore channel may be occluded by a septal pore plug that seems tightly connected to the dolipore swelling (van Driel et al. 2007a, 2008b).



FIGURE 8.27 Budding yeast cell of *Itersonilia perplexans* PD 83/1013 with the top of the nucleus inside the bud. The SPC can be seen located near the nuclear envelope near the top part of the nucleus, whereas the nucleolus remains in the most basal part of the nucleus in the parent cell. Fixation by glutaraldehyde and tannic acid/osmium tetroxide. Reprinted with permission of *Syst. Appl. Microbiol.* 14, 117–123 (1979). Bar = 1.8 μm.

In hyphae of species of Agaricomycotina, the biochemical composition of the septum differs from that of the lateral wall. The lateral cell wall of *Schizophyllum commune* consists of chitin, β-1,3/β-1,6-glucan and α-1,3-glucan. The septal plate contains chitin and β-1,3/β1,6-glucan, but no α-1,3-glucan, whereas the septal swelling contains α-1,3-glucan, β-1,3-glucan and β-1,6-glucan (Janszen and Wessels 1970, Müller et al. 1998, 2000). The dolipore swelling contains more β-1,6-glucan than the septal plate (Müller et al. 1998, 2000). Staining of the polysaccharides, according to Thiéry (1967), showed that filaments of the inner, electron-dense, septal layer radiate into the amorphous matrix of the dolipore and form a distinct rim, which is visible in median and traverse sections. This rim intertwines as a loose network of stained, fibrous material into the non-stained, peripheral part of the septal swelling (Bracker and Butler 1963, Valk and Wessels 1977).

In early electron microscopic studies, chemical fixation and embedding in resin were used to distinguish between the various septal pore cap types. Later, more reliable electron microscopic techniques such as high-pressure freezing, cryofixation and freeze substitution, were used (Hoch and Howard 1981, Orlovich and Ashford 1994). Hoch and Howard (1981) demonstrated that the conspicuous swellings of the dolipore septum, as observed after the application of conventional chemical fixation, are an artifact of this preparatory method, because they are much smaller if freeze substitution methods are used. The application of scanning electron microscopy (Müller et al. 1994, 1998b, 2000) and the development of electron tomography (Müller et al. 2000) has allowed better visualization of the complexity of these structures. Septal pore caps can have different morphologies, and they are usually considered to be reliable phylogenetic markers (Hibbett and Thorn 2001, Lutzoni et al. 2004, McLaughlin et al. 1995). SPCs can be absent, cupulate, ampullate, tubular, vesiculate, non-perforate or perforate (Moore 1985, McLaughlin et al. 1995, Müller et al. 1998, van Driel 2007). The perforate SPC may have small holes as observed in *Schizophyllum commune* or a few large perforations as in *Rhizoctonia solani* (Müller et al. 1994, 1998b, 1999, 2000). The absence or presence of SPCs and the recognized SPC-type reflects the higher-order relationships within the Agaricomycotina to a large extent (Figs 8.19–8.26) (Hibbett and Thorn 2001, Müller et al. 2000, Wells 1994, Wells and Bandoni 2001, van Driel 2008a).

The SPC is a layered structure with inner and outer membranes, which enclose a SPC matrix (Bracker and Butler 1963, Girbardt 1958, 1961, Marchant and Wessels 1973, Moore and McAlear 1962, Müller et al. 1998, 2000). At their base, the SPCs are connected to endoplasmic reticulum (Girbardt 1961, Moore 1975, Müller *et al*. 1998, van Driel et al. 2008b), which is especially clear in young hyphae (Müller et al. 1999). ER is also often observed to be present on top of imperforate SPCs, as reported for *Cyclomyces fuscus*, *Coltricia perennis* (Müller et al. 2000), *Sebacina vermifera* (Currah and Sherburne 1992, Müller et al. 1998), *Basidiodendron cinereum*, *Tremellodendropsis tuberosa* and *Botryobasidium vagum* (Langer 1994, Wells 1994). The outer cap, as observed in perforate SPCs of agaricoid fungi like *Agaricus bisporus* (Craig et al. 1977, Thielke 1972), *Coprinus cinereus* (Valk and Marchant 1978) and *Agrocybe praecox* (Gull 1976), may be similar to the ER plates that are associated with the imperforate SPCs (Gull 1967, Valk and Marchant 1978). The presence of the outer cap in these perforate SPCs may depend on the developmental stage of the hyphal cells, because it occurred at the dolipore septa in subhymenial cells (Craig et al. 1977, Gull 1976).

Due to the connection with the ER, the SPC may be regarded as a specialized subdomain of the ER (Müller et al. 2000, van Driel et al. 2008b, Wilsenach and Kessel 1965). In *Rhizoctonia solani*, a SPC-specific protein, named spc18 (*s*eptal *p*ore *c*ap 18 protein), was characterized, and shown to have characteristics of ER proteins (van Driel 2007, 2008b). Furthermore, fluorescent markers that stain endoplasmic reticulum, such as ER-tracker, DIOC-6 and Brefeldin A conjugated to BODIPY, also stain the SPC region (van Driel 2007, van Driel et al. 2008b, K. van Driel, unpublished observations). In contrast, significant differences in density occur between isolated SPCs of *Rhizoctonia solani* and regular ER (K. van Driel, unpublished observations), thus indicating structural and functional differences between these structures. Moreover staining with wheat germ agglutinin (WGA) and labeling with WGA-gold-antibodies stained the SPC in *R. solani*, but not the ER, when observed by fluorescence microscopy (van Driel et al. 2007b). Differences were also observed with a zinc-iodine osmium tetroxide (ZIO) stain that marks calcium-affinity sites (Gilloteaux and Naud 1979, Müller et al. 1999, 2000). Membranes and matrix of the tubular SPC of *T. gamsii* CBS 8245 (cited as *T. sporotrichoides)* stained similarly to ER. In contrast, in perforate SPCs of *Schizophyllum commune* (Fig. 8.26) and *Rhizoctonia solani,* the SPC inner and outer membranes and the ER stained, and the SPC matrix remained unstained (Müller et al. 1999, 2000).

These results suggest that no structural or functional differences exist between ER and the tubular SPC-type in *T. gamsii* with respect to calcium binding sites, while such differences do exist between the perforate SPCs and ER of *Schizophyllum commune* and *Rhizoctonia solani* (Müller et al. 1995, 1998a, W.H. Müller, unpublished data). Altogether, the observations suggest that the SPC may represent a functionally and structurally different subdomain of the ER, and, moreover, that the SPC structures of fungi belonging to different fungal lineages may differ in functionality.

Although the fine structure of the SPC of many basidiomycetes has been described morphologically, its function is a matter of debate. There is a range of suggested functions, such as:

1. an occlusion function (Thielke 1972);
2. a sieve function to prevent or to regulate migration of larger organelles like nuclei (Wilsenach and Kessel 1965);
3. a protection function against damage during the process of protoplasmic streaming, with the septal pore channel opening ranging between 100 and 500 nm to ease the passage of organelles (Bracker and Butler 1964);
4. a funnel function, to direct small cellular organelles or components towards the septal pore channel opening (Orlovich and Ashford 1994);
5. a repository function for material that is involved in the pore-plugging process (van Driel et al. 2008b).

Immunolabeling of the spc18 protein from *Rhizoctonia solani* demonstrated that this protein localizes in the SPC matrix, along fibrils near the inner side of the SPC, and in pore-occluding electron-dense material, which may be plugs. These observations strongly suggest that SPCs have a role as a repository function for proteins involved in septal pore plugging (van Driel 2007, van Driel et al. 2008b).

Since the last update in *The Mycota* (Hibbett and Thorn 2001, Wells and Bandoni 2001), many new orders have been erected in the Agaricomycotina (Binder et al. 2005, Hibbett et al. 2006, 2007, Larsson et al. 2004). At present the Agaricomycotina represent three classes, namely the Tremellomycetes, Dacrymycetes, and Agaricomycetes with 21 orders (Hibbett et al. 2006).

Dolipore septa are found in yeasts belonging to Tremellomycetidae (Tremellomycetes), which is the basal group of Agaricomycotina. Species of the the orders Cystofilobasidiales, Tremellales, Filobasidiales and Trichosporonales possess dolipores. Cystofilobasidiales, which forms the most basal lineage within the Tremellomycetidae, have a dolipore with slightly inflated pore margins, that lack an elaborated SPC (Fell et al. 1999, Swann and Taylor 1995a, b).

Strands of ER may be present to cover the dolipore, e.g., as observed in *Itersonilia perplexans* (Fig. 8.21) (Boekhout 1991b, Kreger-van Rij and Veenhuis 1971a), *Cystofilobasidium capitatum* (Oberwinkler et al. 1983, Suh et al. 1993a), *Cystofilobasidium infirmo-miniatum* (Suh and Sugiyama 1993) and *Mrakia frigida* (Suh et al. 1993a).

Species of Tremellales have a dolipore covered with a vesicular or tubular SPC, e.g., *Bulleromyces albus* (Fig. 8.19) and dikaryotic hyphae of *Bullera variabilis* (Boekhout et al. 1991a), *Bulleribasidium oberjochense* (Sampaio et al. 2002), *Sirobasidium magnum* (Moore 1979), *Rhynchogastrema coronata* (Metzler et al. 1989), *Trimorphomyces papilionaceus* (Oberwinkler and Bandoni 1983), *Tetragoniomyces uliginosus* (Oberwinkler and Bandoni 1981), *Tremella brasiliensis, Tremella globospora, Tremella mesenterica* (Berbee and Wells 1988, Moore 1987b, Oberwinkler 1985), and *Filobasidiella depauperata* (Kwon-Chung et al. 1995).

The sacculate/vesiculate SPC-type of *Tremella globospora* consists of a cluster of 20 to 40 cylindrical saccules that vary in length from 100 to 400 nm. These saccules are open at the cytoplasm and closed at the dolipore side (Berbee and Wells 1988). *Filobasidiella neoformans* (Kwon-Chung and Popkin 1976, Moore 1985) and the hyphal state of *Cryptococcus flavescens* (cited as *Cr. laurentii*) have a dolipore, but a SPC structure has not been observed (Rhodes et al. 1981). Reports differ with respect to the presence of a cupulate parenthesome in *Filobasidiella depauperata* (see, e.g., Khan et al. 1981, Kwon-Chung et al. 1995). The figures published on the pore structure of *Bulleribasidium oberjochense* showed a variable presence of the cupulate SPC (Sampaio et al. 2002). These observations suggest that this type of SPC may be rather fragile and not well preserved by classical chemical fixation procedures, or, alternatively, the presence or absence of the structure depends on certain, as yet unknown, physiological conditions.

Among Filobasidiales, *Filobasidium capsuligenum* has a dolipore with a cupulate SPC, whereas this observation was less clear in *Filobasidium floriforme* where only vesicles were visible. It should be taken into account, however, that the preservation methods used in these studies were not optimal, and, consequently, the presence or absence of a SPC in this species remains uncertain (Moore and Kreger-van Rij 1972). Species in the Trichosporonales have tubulate, vesiculate or sacculate SPCs (Fig. 8.20), e.g., *Trichosporon asahii, T. coremiiforme, T. cutaneum, T. laibachii* and *T. moniliforme* (Guého et al. 1992b). Some CoQ-9 possessing species, however, seem to lack a SPC structure, e.g*., Trichosporon mucoides* and *Trichosporon gamsii* (cited as *T. sporotrichoides*) (Guého et al. 1992b).

Species of Dacrymycetales, the only order of Dacrymycetes, have an imperforate or continuous SPC type, e.g., *Dacrymyces deliquescens* and *D. stillatus* (Figs 8.24, 8.25) (Moore 1965, 1978, Moore and McAlear 1962). This type consists of a slightly flattened, closed, membranous structure that may have inward growth with reduced thickness in the center of the structure (Müller et al. 2000).

The yeast-like *Cerinosterus* (*Sporothrix*) *luteoalba* has this type of SPC structure (Moore 1987b, Smith and Batenburg-van der Vegte 1985, 1986b), and was recently found to belong to the Dacrymycetales by rRNA gene sequencing (Middelhoven et al. 2000c). The imperforate SPC type is also found in the *Sebacinales*, *Tulasnellales*, *Botryobasidiales* and *Hymenochaetaceae* (Andersen 1996, Khan and Kimbrough 1980, Langer 1994, Moore 1978, Müller et al. 2000). These imperforate SPCs are about 270–800 nm in width (Müller et al. 1998, 2000, Patton and Marchant 1978), and may or may not have a narrow central pore.

The 11 orders of the Agaricomycetes usually contain the imperforate SPC (viz., Auriculariales such as *Auricularia auricula-judae* (Moore 1978, Tu and Kimbrough 1978), Geastrales, Gomphales, Trechisporales, and Sebacinales) or the perforate SPC (viz., Agaricales, Atheliales, Boletales, Phallales, Corticiales, Gloeophorales, Polyporales, Russulales, Thelephorales) (Hibbett and Thorn 2001, van Driel 2007, van Driel et al. 2008a, Wells and Bandoni 2001) (Figs 8.22, 8.23, 8.26). Both types of SPC do occur in Cantharellales and Hymenochaetales (van Driel 2008a), which are basal lineages within Agaricomycetes.

In short, septum morphology reflects fungal phylogeny rather well. Some notable exceptions have been addressed, which need further confirmation and study.

6. OTHER ULTRASTRUCTURAL CHARACTERISTICS

A number of other structures have been investigated for use in fungal phylogeny studies. These include structure of cell walls, ascospores and teliospores, spindle pole bodies (SPBs, also named microtubule organizer center or MTOCs, see also section 2.1 of this chapter), and some miscellaneous structures such as lenticular bodies (also known as colacosomes), symplechosomes, cystosomes, etc. Some of these have already been discussed above, others have been extensively summarized in reviews (e.g., Heath 1978, 1981, McLaughlin et al. 1995, Moore 1998b), and some will be briefly discussed below.

6.1. The Spindle Pole Body

(SPB, see also section 2.1 of this chapter)

Mitosis in ascomycetous and basidiomycetous yeasts shows some differences and the SPB provides additional phylogenetic information. Generally, in ascomycetous yeasts, spindle formation takes place in the parent cell, or in the isthmus between the bud and the parent cell, and spindle elongation occurs towards the bud (see below). In basidiomycetous yeasts, the general pattern is that the DNA migrates to the bud, spindle formation takes place, and elongation of the spindle occurs backwards into the parent cell. However, some noteworthy exceptions have been published. In *S. cerevisiae* (Saccharomycotina), the SPBs are multilayered, diskoidal and occur closely attached to or inserted in an opening of the nuclear envelope (Fig. 8.3). Duplication of the SPB occurs in the parent cell; the nuclear membrane remains intact; and elongation of the mitotic spindle occurs towards the newly formed bud cell. Three types of microtubuli occur. Astral microtubules are oriented into the cytoplasm and may be involved in spindle orientation, kinetochore microtubules connect the chromosomes to the spindle poles and are involved in chromosome movement, and interpolar microtubules connect both spindle poles and are involved in separation of the poles and attached chromosomes (Winey et al. 1995).

In *Schiz. pombe* (Taphrinomycotina), mitosis, in essence, follows the same pattern as in *S. cerevisiae* (McCully and Robinow 1971, Tanaka and Kanbe 1986), but spindle initiation starts in the mid-region of the dividing cell, and spindle elongation (telophase) occurs toward both poles of the dividing cell. The SPBs of *Schiz. pombe* are circular, electron-dense, 300–380 nm in diameter (Ding et al. 1993), and occur closely associated with the nuclear envelope. When entering mitosis, the nuclear envelope invaginates close to the SPB, and forms a pocket in which electron-dense material accumulates. The nuclear envelope opens and allows the duplicated SPB to remain in the nuclear envelope. Small initial spindles that originate from the SPBs are positioned in fenestrae of the nuclear envelope separate, and the spindle elongates. At this stage, cytoplasmic microtubules occur, which are not connected directly with the SPBs. During anaphase, the nuclear fenestrae close and the SPBs again become located in the cytoplasm (Ding et al. 1997).

Some other representatives of Taphrinomycotina, namely *Taphrina maculans, T. farlowii, Protomyces inouyei, P. lactucae-debilis* and *P. pachydermatis*, gave a more diverse picture (Heath et al. 1987). In summary, the *Taphrina* species showed varying patterns, whereas the three *Protomyces* species showed similar mitotic patterns. *T. maculans* showed a basidiomycetous pattern. *T. farlowii* showed both asco- and basidiomycete features, and *T. cerasi* had only ascomycetous characteristics. This clearly indicates the difficulty in using these characteristics for inferring fungal phylogenetic relationships. The three *Protomyces* species, however, all showed a pattern similar to that of ascomycetes (Heath et al. 1987), in which the SPBs remain connected to the outside of the intact nuclear envelope, and the two duplicated SPBs form initial spindles when still close to each other (Heath et al. 1987). Ultrastructural studies of mitosis in "*T. californica*" detected features indicative of a basidiomycete affinity (Heath et al. 1982, 1987). These findings and conclusions were corroborated by subsequent biochemical and molecular data (Sjamsuzidzal et al. 1997, see also Chapter 73).

In basidiomycetous yeasts, the SPBs duplicate before migration of the nucleus into the bud; the nuclear envelope locally disappears to allow migration of the duplicated SPBs into the nucleus (Fig. 8.25); the nuclear membrane extends into the newly formed bud with the SPBs on top; this membrane extension is followed by separation of the SPBs and spindle formation (David et al. 2007a, b, Gabriel et al. 2006, Heath et al. 1987, Kopecká et al. 2001, McLaughlin et al. 1996, 2004, Petersen and Ris 1976).

In *Agaricostilbum pulcherrimum* (Agaricostilbales, Pucciniomycetes, Pucciniomycotina) and *Stilbum vulgare* (Agaricostilbomycetes, Pucciniomycotina), however, spindle formation occurs in the parent cell, and subsequent elongation of the spindle occurs toward the bud (Frieders and McLaughlin 1996, McLaughlin et al. 2004). It is not easy to explain these apparent major different mitotic patterns in mitosis, but is does demonstrate that caution has to be taken in the phylogenetic interpretation of structural differences in mitosis. Among Basidiomycota, the SPBs show a rather wide morphological divergence (McLaughlin et al. 1995, Swann et al. 2001). Pucciniomycotina have morphologically diverse SPBs, which can be discoidal (Bauer et al. 2006) or multilayered and discoidal (e.g., in Uredinales). SPBs in the yeast representatives (e.g., *Leucosporiudium scottii, Rhodosporidium toruloides*) are small, electron-dense disks that occur in the cytoplasm just adjacent to the nuclear envelope. Mitosis in these species occurs in a basidiomycetous manner (Boekhout and Linnemans 1982, McCully and Robinow 1972a, b). In several taxa, endoplasmic reticulum was reported in close connection with SPBs (e.g., Platygloeales and Pucciniales (Bauer et al. 2006). In Ustilaginomycotina, the SPBs of *Ustilago maydis* and *U. avenae* are hemispherical with an internal, concave, electron-dense layer (Celio et al. 2006, O'Donnell 1992, McLaughlin et al. 1995, O'Donnell and McLaughlin 1984, Poon and Day 1976a, b).

SPBs in yeasts and other dimorphic members of Agaricomycotina are small, electron-dense, globular, and without an apparent substructure (e.g., *Bulleromyces albus* [*Bullera alba*], *Cryptococcus neoformans*, *Tremella globospora, Itersonilia perplexans*) (Fig. 8.26), but also in *Auricularia autricula-judae* (Berbee and Wells 1988, Boekhout and Jille 1979, Celio et al. 2006, McLaughlin et al. 1995, Taylor and Wells 1979, Wells and Bandoni 2001).

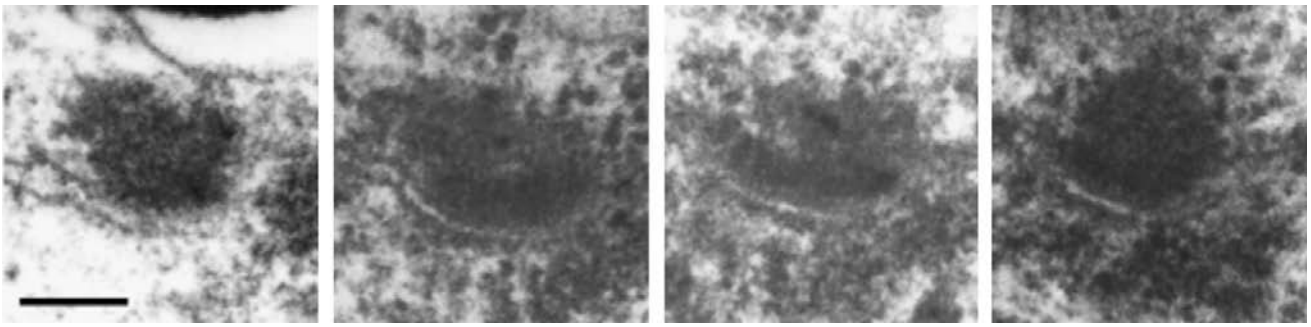


FIGURE 8.28 Morphology of spindle pole body (SPB) of *Itersonilia perplexans* PD 83/1013. Serial section through an electron-dense diglobular spindle pole body connected by a flat disc of high electron density that was located at the tip of a nucleus inside the bud. Fixation by glutaraldehyde and tannic acid/osmium tetroxide. Reprinted with permission of *Syst. Appl. Microbiol.* 14, 117–123 (1979). Bar = 10 nm.

6.2. Lenticular Bodies/Colacosomes and Symplechosomes

Electron-dense lenticular bodies (also referred to as colacosomes) occur in species belonging to some lineages of the Pucciniomycotina, and include species of *Bensingtonia* (Fig. 8.29), *Leucosporidium, Rhodosporidium and Sporidiobolus* (Boekhout et al. 1992b, de Hoog and Boekhout 1982, Kreger-van Rij and Veenhuis 1971b). They also occur in other fungi such as *Colacogloea peniophorae* (Bauer and Oberwinkler 1991b, Oberwinkler et al. 1990b), *Cryptomycocolax abnorme* (Oberwinkler and Bauer 1990) and *Heterogastridium pycnidioideum* (Bauer et al. 2006, T. Boekhout, unpublished data).

The lenticular bodies play a role in in mycoparasitic relationships (Bauer et al. 1991b, 2006), and consist of an electron-translucent, chitin-containing body (Kreger-van Rij and Veenhuis 1971b), with an internal core of high electron density. This core can break through the cell wall of the cell where it is located, as well as that of the target cell (Kreger-van Rij and Veenhuis 1971b). Most likely, this core comprises cell wall degrading enzymes. These structures are also visible as highly refractive spots when using high magnification phase-contrast microscopy. Lenticular-body mediated cell–cell contact, followed by hyper-vacuolization and lysis of one of the cells involved, has also been observed to occur between branches of the same hypha of *Heterogastridium pycnidioideum*. This process of "auto-parasitism" suggests differentiation of the cells involved, and may be a means to redistribute nutrients among the thallus to overcome less favorable conditions (T. Boekhout, unpublished data). The reported presence of lenticular bodies in species of Ustilaginales and Tilletiales (Moore 1972) needs to be verified, as the published pictures are not clear, and could not be confirmed by recent studies (Bauer et al. 2006, Begerow et al. 2006). The presence of lenticular bodies seems to be a good phylogenetic marker for the Pucciniomycotina.

Species of Atractiellomycetes possess symplechosomes (also named microscala), which are intriguing organelles that are formed by stacks of ER cisternea or ER and mitochondria interconnected by transverse and hexagonally arranged filaments (Bauer and Oberwinkler 1991a, Bauer et al. 2006, Swann et al. 2001). Biochemical composition and function of these structures remain to be investigated.

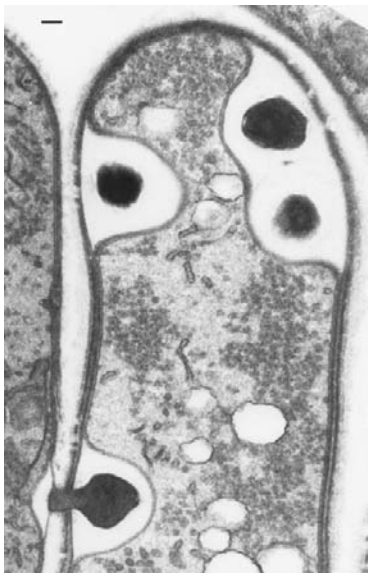


FIGURE 8.29 Lenticular bodies of *Bensingtonia yamatoana* CBS 7243. Note the electron-translucent chitinous part that is covered at the inside by the plasma membrane of the fungal cell. The electron dense core is able to penetrate through the fungal cell wall and most likely contains cell wall degrading enzymes. Fixation with potassium permanganate. Bar = 300 nm.

7. PERSPECTIVE

Biochemical studies of the cell wall and ultrastructural studies contribute greatly to our understanding of fungal (incl. yeasts) cell biology and phylogeny, and biological investigations of yeast cells have increased our understanding of the functioning of eukaryote cells in general. When used in combination with other characteristics, such as rRNA gene sequence analysis or phylogenomics, this may allow the further interpretation of cell biological features in an evolutionary perspective. Unfortunately, due to the time-consuming nature of many of these cell biological studies, most are performed using only a few species. Further improvement in our understanding of yeast cell biology and biochemistry may be obtained by: 1) extending the number of species and phylogenetic lineages to be studied; 2) using the most up-to-date preparatory and visualization techniques (e.g., fluorescence live imaging, advanced electron microscopy such as tomography, and immunolocalization studies) and 3) comparative and functional genomics (e.g., transcriptomics and proteomics, systems biology), in order to unravel the function of the many subcellular whose function is not yet fully known. These structures may include, a.o., Woronin bodies/peroxysomes, SPCs, lenticular bodies, symplechosomes, etc. Eventually, such studies will greatly enhance our understanding of the dynamics of living yeast cells in both functional and evolutionary perspectives.

Chapter 9

Chemotaxonomy of Yeasts

Hansjörg Prillinger, Ksenija Lopandic, Motofumi Suzuki, J. Lodewyk F. Kock and Teun Boekhout

1. INTRODUCTION

This chapter describes the use of some chemotaxonomic approaches used in yeast taxonomy. Emphasis is on cell wall carbohydrate composition, coenzyme Q, electrophoresis of enzymes, and the analysis of fatty acids. For each of these approaches technical protocols are provided.

2. CELL WALL CARBOHYDRATE COMPOSITION

2.1. Introduction

Cell wall composition is a useful marker to indicate taxonomic and phylogenetic affiliations among fungi (Bartnicki-Garcia 1968, 1970, Dörfler 1990, Lopandic et al. 1996, Messner et al. 1994, Prillinger et al. 1990a, b, 1991a, b, 1993a, 1997, 2002, von Wettstein 1921, Weijman and Golubev 1987a). Bartnicki-Garcia (1970) divided the fungi into eight groups using combinations of the two most dominant cell wall carbohydrates present. Using qualitative and semi-quantitative analyses of cell walls, Weijman and Golubev (1987a) distinguished six categories of yeasts and yeast-like fungi based on these carbohydrates. Prillinger et al. (1993a) differentiated seven cell wall types among yeasts and yeast-like fungi, using both quantitative and qualitative analyses. Their typology is a refinement of that of Weijman and Golubev (1987a).

Three cell wall types occur among the ascomycetous yeasts:

1. The mannose, glucose pattern.
2. The glucose, mannose, galactose pattern.
3. The glucose, mannose, rhamnose pattern, with galactose commonly present.

The first patterns are characteristic for the Saccharomycotina. The second and third patterns occur within the Taphrinomycetes (i.e., Taphrinomycotina) and Pezizomycotina (cited as Protomycetes and Euscomycetes, respectively, Prillinger et al. 2002). The presence of glucose, mannose and galactose is found in different orders of Ascomycota (namely some lineages within the Saccharomycetales [note: cited as Dipodascales, Lipomycetales, Stephanoascales (Prillinger et al. 1994)], Schizosaccharomycetales, *Saitoella* and different orders of the Euascomycetes) indicating that the phylogenetic value of the presence of galactose is low (Prillinger et al. 1994).

Among the basidiomycetous yeasts four cell wall types occur:

1. *Microbotryum*-type with mannose dominant, glucose present, fucose usually present and rhamnose sometimes present;
2. *Ustilago*-type with glucose dominant, and mannose and galactose present;
3. *Dacrymyces*-type with xylose present, and glucose and mannose present in equal amounts, traces of galactose may be present, but extracellular amyloid compounds are usually absent;
4. *Tremella*-type with glucose predominant, xylose, mannose and galactose present, and extracellular amyloid compounds are usually present.

The latter four types agree with the cell wall typology of the Basidiomycota given by Dörfler (1990). The data can be used to define classes within the Basidiomycota. The *Microbotryum*-type corresponds with the Pucciniomycotina (cited as Urediniomycetes), the *Ustilago*-type with the Ustilaginomycotina (cited as Ustilaginomycetes) and the *Dacrymyces*- and *Tremella*-types with the Agaricomycotina (cited as Hymenomycetes). From these data it is apparent that cell wall biochemistry is a useful tool in the taxonomy and phylogeny of yeasts and yeast-like organisms. *Rhodotorula yarrowii* is a remarkable exception, having xylose in its cell wall, which would indicate placement in the Agaricomycotina, but dominant amounts of mannose and ribosomal DNA sequences, however, suggest a place within the Pucciniomycotina (Boekhout et al. 2000).

Four main methods have been applied to analyze the carbohydrate composition of the yeast cell wall:

1. Gas chromatographic analysis of acid hydrolysates of whole cells, with derivatization using capillary columns (Weijman 1976, Weijman and Golubev 1987a) or packed columns (Sugiyama et al. 1985);
2. Gas chromatographic analysis of acid hydrolysates of purified cell walls, with derivatization (Dörfler 1990, Lopandic et al. 1996, Messner et al. 1994, Prillinger et al. 1990a, b, 1991a, b, 1993a, 1997b, 2002);
3. High performance liquid chromatographic (HPLC) analysis of acid hydrolysates of whole cells without derivatization (Suzuki and Nakase 1988a);
4. High performance anion-exchange chromatography with pulsed amperometric detection (HPAE-PAD) of cell wall neutral sugars without derivatization (Prillinger et al. 1993a).

2.2. Methods

2.2.1. Analysis of Whole Cells

Analysis of whole cells has the advantage that the isolation of yeast cell walls is not needed. This method is sometimes preferred, because the taxonomic results of both methods are generally concordant. For the analysis of whole cell hydrolysates, Weijman's (1976)

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method can be summarized as follows. Cells are hydrolyzed with 1 N HCl for 12 h at 100°C. During hydrolysis monomeres are formed. Neutral polysaccharides are hydrolyzed completely at low concentrations of HCl (1 N), whereas chitin is converted to glucosamine at high concentrations of HCl (5 N). After hydrolysis, the solubilized components are trimethylsilylated (TMS) prior to gas-liquid chromatography. Sugiyama's (1985) method differs in that dried cells are hydrolyzed in 2.5 N trifluoroacetic acid (TFA) at 100°C for 15 h, followed by reduction of the neutral sugars to their corresponding alditols by borohydride, and acetylation of the alditol derivatives by acetic acid anhydride. The final residues are trifluoroacetylated, and then subjected to gas chromatographic analysis. In Prillinger's (1993a) method, cell walls are isolated and purified before further processing. In order to accurately detect xylose, Suzuki and Nakase (1988a) developed a method using HPLC analysis of whole-cell hydrolysates without derivatization. In brief, whole cells are hydrolyzed with TFA and directly analyzed using HPLC.

2.2.1.1. Analysis of Whole-Cell Hydrolysates Using Trimethyl-Silylation (Weijman 1976, Weijman and Golubev 1987a)

Yeast cells are grown in 100 ml of 0.5% yeast extract, 1% peptone, 2% glucose (YPG) broth, in 300-ml Erlenmeyer flasks on a rotary shaker at 150 rpm and 24°C (psychrophilic species at 17°C). After 5–7 days, the cells are harvested by centrifugation (9000 × g), washed with 0.9% NaCl and washed again with deionized water. The resultant pellet is freeze-dried and powdered. 15 mg of dried cells are hydrolyzed in 6 ml 1 N HCl or 5 N HCl, under nitrogen, in glass tubes with a screwcap, for 12 h, at 100°C in a sandbath. To detect xylose, the cells are hydrolyzed with 2 N trifluoroacetic acid for 3 h at 100°C. After cooling, the hydrolysates are filtered through Whatman No. 1 filter paper, and 1 ml of the filtrate is dried in a rotary evaporator. An additional 100 μl Tri-Sil (Pierce) is used to silylate the sample. The reaction mixture is vigorously shaken and allowed to stand for 15 min. 1 μl is then injected into the gas chromatograph-mass spectrometer (GC-MS), which is equipped with a wall coated open tubular (WCOT) capillary column of 25 meters, coated with CP Sil 5CB with a film thickness of 0.13 μm and an inside diameter of 0.32 mm. The column is programmed from 125 to 175°C with a rate of 10°C/min and an isothermal period of 5 min. Helium is used as the carrier gas at a flow rate of 30 ml/min. Electron Impact (EI) at 70 eV is used for ionization and a quadrupole serves as a massfilter.

2.2.1.2. Analysis of Whole-Cell Hydrolysates Using Trifluoroacetic Acid (TFA) and Reduction of Sugars to Their Alditol Derivatives (Sugiyama et al. 1985)

Yeast cells are grown in liquid Wickerham's basal nitrogen medium, supplemented with 15 ml 1% glucose, at 25°C, for 3–5 days on a test tube shaker. Cells are harvested by centrifugation, and washed with deionized water. The pellet is freeze-dried and powdered. About 30 mg of the dry cell powder is hydrolyzed in 5 ml 2.5 N trifluoroacetic acid at 100°C for 15 h in a sealed tube. The remaining acid is removed by drying over a rotary evaporator, and 50 mg of sodium borohydride in 10 ml distilled water is added to the residue. The reaction mixture is allowed to stand overnight to reduce the sugars to alditols. Excess sodium borohydride is removed by adding dropwise 5% hydrochloric acid in methanol and by evaporating to dryness. Insoluble material and low-polar materials are removed by membrane filtration (0.45 μm, Gelman Sciences, Inc., Ann Arbor, MI, USA), followed by reversed-phase chromatography (Sep-Pak C, Waters Associates, Milford, MA, USA). After drying, 2 ml of methanol are added. The solution is dried in a rotary evaporator to remove the borate complex. This step is repeated several times. To 10 mg of the residue, 0.1 ml of trifluoroacetic anhydride and 0.1 ml of *N*-methyl-bis-trifluoroacetamide are added. The reaction mixture is kept in a sealed tube and left overnight. 1–2.5 μl of the sample is injected in a gas chromatograph equipped with a hydrogen flame ionization detector. The U-shaped glass column (4 m × 3 mm i.d.) is packed with Chromosorb W (HP) 80–100 mesh coated with 2% silicone OV-105, 800 mesh. Nitrogen is used as the carrier gas at a flow rate of 35 ml/min. The column temperature is 140°C, and the injector temperature is 150°C. Carbohydrates are identified on the basis of sample coincidence with the relative retention times for the trifluoroacetyl derivatives of the neutral monosaccharide standards.

2.2.1.3. Analysis of Whole-Cell Hydrolysates without Derivatization Using HPLC (Suzuki and Nakase 1988a)

Yeast cells are grown in a 500-ml Erlenmeyer flask containing 200 ml YM broth supplemented with 2% glucose, on a rotary shaker, at 150 rpm and 25°C (17°C for psychrophilic species). After 4–5 days the cells are harvested by centrifugation (5,000 rpm) and washed twice with deionized water. 50–100 mg of acetone-dried cells are suspended in 2 ml of 2 M trifluoroacetic acid in a test tube (13 × 100 mm) with a teflon-sealed screw cap, and kept at 100°C for 3 h in a metal block bath. After cooling, the hydrolysate is filtered through paper and evaporated to dryness. The residue is dissolved in 0.5 ml water neutralized with small amounts of Amberlite IRA 410 (OH form), filtered with a disposable filter unit (e.g., Shodex DT ED-13), and then subjected to HPLC. HPLC is performed using two different column systems. The two columns are:

1. Ligand exchange type column with water (HPLC grade) as the mobile phase at a flow rate of 0.8 ml/min at 80°C.
2. Sulfonated polymer type or amino type column, with acetonitrile-water (80:20, v/v, HPLC grade) as the mobile phase at a flow rate of 0.8 ml/min at 75°C.

A refractive index detector is used to detect the carbohydrates. Neutral sugars and sugar alcohols are identified by comparing their retention times with those of standard neutral sugars and sugar alcohols.

2.2.2. Analysis of Purified Cell Walls

An attempt has to be made to purify carbohydrates solely from the cell wall, however the results obtained by the analysis of whole cell hydrolysates and purified cell walls are usually concordant. For a detailed understanding of the taxonomic importance of cell wall carbohydrates proper, as well as for a biochemical understanding of these important organelles, they need to be purified, and some protocols are described below. For information on the biochemical structure of cell walls from various groups of yeasts the reader is referred to Chapter 8.

2.2.2.1. Isolation and Purification of Cell Walls (Prillinger et al. 1993a)

Yeast cells are grown in 500 ml YPG broth on a rotary shaker at 150 rpm for 3–5 days, harvested by centrifugation (1000 × g), washed with deionized water until the supernatant is clear, and frozen at −20°C until further use. For disruption, cells are suspended in distilled water (1:1, v/v), and disrupted in a French Press (20,000 PSI) until no intact yeast cells are present under the light microscope. Messner et al. (1994) have shown that disintegration of yeast cells by a Vibrogen Cell Mill (Tübingen, Germany) and 0.5 mm glass beads (yeast pellet/distilled water/glass beads = 1/1/3, w/w) is superior to the disruption achieved with a French Press. Disrupted cells are washed with ice-cold distilled water until the supernatant is clear.

To remove cytoplasmic remnants, the cell walls are thoroughly washed twice with 1% sodium desoxycholate (pH 7.8) with intensive stirring. After each sodium desoxycholate purification, the cell walls are rinsed three times with distilled water. In the case of capsulated yeasts, all the capsular material, which may form a second slimy layer above the cell wall pellet, should be removed. Yeast cells without capsules (i.e., those not having a positive starch test with Lugol's solution) are lyophilized and powdered with a pestle and mortar and further processed.

2.2.2.1.a. High Performance Anion-Exchange Chromatography with Pulsed Amperometric Detection (HPAE-PAD) of Cell Wall Neutral Sugars without Derivatization (Prillinger et al. 1993a) Acid hydrolysis of purified cell walls and removal of TFA are performed according to the method of Sugiyama et al. (1985) (see above). Usually a mixture of 2 mg of powdered cell walls suspended in 2 ml 2 N TFA is hydrolyzed for 2 h at 120°C using teflon-sealed Pyrex test tubes. A standard mixture of monosaccharides containing 90 μg of each neutral sugar is treated in the same way. After evaporating the TFA in an airstream, samples and standards are resolved in 10 ml distilled water. Monosaccharides are separated on a Dionex CarboPac PA-1 column (4.6 × 250 mm), equipped with a guard column, using a flow rate of 1 ml/min at room temperature. They are eluted with NaOH as follows: 10 mM NaOH for 3.9 min isocratic, followed by a step gradient to 100% deionized water for 30 min, and re-equilibration to the initial conditions for 10 min. The system used for monosaccharide analysis consists of a Dionex (Sunnyvale, CA) Gradient Pump Module GPM 2 and a Pulsed Amperometric Detector PAD 2. A Dionex Eluant Degas Module is used to sparge and pressurize the elutants with helium. Eluant 1 is 100 mM NaOH (preparation of a 50% NaOH stock solution with ultrapure distilled water), and eluant 2 is 18 MOhm deionized water. Sample injection is via a Dionex High Pressure Injectio Valve equipped with a 10 μl sample loop. To ensure a carbonate-free eluant, an anion trap column ATC-1 was installed before the injection valve. Detection of the separated monosaccharides is by a PAD, equipped with a gold working electrode. The following pulse potentials are used: $E_1 = 0.1$ V ($t_1 = 300$ ms); $E_2 = 0.6$ V ($t_2 = 120$ ms); $E_3 = -0.6$ V ($t_3 = 60$ ms). The response time of the PAD 2 is set to 1 s. Resulting data are integrated and plotted using Dionex A1-450 software.

2.2.2.1.b. Analysis of Purified Cell Walls Using Trifluoroacetic Acid (TFA) and Reduction of Sugars to Their Alditol Derivatives (Lopandic et al. 1996) Approximately 2 mg of powdered cell walls were suspended in 0.5 ml of 2 M trifluoroacetic acid, overlaid with gaseous nitrogen, and hydrolyzed for 2 h at 120°C. The sediment was separated by membrane filtration (0.45 μm, Millipore, U.S.A.). To remove TFA 30 μl of the supernatant together with 9 μg of *myo*-inositol (internal standard) was evaporated in a water-bath at 36°C under a stream of gaseous nitrogen. After twofold addition of 200 μl methanol, the nitrogen gas evaporation procedure was repeated. The residue was alkalized with 70 μl of 1 M ammonia, and 70 μl of 4% $NaBH_4$ was added. The reaction mixture was left to stand overnight at room temperature. Excess sodium borohydride was decomposed by twofold additions of 50 μl of 2 M acetic acid, 20 μl of 1% acetic acid in methanol, and 200 μl methanol. The resulting mixture was evaporated to dryness under a stream of nitrogen. The residues left were acetylated with 100 μl of acetic acid anhydride for 1 h at 100°C. The remaining anhydride was removed by evaporation under nitrogen-stream. A 500 μl portion of dichlormethane was used to dissolve alditol acetate residues. Extraction of salts with approximately 2 ml of double distilled water was repeated four times. The dichlormethane was evaporated to dryness. Prior to a GLC-analysis the dried residue was dissolved in 50 μl of dichlormethane. Gas-liquid chromatography was performed with a Hewlett Packard model 5890 Series II gas chromatograph (Hewlett Packard, U.S.A.) equipped with a hydrogen flame ionization detector. 1 μl of sample was injected into a type Rtx-225 capillary column (30 m, 0.25 mm ID, 0.1 μm film thickness; Restek Corp., Bellefonte, U.S.A.). Nitrogen was used as a carrier gas at a pressure 1.3×10^5 Pa. The oven temperature was programmed to increase from 140° to 190°C at a rate of 20°C/min, and then to 225°C at a rate of 3°C min^{-1}.

3. COENZYME Q (UBIQUINONE) COMPOSITION

3.1. Introduction

Coenzyme Q (ubiquinone, CoQ) plays a primary role as an essential component of the respiratory electron transport chain of the inner mitochondrial membranes of eukaryotes, and in the plasma membrane of prokaryotes. It is also found in other organelles, and in the plasma membrane of eukaryotes, where it participates in a plasma membrane electron transport system. Furthermore, multiple additional functions of CoQ (e.g., a role as a lipid-soluble antioxidant) have been observed (Kawamukai 2002). The natural CoQ series encompasses 2,3-dimethoxy-5-methyl-6-polyprenyl-1,4-benzoquinone nucleus with side chains containing 1 to 12 isoprenoid units (Crane and Barr 1985).

The length of the isoprenoid side chain varies among organisms. The CoQ homologues (isoprenologues) of yeasts range from CoQ-5 to CoQ-10 (Billon-Grand 1985, Suzuki and Nakase 1998a, Yamada and Kondo 1973, Yamada et al. 1976b, 1981). A dihydrogenated isoprenoid side-chain CoQ homologue, CoQ-10(H_2), occurs in some basidiomycetous yeasts (Bai et al. 2001c, Hamamoto et al. 2002a, Nakase and Suzuki 1986, Yamada et al. 1973c) as well as in euascomycetes (Kuraishi et al. 1985, Suzuki and Nakase 1986). The major types of CoQ among the following three major groups of yeasts are as follows:

1. Yeasts belonging to the Taphrinomycotina (i.e., former Archiascomycetes) have CoQ-9 or CoQ-10.
2. Members of Saccharomycotina have CoQ-5, CoQ-6, CoQ-7, CoQ-8, CoQ-9 or CoQ-10
3. The various lineages of Basidiomycota have CoQ-7, CoQ-8, CoQ-9, CoQ-10 or CoQ-10(H_2).

The CoQ composition (i.e., the major type of coenzyme Q) is considered to be important as a useful criterion to classify yeasts and yeast-like fungi, at the generic or family level (Billon-Grand 1985, 1989, Suzuki and Nakase 1986, Yamada and Kondo 1972b, Yamada et al. 1976a).

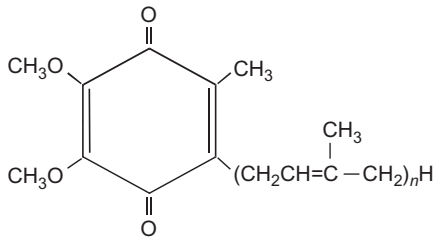


FIGURE 9.1 Diagrammatic representation of coenzyme Q. The coenzyme Q homologues are expressed as Q-n, with n denoting a specified number of isoprene units in a side chain, e.g., Q-6, Q-10. If there are two hydrogen atoms saturating the isoprene units in the side chain the formular becomes Q-n(H_2), e.g., Q-10(H_2). After Yamada (1998), with permission of the publisher).

Recently, the biosynthetic pathway of CoQ has been unraveled in *Saccharomyces cerevisiae* (Kawamukai 2002, Meganathan 2001, Okada et al. 1998) and was found to comprise 10 steps, including methylation, decarboxylation, hydroxylation and isoprenoid transfer. The length of the side chain appears to be determined by polyprenyl diphosphate synthase, but not by the 4-hydroxybenzoate-polyprenyl-diphosphate transferase, which catalyzes the condensation of 4-hydroxy-benzoate and polyprenyl diphosphate. Further genetic and biochemical studies on these key enzymes may help us to understand the taxonomic significance of CoQ composition.

3.2. Methods

Yeast strains are aerobically grown in a 2% glucose-0.4% peptone-0.3% (w/v) yeast extract medium (YPG) on a rotary shaker for 24–72 h (Yamada and Kondo 1973, Yamada et al. 1989c) or in YM broth medium on a rotary shaker for 3–7 days until stationary phase (Nakase and Suzuki 1985a, Suzuki and Nakase 1986, 1998). The cells are harvested by centrifugation. Wet packed cells (5–10 g) are saponified with methanol-sodium hydroxide-pyrogallol (80 ml, 8 g, 1 g, respectively) at 75–80°C for 1 h. Ubiquinone is extracted with hexane and isolated by preparative thin layer chromatography using 0.5 mm silica gel 60F254 layer on 20 × 20 cm glass plate (Merck, Darmstadt, Germany). Benzene is used as solvent for development. A yellow band region, which is visualized as a dark band under a short-wave UV light (wave length 254 nm), is scraped off. The powdery materials are transferred to a small flask, and acetone is poured into it for extraction of CoQ. The yellow acetone extract is concentrated to dryness using a rotary evaporator. The yellow materials are redissolved in a small amount of ethanol and stored in the freezer.

For routine identification of CoQ homologues, the following two methods are recommended:

1. Reversed-phase thin layer chromatography for the qualitative analysis. The purified CoQ samples are spotted on a reversed-phase thin layer plate (HPTLC RP-18F254S, 10 × 10 cm, 0.2 mm, Merck, Germany), which is then developed with acetone/acetonitrile (4:1, v/v) (Collins and Jones 1981, Nakase and Suzuki 1985a). The coenzyme Q homologues can be visualized under a short-wave UV light (wave length 254 nm) and by iodine vapor.
2. High performance liquid chromatography (HPLC) for the qualitative and quantitative analyses. HPLC is performed on a liquid chromatograph fitted with an ODS (C_{18}) column (4.6 mm × 250 mm or 4.6 mm × 150 mm) (Billon-Grand 1985, Collins and Jones 1981, Nakase and Suzuki 1985a, Tamaoka et al. 1983, Suzuki and Nakase 1986). The CoQ homologues are eluted with a mobile phase of methanol-propan-2-ol (2:1, v/v) at 2.0 ml/min or 1.0 ml/min, and monitored at 275 nm. The homologues are identified by comparing their retention times with those of standard CoQ from CoQ5 to CoQ10 and C0Q10(H_2), and are quantitated on the basis of each peak area ratio.

Other methods such as reversed-phase paper chromatography and mass spectroscopy may also be useful for the identification of CoQ composition (Yamada 1998, Yamada and Kondo 1973, Yamada et al. 1969, 1989c).

4. ELECTROPHORETIC COMPARISON OF ENZYMES

4.1. Introduction

Differences in amino acid sequences found among the enzymes of different organisms are a reflection of organismal genetic divergence, based on differences in the nucleotide sequence of the DNA that codes for the enzyme protein. Amino acid substitutions can be detected from the extent of migration shown by enzymes on electrophoretic gels, and the visualized patterns are termed zymogram and isozyme patterns. The term "allozyme" is actually a shortened version of "allelic isozyme" where the term isozyme refers to multiple forms of the same enzyme that have different electrophoretic mobilities. The isozymes detected can arise from multiple alleles at a single locus, single or multiple alleles at multiple loci, and secondary isozymes arising from post-translational processing (Micales and Bonde 1995).

In the previous edition of this book, Yamazaki et al. (1998) gave an excellent review of the application of enzyme electrophoresis to yeast taxonomy. Concerning studies of taxonomic relationships of filamentous fungi, only references were listed, i.e., Blaich and Esser 1975, Jones and Noble 1982, Micales et al. 1986, Nasuno 1971, Nealson and Garber 1967, Okunishi et al. 1979, Royse and May 1982, Schmidt et al. 1977, Stout and Shaw 1973, 1974, Sugiyama and Yamatoya 1990, Toyomasu and Zennyozi 1981, Yamatoya et al. 1990, Zambino and Harrington 1992, and Zamir and Chet 1985.

Electrophoretic comparisons of enzymes is one of the useful tools for taxonomic resolution at specific and infraspecific levels as briefly exemplified below.

1. Baptist and Kurtzman (1976) first applied enzyme electrophoresis to yeast taxonomy, and separated *Cryptococcus laurentii* from *Cr. magnus* and *Cr. flavescens* cited as varieties *magnus* and *flavescens*, respectively.
2. Yamazaki and Komagata (1981, 1982a, b) comprehensively used zymographic comparisons to investigate the taxonomic affinities of species of *Rhodotorula* with those of *Rhodosporidium* as well as the relationships between asporogenous yeast species of the genera *Candida*, *Torulopsis*, and *Kloeckera* with their presumed teleomorphs. Subsequently, Hamamoto et al. (1986a) numerically analyzed their data on patterns of 7 enzymes from 108 strains belonging to the genera *Rhodotorula* and *Rhodosporidium*.
3. Holzschu et al. (1983) first used the allozyme patterns in the formal description of yeast species. They showed that *Pichia pseudocactophila* could be differentiated from its sibling species *Pichia cactophila*.
4. Sidenberg and Lachance (1983) examined the type strains of 20 phenotypically defined species of the genus *Kluyveromyces*. The results of a multivariate analysis of the electrophoretic patterns supported the division of the genus into 13 species.
5. Smith et al. (1990b) examined the taxonomic status of various species of the teleomorphic genus *Dekkera* and the anamorphic genera *Brettanomyces* and *Eeniella* by electrophoretic comparison of five enzymes with respect to nDNA relatedness, and with respect to physiological reactions. Enzyme patterns demonstrated the presence of two *Dekkera* species [*D. anomala* with anamorph *B. anomalus* (= *B. claussenii*), *D. bruxellensis* (= *D. intermedia*) with anamorph *B. bruxellensis*] and three *Brettanomyces* species [*B. bruxellensis* (= *B. abstinens*, *B. custersii*, *B. intermedius*, *B. lambicus*), *B. custersianus* and *B. naardenensis*] that were recognized from low (0–29%) similarity values. *Eeniella nana* showed an unique enzymic pattern that differed from other *Brettanomyces* and *Dekkera* species (0–5% similarity).
6. Naumova et al. (2003b) showed that six sibling species in the *Saccharomyces sensu stricto* complex (*S. cerevisiae*, *S. bayanus*, *S. cariocanus*, *S. kudriavzevii*, *S. mikatae* and *S. paradoxus*) could be distinguished from each other by multilocus enzyme electrophoresis (MLEE).

Additionally, in the field of clinical yeasts (*Candida albicans*, *C. tropicalis*, *C. guilliermondii*, *C. krusei*, *C. parapsilosis*, *C. lusitaniae*, *C. glabrata* and *Cryptococcus neoformans*), MLEE has been applied to epidemiology, evolutionary biology and population genetics as a typing or a fingerprinting method (De Meeus et al. 2002, Soll 2000,

Taylor et al. 1999). The power of MLEE is that if the enzymes are carefully selected, one can discriminate among the gene products of different alleles for a number of loci (Soll 2000). It should be noted, however, that the use of enzyme electrophoresis has been criticized for the following reasons:

1. The method assays the genotype only indirectly, so that much variation at the nucleotide level may go undetected because nucleotide substitutions do not necessarily change the amino acid composition;
2. Changes in amino acid composition do not necessarily change the electrophoretic mobility of the protein and, as a consequence, alleles that are considered to be the same protein alleles from different individuals may represent different gene alleles; and
3. different polymorphisms may be under different selection presures, so that anonymous DNA markers may give a different picture as allozyme markers, presumably because the former are neutral and the latter are under some sort of selection (Taylor et al. 1999).

4.2. Methods

This method is straightforward. Enzyme protein molecules in cell extracts are separated from each other by using starch gel electrophoresis, polyacrylamide gel electrophoresis and isoelectric focusing under native conditions. The enzymes are then visualized in the gels by specific enzyme-staining procedures. Murphy et al. (1990, 1996) discussed the advantages of the different methods of electrophoresis. The method used will be determined by availability of equipment and expertise. As the gel support media, polyacrylamide gels and starch gels have been used (Davis 1964, Sidenberg and Lachance 1983, 1986, Yamazaki and Komagata 1981 for polyacrylamide gels; Baptist and Kurtzman 1976, Holzschu et al. 1983, Nealson and Garber 1967, Rosa et al. 2000, Royse and May 1982, Singh and Kunkee 1977, Zamir and Chet 1985 for starch gels).

An example of using polyacrylamide gel electrophoresis (Nakase and Suzuki 1985a, b, Yamazaki and Komagata 1981) is introduced here as follows. Cells are suspended in 0.05 M Tris-HCl buffer (pH 7.8), and disrupted in a Braun cell homogenizer (Braun, Melsungen, Germany) for 2 min (30 second, 4 times) at 4000 rpm in a 50-ml glass vessel, containing glass beads (0.45−0.50 mm, 35 g), cooled with ice water. The homogenate is centrifuged at 11,000 rpm for 50 min at 4°C. The supernatant is then used as an enzyme source for the electrophoresis.

The electrophoretic apparatus used is for disc electrophoresis. "Disc" is used as an abbreviation for "discontinuous", referring to the buffers employed (Andrews 1986) using vertical slab gels. In this type of electrophoresis, separation takes place in a gel in the usual way, and is determined by both charge effects and molecular size differences. Above this separation gel is added a stacking gel layer in which the sample components are stacked into thin, and hence concentrated, starting zones before the actual separation. The formation of sharp zones produced by the gel and buffer discontinuities determines the subsequent sharpness of the separations. A 3.0% large-pore upper stacking gel and 7.5% small-pore separation gel are prepared by the method of Davis (1964). The separation gel is chemically polymerized and the stacking gel is photopolymerized. Addition of sucrose to increase the sample density followed by direct application of sample solution is widely used and is generally satisfactory. For example, addition of the same volume of 40% sucrose to the sample solution is recommended. The tracking dye (e.g., 2 ml/l of 0.001 per cent bromophenol blue) can be added to the upper electrode buffer. Slab-gel electrophoresis was conducted for 3−5 h at a regulated current of 20 mA per gel slab at 4°C. Tris-glycine buffer (pH 8.3) was used as an electrode buffer.

The staining procedures for detection of enzymes in electrophoretic gels have been described by Siciliano and Show (1976). Enzymes compared are as follows (Sidenberg and Lachance 1983, 1986, Yamazaki and Goto 1985, Yamazaki and Komagata 1981 1982a, b, 1983a, b, Yamazaki et al. 1982 1983, 1985): Fructose-1,6-bisphosphate aldolase (EC 4.1.2.13), hexokinase (EC 2.7.1.1), phosphoglucomutase (EC 2.7.5.1), alcohol dehydrogenase (EC 1.1.1.1), lactate dehydrogenase (EC 1.1.1.27), malate dehydrogenase (EC 1.1.1.37), 6-phosphogluconate dehydrogenase (EC 1.1.1.41), glucose-6-phosphate dehydrogenase (EC 1.1.1.49), glutamate dehydrogenase (EC 1.4.1.4), fumarase (EC 4.2.1.2), esterase (EC 3.1.1.1), catalase (EC 1.11.1.6) and terazolium oxidase, superoxide dismutase (EC 1.15.1.1), alkaline phosphatase (EC 3.1.3.1), α-glucosidase (EC 3.2.1.20), β-glucosidase (EC 3.2.1.21), and exo-β-glucanase (EC 3.2.1.58).

After staining, the gels were dried under vacuum with warming, and the relative mobilities (Rm) of the enzyme bands were calculated as the ratio of the distance that the enzyme moved from the origin to the distance that the tracking dye moved (Yamazaki and Komagata 1981).

An example using a starch gel electrophoresis (Holzschu et al. 1983) is introduced here as follows. Cells are suspended in approximately 15 ml of 0.1 M Tris-HCl buffer, pH 7.4, and disrupted in a Bronwill cell homogenizer (0.5 mm glass beads) for 3 min with CO_2 cooling. After cell breakage, a 1−2 ml portion of each suspension is removed by Pasteur pipette and placed in a single well of a plastic tray (24 samples/tray), covered, and frozen immediately. The samples are stored at −20°C for not more than 3 days before transfer to −80°C.

Protocols for starch gel preparation, buffer preparation, horizontal electrophoresis, gel cutting and staining procedures have been presented in detail by Ayala et al. (1972), Harris and Hopkinson (1976), Murphy et al. (1990, 1996), Shaw and Prasad (1970), and Tracey et al. (1975).

Four buffer systems are used: (A) discontinuous, Tris-citrate electrode buffer, pH 8.65, and borate (NaOH) gel buffer, pH 8.1; (B) continuous, Tris-borate-EDTA, pH 9.1, electrode and gel buffer; (C) continuous, Tris-citrate-EDTA electrode buffer, pH 7.0, and for gel buffer a 15-fold dilution of electrode buffer; and (D) continuous, phosphate-citrate, pH 7.0, electrode and gel buffer.

Banding patterns of the following enzymes are resolved by specific staining after horizontal electrophoresis in the buffer system indicated in parentheses; alcohol dehydrogenase, (B); fumarase (C); glucose-6-phosphate dehydrogenase (A); hexokinase (B); leucine amino peptidase (A); phosphoglucose isomerase (D); tetrazolium reductase (B); and triosephosphate isomerase (B). Activity stains were prepared 30−60 min prior to use, and slices of the starch gels were incubated in the staining solutions in the dark until indicator dyes appeared. Gels were fixed and stored as reported by Ayala et al. (1972); 26 samples were run in each starch gel (19.5 × 17.5 × 1 cm).

The application of electrophoretic data in systematic studies has been discussed in detail (Buth 1984, Murphy et al. 1990, 1996). Three methods that have been applied to yeast taxonomic studies are as below:

1. Similarity values for the electrophoretic patterns of the enzymes are calculated by the formula:

$$\%S = NS/(\mathrm{NS} + \mathrm{ND}) \times 100,$$

with S = similarity value; NS = number of enzymes showing identical mobilities; ND = number of enzymes showing different mobilities.

2. Similarity for each enzyme is calculated by the following formula:

$$\%S = 2\mathrm{NAB} / (\mathrm{NA} + \mathrm{NB}) \times 100,$$

with S = similarity value; NAB = the number of enzyme bands with identical relative mobilities; NA = the number of enzyme bands of strain A; NB = the number of enzyme bands of strain B. Clustering is performed by the unweighted average linkage method (Sneath and Sokal 1973).

3. Sidenberg and Lachance (1983, 1986) used reciprocal averaging to ordinate the strains as a function of correlated electromorphs. The amount of information provided by each enzyme is evaluated by the following measure of entropy (Ij):

$$Ij = (n \times tj \times \ln \quad tj)$$

$$n$$

$$-S[(aij \times \ln aij) + (tj - aij) \times \ln(tj - aij)],$$

$$i = 1$$

where n is the number of strains, tj is the total number of different electromorphs for the j^{th} enzyme, and aij is the number of electromorphs of that enzyme present in the i^{th} strain.

The results are expressed in a matrix having the dimensions n × p, where n strains are described by the presence (scored as 1) or absence (scored as 0) of each of p electromorphs. Reciprocal averaging is used to ordinate rows and columns of a frequency matrix and simultaneously reveals correspondences between two kinds of information (i.e., strains and electromorphs).

5. LIPIDS IN CHEMOTAXONOMY

5.1. Introduction

A diverse variety of fungal lipid types occurs, including compounds based on long-chain fatty acids (FAs) and those derived from isoprene units such as terpenoid lipids (Kock and Botha 1998). In this chapter, emphasis will be placed on FA based lipids and their taxonomic value in yeasts. The predominant FA-families, i.e., ω-3 and ω-6, are both known to be present in fungi (Kock and Botha 1998). In either case, the ω-3 and ω-6 polyunsaturated fatty acid (PUFA) series are derived from linoleic acid (18:2 ω-6) by the participation of different desaturase and elongase enzymes (Certik and Shimizu 1999). These FAs can also be oxygenated derivatives produced from hydroxylated PUFAs via lipoxygenase, P450 pathways and others (Kock and Botha 1998). It has been reported that long chain FAs of C16 and C18 chain lengths predominate in fungi (including the yeasts) and include palmitic- (16:0), palmitoleic- (16:1), stearic- (18:0), oleic- (18:1), linoleic- (18:2) and linolenic acids (18:3). Growth rate, culture age, oxygen availability, temperature, pH and composition of the growth medium are all factors that can affect the cellular FA profiles of microorganisms in general and must be taken into account when comparisons of FA compositions in fungi are made (Erwin 1973, Rattray 1988).

The presence of ω3 and ω6 series of PUFAs in fungi seems to be conserved at higher taxonomic levels, and is influenced only quantitatively by the above factors. Kock and Botha (1998) reported that the Oomycetes, Chytridiomycetes and Hyphochytridiomycetes are characterized mainly by the presence of the ω6 series of PUFAs with chain lengths from 18 carbons (C18) to 20 carbons (C20). The zygomycetes also contain the ω6 series of PUFAs, although most representatives only produce C18 and not C20 PUFAs. In contrast, members of the Dikarya and affiliated anamorphs do not produce the ω6 series of PUFAs. Some are characterized by the presence of 18:3 (ω3) and others can only produce FAs up to 18:2 (ω6). Some strains of *Saccharomyces cerevisiae* do not produce the ω3 or ω6 series of FAs. Some of these organisms (including some *S. cerevisiae* strains) are, in fact, not able to produce FAs greater than C18 mono-enoic acids. The separation of three groups (i.e., Chytridiomycota, Mucoromycotina and Dikarya) coincides with the scheme inferred from SSU rRNA sequence analysis (Wilmotte et al. 1993). The highly conserved status of PUFAs can probably be ascribed to their crucial role in the survival of the fungal cell, i.e., in maintaining membrane integrity and function.

5.2. Fatty Acid Profiles and Yeast Taxonomy

The use of long chain FA profiles for yeast identification is well reported (Botha and Kock 1993a). Various studies have shown that some variations in the mean relative percentages of FAs present in the cellular material from different strains within the same species can occur (Augustyn 1992, Kock and Botha 1998). Thus, to obtain a representative FA profile of a particular yeast species, as many representative strains as possible must be examined. When interpreting the FA composition of yeasts representing the different yeast families (Kurtzman 1998d), it was found that large overlaps occur. This of course renders this phenotypic characteristic not conserved at the family level (Kock and Botha 1998), and can therefore not be used to differentiate at this taxonomic level.

Within genera, long-chain FA composition seems to be of more value. For instance, within *Kluyveromyces*, *Lipomyces*, *Nadsonia*, *Rhodosporidium*, *Saccharomyces* and *Schizosaccharomyces* it was possible to distinguish between a selection of species using FA composition. For instance, Golubev *et al.* (1989) used FA composition as one of several phenotypic characteristics to revise the genus *Nadsonia.* Van der Westhuizen et al. (1987) found that rapid differentiation between species in the genus *Rhodosporidium* was possible using this phenotypic characteristic. Augustyn and co-workers (1989, 1990, 1991) demonstrated that minor FAs were useful for discrimination of 46 of the 50 *Saccharomyces cerevisiae* strains studied. In addition, they found that it was also possible to separate *S. cerevisiae*, according to the range of its cellular FA profiles, from the other members of the *Saccharomyces sensu lato* complex. However, they were not able to separate *S. cerevisiae* from the other members of the industrially important *sensu stricto* complex. Augustyn and co-workers were able to distinguish 105 strains representing *Arxiozyma*, *Hanseniaspora*, *Kluyveromyces, Pachytichospora*, *Saccharomycodes*, *Torulaspora* and *Wickerhamiella* from the species of *Saccharomyces sensu stricto* complex. They were, however, unable to differentiate between several *Hanseniaspora* and *Kluyveromyces* species, indicating that cellular long-chain FA profiles cannot be used as the sole criterion for differentiating yeasts at the species level. Cellular FA profiles discriminated between various yeasts associated with wine spoilage (Malfeito-Ferreira et al. 1989). Using principal component analysis (PCA), they were able to differentiate between *Torulaspora delbrueckii* and *Zygosaccharomyces bailii*. In 1989, Cottrell and Kock concluded that *Dipodascopsis* was closely related to *Lipomyces* when using linolenic acid (18:3) as taxonomic marker. The percentage palmitoleic acid (16:1) and oleaginicity in the neutral lipid (NL) fraction of yeasts representing the Lipomycetaceae made it possible to distinguish between the genera *Babjevia*, *Dipodascopsis*, *Lipomyces* and *Zygozyma* (Kock and Botha 1998). It was, however, not possible to distinguish *L. japonicus* and *Zygozyma*. On the basis of lipid composition, ascospore topography and rRNA sequence analysis, Kock et al. (1995) re-classified *L. japonicus* under the new genus *Smithiozyma* as *S. japonica* (but see Chapter 43, *Lipomyces*).

Cellular FA analysis was not satisfactory as a sole identification method to distinguish between oral yeast species (Blignaut et al. 1996). However, when performed together with other relatively simple and rapid tests, such as cycloheximide sensitivity, the distinguishing performance increased. Cellular FA analysis alone clearly

distinguished *Candida albicans* from *C. glabrata*, *C. holmii*, *C. parapsilosis, Cryptococcus albidus*, *Exophiala jeanselmei*, *Lecythophora mutabilis* and *S. cerevisiae*. Within the genus *Schizosaccharomyces* it was possible to distinguish between *Schiz. pombe* and *Schiz. japonicus* on the basis of the percentage 18:1 and 18:2 in the total lipid (TL)-, neutral lipid (NL)-, phospholipid (PL)- and glycolipid (GL) fractions (Jeffery et al. 1997, Kock and van der Walt 1986). On the basis of long-chain FA profiles, i.e. the detection of linoleic acid (18:3) in the total lipid fraction, ascospore morphology and the absence of CoQ-10, Yamada and Banno (1987a) proposed the new genus *Hasegawaea* (but see Chapter 66, *Schizosaccharomyces*). FA composition distinguished between *Candida albicans* and *C. dubliniensis* as well (Peltrochellacsahuanga et al. 2000).

5.3. The Distribution of Oxylipins in Yeasts

Hydroxy FAs are widely distributed in nature, and occur in plants, animals and in some microorganisms or as constituents of various complex lipids or free carboxylic acids (Van Dyk et al. 1994). Kock and Botha (1998) reported the possible presence of prostaglandins in yeasts as determined by radio immunoassay and radio TLC techniques. However, these results await further confirmation using more advanced analytical methods, such as gas chromatography-mass spectrometry analyses.

The production of 3-hydroxy FAs (3-OH-FAs) in fungi was first reported in 1967, with the presence of 3(D)-OH 16:0 and 3(D)-OH 18:0 acids in the extracellular glycolipids of strains of *Rhodotorula graminis* and *Rh. glutinis* (Stodola et al. 1967). The formation of large quantities of extracellular 3(D)-OH 16:0 by *Saccharomycopsis malanga* was later reported by Kurtzman et al. (1974) and Vesonder et al. (1968).

In 1991, a novel eicosanoid, namely 3-hydroxy-5, 8,11,14-eicosatetraenoic acid (3-HETE), was found in the yeast *Dipodascopsis uninucleata* after it was exogenously fed with arachidonic acid (AA) (Van Dyk et al. 1991). Utilizing immunofluorescence microscopy, this compound was found to be closely associated with the released aggregating ascospores. By adding inhibitors for oxylipin production during ascospore development of this yeast, it was concluded that 3-OH oxylipins are responsible for ascospore aggregation. It is interesting to note that immunofluorescence studies (Smith et al. 2000a) on *Dipodascopsis tothii* showed that 3-OH oxylipins such as 3-HETE accumulate on the ascus tip and were not associated with the aggregating ascospores.

Dipodascopsis uninucleata produces a 3-OH derivative not only from AA but also from a variety of other exogenous polyenoic FAs (Venter et al. 1997). This yeast was found to produce 3-OH 14:2 from the start of growth. 3-OH oxylipins are present in the teleomorphic stages of most species from the genera *Dipodascopsis*, *Lipomyces*, *Smithiozyma* and *Zygozyma* of the Lipomycetaceae (Smith et al. 2000b), but the structures of these metabolites await clarification. Oxylipins such as 3-OH 8:0, and 3-OH 10:0 are produced during the growth cycle of a flocculating yeast strain of *S. cerevisiae* (Kock et al. 2000). Furthermore, their studies demonstrated that these compounds were synthesized from an early stage of growth in association with the cell wall. Since these compounds are present between flocculating cells, these observations implicate the involvement of these oxylipins in cell aggregation or flocculation.

A novel oxylipin derived from AA, namely 3,18-dihydroxy-5,8,11,14-eicosatetraenoic acid (3,18 diHETE), that revealed immunoreactivity with an antibody against 3(R)-OH oxylipins, was detected recently in *C. albicans* (Deva et al. 2000, 2001). Using immunofluorescence microscopy, endogenous 3(R)-OH oxylipins were found in pseudohyphae but not in unicellular yeast cells of this species. These authors proposed that infection-mediated release of AA from mammalian host cells may modulate cell growth, morphogenesis and invasiveness of *C. albicans*. The administration of aspirin, a 3(R)-OH oxylipin inhibitor, may be beneficial in the treatment of vulvovaginal candidiasis by (i) inhibition of 3(R)-OH oxylipin formation, and (ii) inhibition of prostaglandin PGE_2 formation in the infected host tissue (Deva et al. 2000, 2001).

So far, a wide variety of 3-OH oxylipins ranging from 3-OH 8:0 to 3-OH 20:4 has been identified in yeasts. These compounds seem to vary between different species. However, more strains of a species should be analyzed in this regard, to assess the taxonomic value of this phenotypic characteristic. It is also clear that these compounds are associated with surfaces of aggregating cells such as *S. cerevisiae*, as well as with surface ornamentations of ascospores (Kock et al. 2003). The question of the function of these oxylipins still remains. Kock et al. (2004) suggested a lubricating function for these compounds when the ascospores are released from the asci (see: http://www.sajs.co.za/) (Van Heerden et al. 2005).

5.4. Methods

5.4.1. Fatty Acid Analysis (After Botha and Kock 1993a, Jeffery et al. 1997)

5.4.1.1. Cultivation

Stock cultures are maintained on YM (yeast-malt) agar slants (Wickerham 1951) at optimal growth temperature. Yeasts are then inoculated into 250-ml conical flasks containing 40 ml medium (4% glucose and 0.67% yeast nitrogen base in dH_2O). Flasks are incubated at 28°C (psychrophilic species at 17°C) for 18 h while shaking at 150 rpm, after which the 40 ml culture is transferred into 1-liter conical flasks containing 400 ml of the same medium. These flasks are incubated again as described above. Growth is monitored by measuring the optical density of each flask at 640 nm with a Klett-Summerson colorimeter (red filter, Klett MFG CO, Philadelphia, USA). This experiment is performed in triplicate. When cells reach stationary growth phase, they are harvested by centrifugation at 8,000 rpm for 10 min and washed twice with dH_2O. The centrifuged cells are then frozen rapidly by liquid nitrogen followed by freeze drying.

5.4.1.2. Lipid Extraction

Pre-weighed freeze-dried cells are dissolved in a mixture of chloroform:methanol (2:1, v/v) overnight and then washed twice with distilled water. The organic phase is then evaporated while the lipid samples are dried in an oven at 50°C over P_2O_5 overnight and measured weight.

5.4.1.3. Lipid Fractionation

Lipid samples are dissolved in a minimal volume of chloroform and applied to a clean column (140 mm × 20 mm) of activated silicic acid. The different solvents with different polarities are applied to a column to elute neutral, glyco- and phospholipids fractions respectively. The total and fractionated lipid samples are dried in an oven over P_2O_5 at 50°C and weighed. All lipid samples are stored under a blanket of N_2 at −20°C.

5.4.1.4. Fatty Acid Determination

All lipid samples are dissolved in a minimum volume of chloroform. Then 200 μl of the sample is transferred to a gas chromatography (GC) vial and transesterified by the addition of 200 μl trimethylsulphonium hydroxide (TMSOH). The fatty acid methyl esters are

analyzed by GC with a flame ionization detector, and Supelcowax 10 capillary column (30 m × 0.75 mm). The initial column temperature of 145°C is increased by 3°C/min to 225°C and, following a 10 min isothermal period, increased to 240°C at the same rate. The inlet and detector temperatures are 170°C and 250°C respectively. Nitrogen is used as carrier gas at 5 ml/min. Peaks are identified by reference to standards.

5.4.2. Oxylipin Analysis

5.4.2.1. Immunofluorescence Microscopy (Kock et al. 1998)

Yeasts are grown on YM agar medium (Wickerham 1951) at 25°C until asexual and sexual stages are formed. Primary antibodies against 3-hydroxy oxylipins used for immunofluorescence microscopy are raised in a rabbit and characterized according to titer, sensitivity and specificity. Cells are prepared for immunofluorescence studies as described. Briefly, cells are suspended in a buffer in 2-ml plastic tubes and treated with primary antibody. This suspension is incubated for 1 hour at room temperature and immediately washed with a phosphate buffer. Fluorescein isothiocyanate (FITC)-conjugated secondary antibody (Sigma, St Louis, MO, USA) is added, and the preparation is incubated in the dark for 1 hour at room temperature, followed by washing. The fluorescent material is prepared on microscope slides, and photographed using a digital or analogue microscope camera (e.g., using Kodak Gold Ultra 200 ASA film, Kodak, Johannesburg, South Africa) attached to a fluorescence microscope (e.g., Zeiss Axioskop [Zeiss, Jena, Germany]) equipped for epifluorescence with a 50 W high-pressure mercury lamp (excitation filter: Blue, 460 nm). The fluorescing cells are compared with appropriate controls such as the addition of FITC-conjugated secondary antibody alone.

5.4.2.2. Gas Chromatography Mass Spectrometry Analysis (Van Dyk et al. 1991, Venter et al. 1997)

Cells are subjected to 3-hydroxy oxylipin extraction. This is done by suspending the cells in 100 ml dH_2O water after which the pH is decreased to below pH 4 by the addition of 3% formic acid. Lipids from the cells are extracted with two volumes of ethyl acetate (200 ml) and the organic solvent is evaporated. Extracted lipids are methylated and silylated, dissolved in a mixture of chloroform:hexane (4:1, v/v) and eventually analyzed by GC-MS. A Finnigan Trace GC Ultra gas chromatograph (San Jose, California, USA) equipped with a HP5 (60 m × 0.32 mm) fused silica capillary column, coupled to a Finnigan Trace DSQ MS, is used. Helium is used as a carrier gas at 1.0 ml/min. The initial oven temperature is 110°C which was increased at 5°C/min to a final temperature of 280°C. The GC-MS was auto-tuned for m/z 62 to 512. A sample volume of 1 μl was introduced at an inlet temperature of 230°C and a split ratio of 1:60. All chemicals used in this study were of highest purity grade and obtained from reputable dealers.

Chapter 10

Gene Sequence Analyses and other DNA-Based Methods for Yeast Species Recognition

Cletus P. Kurtzman, Jack W. Fell and Teun Boekhout

1. INTRODUCTION

DNA sequence analyses, and other DNA-based methodologies, have transformed the way in which yeasts are identified. The focus of this chapter will be on the resolution of species using various types of DNA comparisons. In other chapters in this book, Rozpedowska, Piškur and Wolfe discuss multigene and whole genome analyses to understand species relationships (Chapter 11), and Weiss and Göker examine the phylogenetic methods used to determine these relationships (Chapter 12).

DNA comparisons of yeasts have paralleled the increasing sophistication of methods for nucleic acid characterization in general. Initial studies were restricted to determination of the mol% guanine + cytosine (G + C) content of DNA. From this work, it was seen that ascomycetous yeasts had a nuclear DNA content of ca. 28–50 mol%, whereas basidiomycetous yeasts had a noticeably higher range of 50–70 mol% (Nakase and Komagata 1968, Price et al. 1978). These studies suggested that strains differing by 1–2 mol% were likely to represent different species, thus providing a means for excluding strains incorrectly assigned to a particular species. Determination of mol% G + C can be done by a variety of methods, the most commonly used being cesium chloride gradients generated by ultracentrifugation, thermal melting profiles and high pressure liquid chromatography (HPLC) (Kurtzman 1993b, Price et al. 1978, Tamaoka and Komagata 1984). Despite the usefulness of mol% G + C values, further progress in taxonomy and systematics required methods that provided a quantitative assessment of genome similarities.

2. NUCLEAR DNA REASSOCIATION

Quantitation of the degree of gene sequence similarity between strains became possible with the development of DNA reassociation techniques, which measure the extent of pairing of nucleotide sequences when DNA is made single-stranded, and then allowed to repair as a double strand. There are two basic methods. One is "free solution", in which both DNAs of the test pair react while dissolved in a buffer solution, and the second relies on binding of one of the pair as single-stranded DNA to a matrix, such as a nitrocellulose filter, while the other strand of DNA remains free in the buffer surrounding the bound DNA. Free solution assays may be done spectrophotometrically or with the use of radioisotopes. The spectrophotometric method relies on separation of double stranded DNA by heating ("melting") – at which time the reaction buffer containing the separated strands has maximum absorbance at 260 nm (A_{260}). DNA reassociates optimally at 25°C below the midpoint of the melting curve (T_m-25) that results from DNA dissociation by heating. Consequently, after strand separation, the temperature is lowered to T_m-25, and the reassociation is monitored by measuring the decreasing A_{260}. The reassociation process is typically conducted with a recording spectrophotomer equipped with thermally controlled cuvettes. Generally, four of these are monitored; a blank, a mixture of DNAs from the two strains being compared, and each of the DNAs alone. The reaction is concentration dependent, and if the two strains are from the same species, the mixture of DNAs will reassociate as rapidly as the same concentration of DNA from single strains. If the strains are unrelated, the reassociation will take twice as long because each DNA reacts independently of the other, i.e., two independent populations of DNA molecules that are at half the concentration of single strain DNAs. The extent of DNA reassociation can be calculated as percent relatedness by the equation of Seidler and Mandel (1971):

$$\{1-[\text{obs. } C_o t_{0.5}{}^{\text{mix}} + (C_o t_{0.5}{}^{100} - C_o t_{0.5}{}^{0})]/C_o t_{0.5}{}^{100}\} \times 100 \qquad (10.1)$$

where:

obs. $C_o t_{0.5}{}^{\text{mix}}$ is the observed $C_o t_{0.5}$ of a renatured mixture,
$C_o t_{0.5}{}^{100}$ is the $C_o t_{0.5}$ of the mixture expected if the two DNA molecules are identical in sequence,
$C_o t_{0.5}{}^{0}$ is the $C_o t_{0.5}$ of the mixture expected for no sequence similarity (complete additivity of the independently measured $C_o t_{0.5}$ values).

When free solution assays use isotopes as markers, the reassociated DNA is recovered on a matrix that binds double-stranded DNA, such as hydroxyapatite (Price et al. 1978). If a filter or other binding methods are employed, the extent of reassociation is determined by measuring the radioactivity bound to the DNA on the filter (Meyer et al. 1975).

Measurements of DNA complementarity are commonly expressed as percent relatedness. This usage can be misleading because DNA strands must show at least 75–80% base sequence similarity before duplexing can occur and a reading is registered on the scale of percent relatedness (Bonner et al. 1973, Britten et al. 1974).

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Experimental conditions can greatly influence the extent of duplex formation, but when measured under optimum conditions, different methods of assessing DNA relatedness give essentially the same result (Kurtzman 1993b). Percent DNA relatedness provides an approximation of overall genome similarity between two organisms, but the technique does not detect single gene differences, or exact multiples of ploidy, although aneuploidy can sometimes be detected (Vaughan-Martini and Kurtzman 1985).

An interpretation of DNA reassociation data was provided by Martini and Phaff (1973) and Price et al. (1978), who suggested that, on the basis of shared phenotype, strains that showed 80% or greater nuclear DNA relatedness are members of the same species. Correlation of DNA relatedness with the biological species concept has been examined from genetic crosses utilizing both heterothallic and homothallic species. In one of these studies, the heterothallic species *Lindnera* (*Pichia*) *amylophila* and *L.* (*P.*) *mississippiensis*, which showed 25% DNA relatedness, gave abundant interspecific mating, but ascus formation was limited and no ascospores were formed (Kurtzman et al. 1980a). Similar results were found for crosses between *L.* (*P.*) *americana* and *L.* (*P.*) *bimundalis* (21% DNA relatedness) (Kurtzman 1984b) and between *Wickerhamomyces* (*Pichia*) *alni* and *W.* (*P.*) *canadensis*, the latter pair showing just 6% DNA relatedness (Fuson et al. 1979). *Pichia* (*Issatchenkia*) *scutulata* and *P.* (*I.*) *exigua* exhibited 25% DNA relatedness, but crosses between the two species gave mating and ascospore formation that was comparable to intraspecific crosses. Ascospore viability from interspecific crosses was about 5%, but sib-matings of the progeny had 17% ascospore viability. However, backcrosses to the parentals gave poor ascosporulation and very low viability (Kurtzman et al. 1980b), which suggested that these two taxa, formerly considered to be varieties, actually represent separate species.

Smith et al. (2005) discovered four intermating populations of differing levels of DNA relatedness among isolates assigned to the heterothallic species *Zygoascus hellenicus*. Two of the populations gave poor ascospore formation when intermated and showed only 25% DNA relatedness. These two populations were considered to be separate species, *Z. hellenicus* and *Z. meyerae*, the latter being newly described in the study. Strain matings within each of these two species gave a much higher frequency of ascospore formation than was observed for interspecific crosses. However, DNA reassociation resolved two populations within both species, each with 70% relatedness. Despite this reduced DNA relatedness, the two subpopulations within each species were considered to be conspecific because of the high frequency of ascospore formation, although ascospore viability was not determined.

Species of *Saccharomyces* are heterothallic and have been recognized from extent of nuclear DNA relatedness and/or multigene sequencing, as well as from the biological species concept. One of the species, *S. pastorianus*, represents a hybrid between *S. cerevisiae* and *S. bayanus* (Vaughan-Martini and Kurtzman 1985, Vaughan-Martini and Martini 1987a, Yamada et al. 1993a). Naumov et al. (2000) reported that with the exception of *S. pastorianus*, which appears sterile, the remaining six species of *Saccharomyces* can be crossed in any combination, but interspecific hybrids are sterile. With one exception, there is strong correlation between species defined from DNA reassociation and from traditional genetic crosses. The exception is the species pair *S. cariocanus* and *S. paradoxus*, which gave 97% nuclear DNA relatedness when measured by spectrophotometic reassociation (A. Vaughan-Martini, personal communication).

Studies of homothallic yeasts have given results that are similar to those from comparisons of heterothallic species. Although self-sporulating, cultures of homothallic species often show conjugation between independent cells, and can function as heterothallics in terms of genetic exchange. An example is a study of the five varieties of *Williopsis saturnus* in which auxotrophic markers were used to follow the mating process. The varieties of *W. saturnus* range in DNA relatedness from 37 to 79%. Intervarietal fertility was reduced and generally correlated with extent of DNA relatedness (Kurtzman 1987b, and references therein). However, in some crosses, less related pairs showed greater fertility than found among pairs with higher DNA relatedness. In other crosses, pairs with similar DNA relatedness showed somewhat different levels of fertility. A multigene phylogenetic comparison led to elevation of the five varieties to species level and their reclassification in the genus *Lindnera* (Kurtzman et al. 2008).

Conclusions are tentative from many of the genetic studies cited because they often did not involve a full test of the biological species concept. For a conclusive test, crosses must give meiotic spores with high viability, which when crossed, produce a highly fertile F2 generation. Backcrosses to parentals should be highly fertile to rule out the possibility that the F1 hybrids are allopolyploids (amphidiploids). Thus, a full test of the biological species concept can be quite time consuming, and when applied to homothallic species, reversion of auxotrophic markers can be a serious problem.

Despite the limitations discussed, the preceding studies show that mating among heterothallic as well as homothallic taxa can occur over a wide range of DNA relatedness values, but that highly fertile crosses, which demonstrate conspecificity, seem to exhibit 70% or greater DNA relatedness. Because species barriers are complex, and involve a number of factors, the numerical range of 70–100% DNA relatedness should be viewed as a prediction of conspecificity. This prediction has been applied to anamorphic as well as to teleomorphic species, because many anamorphs have been shown to represent mating types, and the genetic constraints that affect them may be no different than those affecting teleomorphs.

3. GENE SEQUENCE COMPARISONS

3.1. Ribosomal rRNA Genes

A limitation of DNA reassociation experiments has been that genetic resolution extends no further than to closely related species. In contrast, gene sequence comparisons offer the opportunity to resolve closely related species, as well as more distantly related taxa, and a database of sequences can be developed and expanded for further use.

The variable domain 2 (D2) from nuclear large subunit ribosomal RNA (LSU rRNA) was initially examined and found to resolve closely related species that had been circumscribed from genetic crosses and DNA reassociation experiments (Peterson and Kurtzman 1991). This work was expanded to include domains 1 and 2 (D1/D2) and applied to all described species of ascomycetous yeasts, resulting in a diagnostic database (barcode) useful for rapid species identification (Kurtzman and Robnett 1998a). Fell et al. (2000) developed a complementary D1/D2 database for known basidiomycetous yeasts. By comparing divergence among ascomycetous strain pairs with previously determined nuclear DNA reassociation values, it appeared that conspecific strains differed by no more than 3 nucleotides among the 500–600 nucleotides of the D1/D2 domains, whereas differences of 6 or more nucleotides (1%) indicated that the strains were different species (Table 10.1).

The preceding guidelines were treated as a prediction (Kurtzman and Robnett 1998a), because exceptions had been found earlier. DNA reassociation studies revealed that *Saccharomyces pastorianus* had intermediate relatedness with *S. cerevisiae* (57%) and *S. bayanus* (72%) (Vaughan-Martini and Kurtzman 1985) (Fig. 10.1), and D2 LSU rRNA sequence analysis found *S. bayanus* and *S. pastorianus* to have identical D2 sequences (Peterson and Kurtzman 1991). These results

TABLE 10.1 Correlation of Nuclear DNA Relatedness Determined from Reassociation Experiments and LSU D1/D2 rRNA Gene Sequence Divergence among Ascomycetous Yeasts[1]

Strain Pairs	% nDNA Relatedness	D1/D2 Nucleotide Differences
70 Conspecific pairs	70–100	0–3
Ca. 200 Unrelated pairs	0–20	6–250

[1]*Data from Kurtzman and Robnett (1998a, and references therein).*

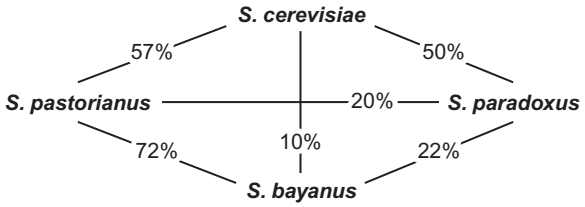


FIGURE 10.1 Percent nuclear DNA relatedness among *Saccharomyces* species as determined from reassociation experiments (Vaughan-Martini and Kurtzman 1985). As discussed in the text, *S. pastorianus* appears to be a hybrid of *S. cerevisiae* and *S. bayanus*. These data also suggest that *S. paradoxus* is a hybrid.

were interpreted to mean that *S. pastorianus* was a hybrid of *S. bayanus* and *S. cerevisiae* and that *S. pastorianus* received its D2 LSU rRNA sequence from *S. bayanus*. Later, *S. pastorianus* and *S. bayanus* were shown to share the entire rRNA repeat (Kurtzman and Robnett 2003); consequently, neither D1/D2 rRNA, SSU rRNA or ITS would separate these two sister species. The problem of resolving hybrids was further illustrated by Groth et al. (1999) from the discovery that *Saccharomyces* sp. CID1 was actually a triparental hybrid with DNA from *S. cerevisiae*, *S. bayanus* and *S. kudriavzevii* (Fig. 10.2). Additionally, Lachance et al. (2003c) found certain strains of *Clavispora lusitaniae* to be highly polymorphic in the D1/D2 domains of the LSU rRNA gene (Fig. 10.3). Polymorphic strains mated and formed ascospores, although ascospore viability was not tested. For comparison, the nucleotide divergence in the gene for actin-1 was determined for selected strains, and this gene appeared not to be polymorphic in strains with D1/D2 polymorphisms.

Another example of hybrids was found in the *Cryptococcus neoformans*/*Cr. gattii* complex where diploid or aneuploid isolates, such as serotype AD, BD or AB hybrids, occasionally occur (Boekhout et al. 2001, Bovers et al. 2006, 2008a, Cogliati et al. 2001, 2006, Litvintseva et al. 2007, F. Hagen and T. Boekhout, unpublished data). Hybrids usually possess both mating type loci, which indicates that they most likely result from a mating between isolates of opposite mating types. Genetic and molecular studies performed on serotype AD hybrid isolates showed that these were formed multiple times (Xu et al. 2002, 2003) and serotype AD and BD hybrids have been generated in the laboratory (Cogliati et al. 2006, Kwon-Chung and Varma 2006, Lengeler et al. 2001, Sia et al. 2000, Tanaka et al. 2003).

Interspecific *Cr. neoformans* × *Cr. gattii* hybrids serotype AB and BD have recently been described (Bovers et al. 2006, 2008b) based on extensive analyses including flow cytometric analysis of ploidy, serotyping, mating- and serotype-specific PCRs, genotyping using amplified fragment length polymorphism (AFLP), and sequence analysis of a set of cloned genes [viz. internal transcribed spacer (ITS), intergenic spacer (IGS), laccase (*CNLAC1*), the largest and second largest subunit of RNA polymerase II (*RPB1* and *RPB2*) and translation

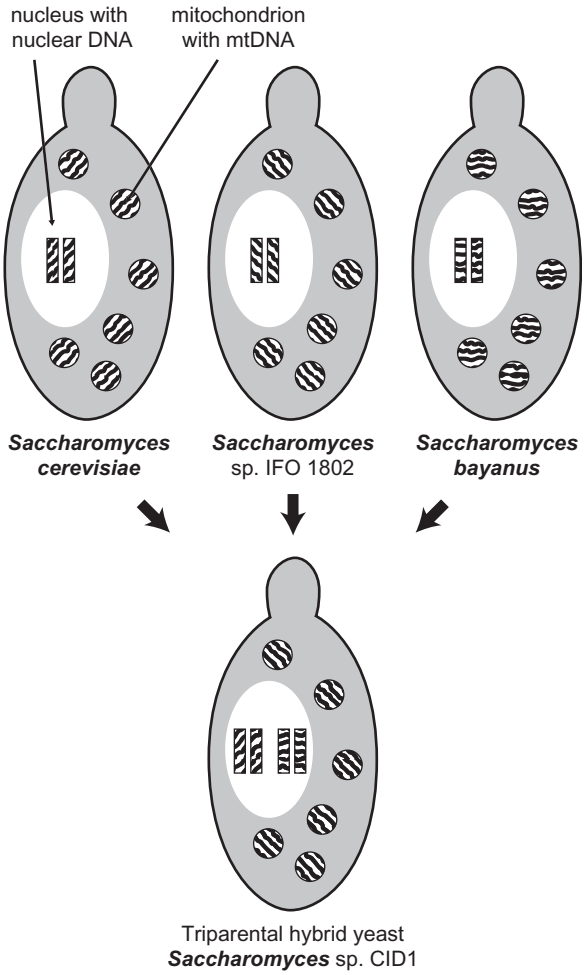


FIGURE 10.2 *Saccharomyces* sp. CID1 is a triparental hybrid with mitochondria from *S. kudriavzevii* (IFO 1802) and nuclear DNA from *S. cerevisiae* and *S. bayanus*. As discussed in the text, multiple diagnostic genes are required to detect hybrids. Redrawn from Groth et al. (1999).

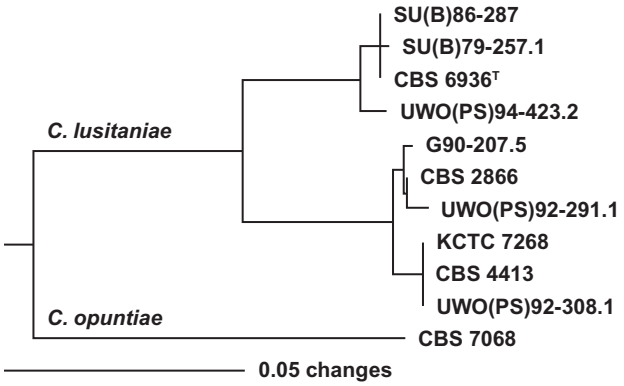


FIGURE 10.3 Gene tree demonstrating the sequence polymorphisms for D1/D2 LSU rRNA that were found among strains of *Clavispora lusitaniae*. Adapted from Lachance et al. (2003a).

elongation factor-1α (TEF1α) and two mitochondrial regions, ATP synthase subunit 6 (*ATP6*) and mitochondrial LSU rRNA]. Hybrids such as these have been found in patients in South America (Peru), North America (Canada), and Europe (Netherlands and Germany) (F. Hagen and T. Boekhout, unpublished data).

Apparent differences in substitution rates can also impact the diagnostic value of genes. For example, the closely related species *Meyerozyma guilliermondii*, *M. caribbica* and *Candida carpophila* differ from one another by one to three nucleotides in D1/D2 and will not be recognized as separate species using the guideline that zero to three substitutions indicate conspecificity (Table 10.2). Examples of lineage-specific differences in the extent of substitutions among other genes are given in the following sections.

The internal transcribed spacers 1 and 2 of the rDNA, which are separated by the 5.8S rRNA gene, are located between the SSU and LSU rRNA genes of the rDNA repeat. ITS sequences are commonly used to resolve species, often in conjunction with those from the D1/D2 LSU rRNA gene. The resolution provided by ITS sometimes exceeds that of D1/D2, but the reverse is also true. For species of *Bensingtonia* and *Kondoa*, ITS clearly provides greater resolution of species (Fig. 10.4), but species of *Trichosporon* were less well resolved by ITS (Scorzetti et al. 2002) (Fig. 10.5).

Of rDNA regions used for species identification, the intergenic spacer (IGS) appears the most substituted and offers the greatest resolution of closely related species and subspecific lineages. The IGS is comprised of two regions, IGS1 and IGS2, which are often separated by the 5S rRNA gene. IGS sequences have been used to resolve lineages within *Cryptococcus neoformans* and closely related taxa (Diaz and Fell 2005b, Diaz et al. 2000, 2005, Sugita et al. 2001a). The IGS has also been employed for resolution of closely related species of *Trichosporon* (Diaz and Fell 2004, Sugita et al. 2002), *Mrakia* (Diaz and Fell 2000) and *Xanthophyllomyces* (Fell and Blatt 1999, Fell et al. 2007). A characteristic of IGS is the diversity of length polymorphisms. Sugita et al. (2002) reported that the IGS1 region among *Trichosporon* species ranged in length from 195 to 704 nucleotides. The IGS region includes a series of multiple repeat units with numerous deletions and insertions (indels). These repeat units and indels provide characteristics for defining strains and species, and may delineate geographical strain distributions (Fell et al. 2007, Libkind et al. 2007). In practice, however, the sequence alignments take considerable time and patience to prepare. Intragenomic sequence heterogeneity is another factor to consider for IGS analysis. Fell et al. (2007) reported sequence heterogeneity in the ITS and IGS regions among certain strains of *Xanthophyllomyces*, which required cloning prior to sequence analysis. Intragenomic variation in the rDNA spacer regions is not uncommon among fungi, and reports include ITS variation in *Fusarium* (O'Donnell and Cigelnik 1997) and IGS variability in hybrids of *Cryptococcus neoformans* (Bovers et al. 2006), which may be used as a tracking tool for investigations of the origin and distribution of strains and species.

3.2. Genes Other than for rRNA

A significant advantage to the use of rRNA gene sequences is that ribosomes have a common evolutionary history, and within the sequences there are highly conserved regions between the variable regions that serve as a pan-specific primer attachment for PCR amplification and sequencing. In contrast, protein-coding genes tend to be variable across the entire gene, often making primer design difficult. Nonetheless, several protein sequences have been examined for phylogenetically divergent groups of species. Daniel et al. (2001) compared *Candida* spp. from several clades and showed that phylogenetic trees generated from actin sequences were congruent with rRNA gene trees. Daniel and Meyer (2003) compared resolution of closely related species from actin sequences and from D1/D2 LSU. As with D1/D2, actin did not always provide a clear separation of species but,

TABLE 10.2 Percent Nuclear DNA Relatedness and LSU D1/D2 Nucleotide Divergence among Closely Related Species of the *Meyerozyma guilliermondii* clade[1,2]

Species	% Nuclear DNA Relatedness and D1/D2 Nucleotide Substitutions					
	M. guilliermondii		*M. caribbica*		*C. carpophila*	
	% DNA	D1/D2	% DNA	D1/D2	% DNA	D1/D2
M. guilliermondii	100	0	37	3	55	1
M. caribbica			100	0	68	2
Candida carpophila					100	0

[1]*Data from Vaughan-Martini et al. (2005).*
[2]*DNA reassociation values are an average from five strain pairs of each species. All strains of each species had the same D1/D2 sequence.*

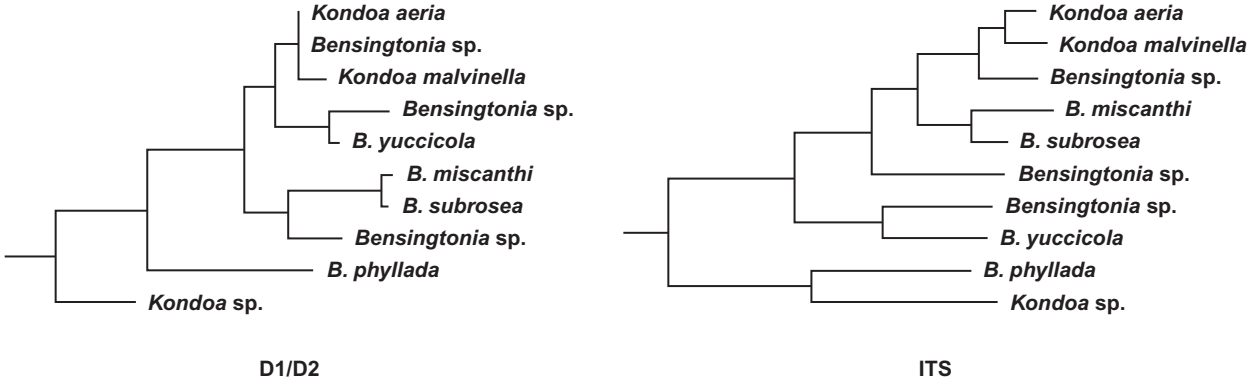


FIGURE 10.4 Contrasting resolution of *Bensingtonia* and *Kondoa* species when analyzed from gene sequences of D1/D2 LSU rRNA and from sequences of ITS. Lineages in this clade are more highly resolved from ITS sequences than from D1/D2. Adapted from Scorzetti et al. (2002).

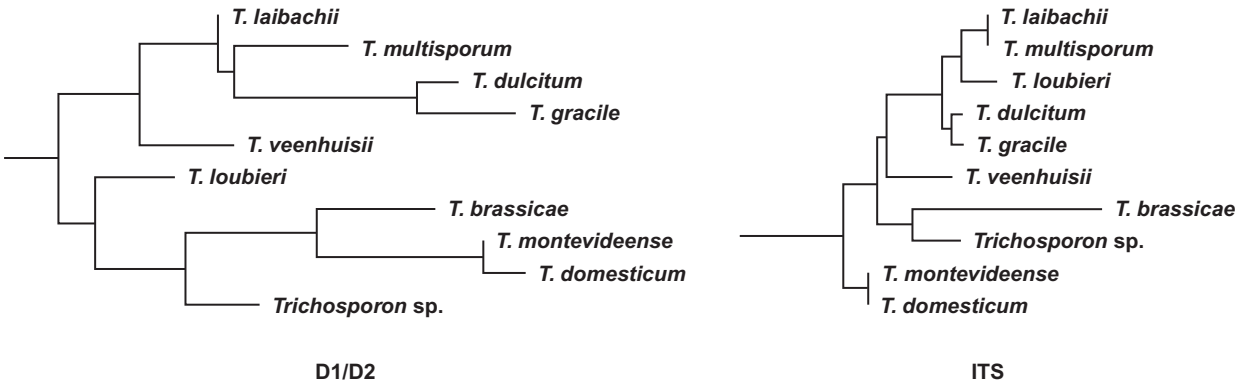


FIGURE 10.5 Resolution of *Trichosporon* species from analysis of D1/D2 LSU rRNA gene sequences and from ITS sequences. Greater species resolution is provided by D1/D2 than from ITS, which is in contrast to resolution of species in the *Kondoa* clade (Fig. 10.4). Adapted from Scorzetti et al. (2002).

TABLE 10.3 Extent of Nuclear DNA Reassociation and Gene Sequence Divergence between Closely Related Species in Several Ascomycetous Genera

Species Pair[1]		Genes (Substitutions − Indels)[3]			
	Percent[2] DNA Reassoc.	D1/D2	SSU	EF-1α	MtSm
Lindnera (*Pichia*) *amylophila* − *L.* (*P.*) *mississippiensis*	25	2 − 2	4 − 0	19 − 0	
L. amylophila − *L.* (*P.*) *fabianii*		9 − 2	19 − 2	39 − 0	
L. mississippiensis − *L. fabianii*		7 − 0	15 − 2	51 − 0	
Lindnera (*Pichia*) *americana* − *L.* (*P.*) *bimundalis*	21	2 − 0	0 − 0	22 − 0	
Lindnera (*Williopsis*) *saturnus* − *L.* (*W.*) *mrakii*	52	1 − 0	0 − 0	12 − 0	
L. mrakii − *L.* (*W.*) *subsufficiens*	44	4 − 0	0 − 0	12 − 0	
L. saturnus − *L. subsufficiens*	56	5 − 0	0 − 0	12 − 0	
Pichia cactophila − *P. pseudocactophila*	34	11 − 8	1 − 3	14 − 0	0 − 0
P. cactophila − *Candida inconspicua*[4]		1 − 1	0 − 0	0 − 0	0 − 0
Pichia kluyveri − *P. eremophila*	66	7 − 1	5 − 0	26 − 0	1 − 0
P. kluyveri − *P. cephalocereana*	72	3 − 0	2 − 0	11 − 0	1 − 0
P. eremophila − *P. cephalocereana*	69	7 − 1	4 − 0	25 − 0	1 − 0
Pichia (*Issatchenkia*) *scutulata* − *P.* (*I.*) *exigua*	25	20 − 7	7 − 1	36 − 0	10 − 4
Starmera (*Pichia*) *amethionina* − *S.* (*P.*) *pachycereana*	65	8 − 10	5 − 3	12 − 0	
S. amethionina − *S.* (*P.*) *caribaea*	40	21 − 2	8 − 3	11 − 0	
S. pachycereana − *S. caribaea*	37	17 − 5	9 − 5	6 − 0	

[1]*Species pairs are type strains. Genus names in parentheses were those used in the publication describing these results.*
[2]*Data are from Holzchu et al. 1983, Kurtzman 1984b, 1991a, Kurtzman et al. 1980 a, b, Phaff et al. 1976, 1987b, 1992, Shen and Lachance 1993.*
[3]*D1/D2 = domains 1 and 2, large subunit rRNA; SSU = small subunit rRNA, EF-1α = translation elongation factor-1α; MtSm = mitochondrial small subunit rRNA (Kurtzman et al. 2008).*
[4]*From these data,* Pichia cactophila *and* Candida inconspicua *are considered to be conspecific.*

in general, actin sequences had a greater number of substitutions, thus providing easier recognition of closely related species. Similar resolution was reported for the translation elongation factor-1α gene (Kurtzman et al. 2008) (Table 10.3) and the cytochrome oxidase II (COX II) gene (Belloch et al. 2000, Kurtzman and Robnett 2003). Comparisons presented in Table 10.3 show a lack of proportionality for substitutions among the genes for D1/D2, SSU and EF-1α for some species pairs.

4. RECOGNITION OF SPECIES FROM MULTIGENE PHYLOGENETIC ANALYSIS

In the examples presented, determination of whether strains are conspecific or members of separate species can be confused by hybridization events (Figs. 10.1, 10.2), by unexplained sequence polymorphisms (Fig. 10.3), and by differences in nucleotide substitution rates (Figs. 10.4, 10.5). Multigene analyses offer a means for detecting these changes, which would be signaled by lack of congruence for a particular gene tree. This approach was recommended by Goodman (1976) for vertebrates, for bacteria by Dykhuizen and Green (1991), and for fungi by O'Donnell et al. (2000) and Taylor et al. (2000). The paper by Taylor et al. (2000) provides an inclusive review of species concepts, and the term Genealogical Concordance Phylogenetic Species Recognition (GCPSR) was introduced to describe the concept of multigene analysis for species recognition. An example of GCPSR is found in a multigene sequence analysis of the *Kazachstania* (*Arxiozyma*) *telluris* species complex. D1/D2 LSU rRNA gene sequence analysis resolved the complex into five species, as did analysis of mitochondrial SSU rRNA gene sequences. However, analysis of RNA polymerase II (Fig. 10.6) detected four species because *K. pintolopesii* and *K. heterogenica* had nearly identical sequences for this third gene (Kurtzman et al. 2005). From the preceding analyses, it appears that *K. heterogenica* is a hybrid between *K. pintolopesii* and an undescribed species of *Kazachstania* (Fig. 10.6).

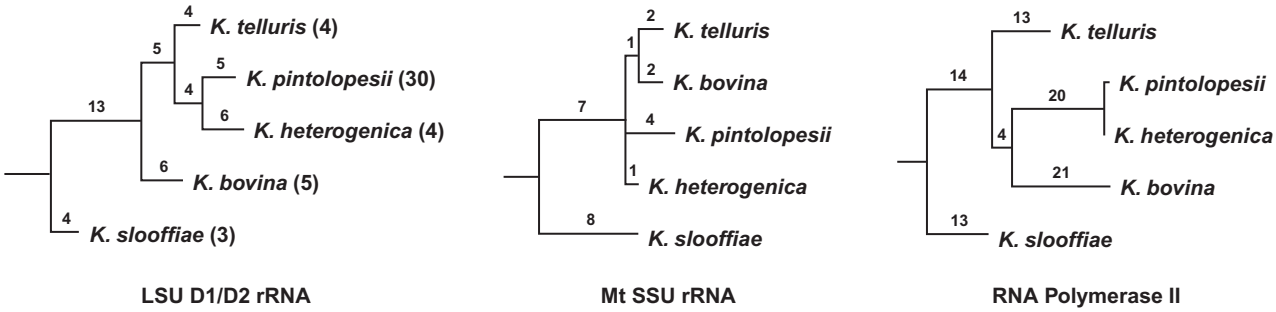


FIGURE 10.6 Maximum parsimony analyses of gene sequences for D1/D2 LSU rRNA, mitochondrial SSU rRNA and RNA polymerase II from *Kazachstania* species. The gene trees show overall congruence, but for RNA polymerase II, *K. pintolopesii* and *K. heterogenica* are nearly unresolved, suggesting that the latter species is a hybrid. The mitochondrial SSU rRNA tree shows *K. telluris* and *K. bovina* to be more closely related than is indicated by the other two gene trees, again suggesting an interspecific hybridization event. Numbers above branches reflect nucleotide substitutions and numbers in parentheses are the number of strains sequenced for each species for all three genes. Adapted from Kurtzman et al. (2005).

Multilocus sequence typing (MLST) has become an important application of GCPSR for the study of genetic structure in a number of important yeast species, such as *Candida albicans, C. dubliniensis, C. tropicalis, C. glabrata* and *C. krusei* (Bougnoux et al. 2003, Dodgson et al. 2003, Jacobsen et al. 2007, McManus et al. 2008, Odds and Jacobsen 2008, Tavanti et al. 2005b). Sequence analysis is usually based on multiple house-keeping genes, and the data are stored in an electronic database and made available through a dedicated website, such as www.mlst.net/. MLST schemes have been developed for the above listed clinically important yeasts, and also for *Saccharomyces cerevisiae* (Ayoub et al. 2006) and *Cryptococcus neoformans* (Meyer et al. 2009), as described below.

Gene sequence analyses of *Cryptococcus neoformans* and *Cr. gattii* have employed single genes as well as MLST. Most of the studies utilized a single locus (Biswas et al. 2003, Butler and Poulter 2005, Chaturvedi et al. 2002, Diaz et al. 2005), but studies of multiple loci used either *Cr. neoformans* (Litvintseva et al. 2006) or *Cr. gattii* isolates (Fraser et al. 2005, Kidd et al. 2005). Three studies included both *Cr. neoformans* and *Cr. gattii* isolates. In the first study, only a few *Cr. gattii* isolates were included (Xu et al. 2000). Two extensive studies were published recently (Bovers et al. 2008a, Ngamskulrungroj et al. 2009) with concordant results. One study (Bovers et al. 2008a) examined six nuclear loci, namely two rDNA regions (ITS1 and two including 5.8S rDNA and IGS1), and the laccase gene (*CNLAC1*), RNA polymerases 1 and 2 (*RPB1, RPB2*), and translation elongation factor-1α (*TEF1*α) in 117 haploid isolates (Bovers et al. 2008a, b). The second study included four genes [*ACT1*, orotate-phosphoribosyl transferase (*URA5*), phospholipase B (*PLB1*) and a 110-kDa neutral metalloendopeptidase (*IDE*)] that were studied in 73 globally collected isolates (Ngamskulrungroj et al. 2009). The results from these two studies agreed to a large extent. In *Cr. neoformans*, two main phylogenetic lineages occurred that correspond to either serotype A or D, and within *Cr. gattii*, four lineages could be discerned. Within each of the lineages, subclades occurred, which indicates the presence of extensive genetic diversity. An analysis of a combined dataset including *ACT1, IDE,* ITS1/2, IGS, *LAC1, PLB1, RPB1, RPB2, TEF1*α and *URA5* clearly supported these findings and indicated that within serotype A isolates, three sublineages occur. Moreover, within *Cr. gattii,* the lineage *VG11*/*AFLP6* was found to occur in a basal position (Meyer et al. 2010). Another study that included two mitochondrial genes (LSU rRNA and ATP synthase subunit 6 (*ATP6*)) gave somewhat different results from the above-mentioned studies as it seems likely that mitochondrial recombination occurred between two or three of the lineages within *Cr. gattii* (Bovers et al. 2009). A MLST scheme was proposed for epidemiological studies of the *Cr. neoformans*/*Cr. gattii* complex. The seven genes included are *CAP59*, *GPD1*, *LAC1, PLB1*, *PD1*, *URA5* and the IGS1 region (Meyer et al. 2009), and the data will be released via a webtool at www.mlst.net/.

Many yeast species have been described almost exclusively from divergence in D1/D2 LSU rRNA gene sequences and/or from ITS sequences. However, from the examples presented, it is apparent that single gene analyses can lead to incorrect interpretations. Consequently, it appears that in addition to D1/D2 and/or ITS, one or more protein coding gene sequences should be utilized as well. This would also apply to rapid molecular detection methods that are now being widely adopted. It is beyond the capacity of this book to include all species-specific loci that are included in multigene analyses, such as those used in MLST schemes, but reference to the above-mentioned website will provide much of this information.

5. RAPID MOLECULAR METHODS FOR SPECIES IDENTIFICATION AND QUANTITATION

Rapid molecular-based methods commonly used for species identification include species-specific primer pairs and probes, randomly amplified polymorphic DNA (RAPD), amplified fragment length polymorphisms (AFLP), restriction fragment length polymorphisms (RFLP) and karyotyping. In this section, some of the commonly used methods are described.

5.1. Species-Specific Primers

The use of species-specific primer pairs is effective when used for PCR-based identifications involving a small number of species, or when a particular species is the subject of the search (Chapman et al. 2003, Fell 1993, Mannarelli and Kurtzman 1998) (Fig. 10.7). However, PCR mixtures that contain large numbers of species-specific primer pairs may lead to uncertain banding patterns.

5.2. PNA

Peptide nucleic acid (PNA) probes offer a means for detection and quantitation of species in clinical samples and food products, through fluorescence *in situ* hybridization (FISH). PNA probes have a peptide backbone to which is attached nucleotides complementary to a species-specific target sequence, and a fluorescent label is added for detection by fluorescence microscopy (Stender et al. 2001). If

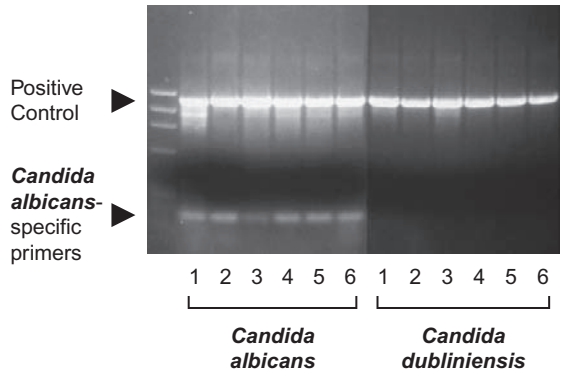


FIGURE 10.7 Use of species-specific PCR primer pairs for rapid identification of a target species. In this example, the primer pairs were designed to detect *Candida albicans* but not the closely related species *C. dubliniensis*. The PCR mixture included species-specific D1/D2 primers and pan-specific SSU primers to serve as a positive control (Mannarelli and Kurtzman 1998).

probes are complementary to rRNA, the whole cell of the target species will "glow" when visualized, which will also allow quantitation by cell counts. An advantage is that a sample can be diluted and directly probed. One disadvantage is that probes must be developed for each species of interest, a problem common to most probe technology. PNA technology has been effective for detection of *Dekkera* (*Brettanomyces*) *bruxellensis* in spoiled wine (Stender et al. 2001) and for detection of *Candida albicans* in blood samples (Rigby et al. 2002).

5.3. RAPD/AFLP

Microsatellite-primed RAPDs (Gadanho et al. 2003) and AFLP fingerprints (de Barrios Lopes et al. 1999) have been effectively used for rapid preliminary identification of large numbers of isolates, and the pattern-based identification is then often followed by gene sequencing of representative strains from each group having a unique pattern. RAPD analysis has also been used to resolve populations in various species, such as *S. cerevisiae, S. bayanus* var. *uvarum, C. albicans* and *C. glabrata* (Botterel et al. 2001, Fan et al. 2008, Foulet et al. 2005, Garcia-Hermoso et al. 2007, Hennequin et al. 2001, Legras et al. 2005, Malgoire et al. 2005, Masneuf-Pomarède 2007). One concern over the use of pattern-based identification techniques is reproducibility between laboratories, since small differences in PCR conditions may impact the species-specific patterns that serve as reference. Karyotyping with pulse field electrophoresis and RAPD on mitochondrial DNA can also serve in the initial characterization and identification of yeast species, but the interpretation of chromosomal banding patterns and mitochondrial restriction fragments for taxonomic purposes is complicated by a high degree of polymorphisms, such as chromosomal rearrangements within some yeast taxa (Špírek et al. 2003a).

5.4. Real Time PCR

The technique of real time PCR has also been widely studied for applications in medical mycology, especially those aiming to detect and quantify loads of *C. albicans*. In typical assays, 5 cfu/ml could be detected. Furthermore, clinically relevant *Candida* and *Cryptococcus* species could be identified. An advantage of this method is the potential early detection of the pathogen, thus contributing to the early start of treatment. The most commonly used primers are based on sequences of the rDNA repeat, such as ITS 1 and 2, or the 18S rRNA gene (Bergman et al. 2007, Khlif et al. 2009, Klingspor and Jalal 2006, Loeffler et al. 2000, Wellinghausen et al. 2009). This technique is also becoming widely employed in food and beverage analyses, and has been used for detection and quantitation of spoilage yeasts in orange juice (Casey and Dobson 2004) as well as in wine fermentations (Cocolin et al. 2001).

5.5. DGGE

Denaturing gradient gel electrophoresis (DGGE) is a promising technique that has been used for species identification and quantitation of yeast populations in foods and beverages. The technique is based on separation of DNA fragments of differing nucleotide sequences (e.g., species-specific), using the decreased electrophoretic mobility of partially melted double-stranded DNA amplicons in a polyacrylamide gel containing a linear gradient of DNA denaturants (i.e., a mixture of urea and formamide). A related technique is temperature gradient gel electrophoresis (TGGE), in which the gel gradient of DGGE is replaced by a temperature gradient (Muyzer and Smalla 1998). Recent applications of DGGE include identification and population dynamics of yeasts in sourdough bread (Meroth et al. 2003), in coffee fermentations (Masoud et al. 2004) and on wine grapes (Prakitchaiwattana et al. 2004). Levels of detection are often around 10^3 cfu/ml, but 10^2 cfu/ml have been reported, which compares favorably with standard plate count methods. Prakitchaiwattana et al. (2004) provided information on mixed species populations, noting that when the ratio of species is not greater than 10–100-fold, detection of individual species was possible, but if the ratio exceeds 100-fold, the low population species will not be detected. Masoud et al. (2004) and Prakitchaiwattana et al. (2004) reported detection of species by DGGE that were not recovered by plating, suggesting that some yeasts may establish significant populations in a product and then die.

5.6. Flow Cytometry

High throughput probe hybridization methods are available for detection of multiple species in multiple samples. One method that is effective for yeasts (Diaz and Fell 2004, Page and Kurtzman 2005) is an adaptation of the Luminex xMAP technology (Luminex Corp), which consists of a combination of 100 different sets of fluorescent beads covalently bound to species-specific DNA capture probes (Fig. 10.8). Upon hybridization, the beads bearing the target amplicons are classified in a flow cytometer by their spectral addresses with a 635 nm laser. The hybridized biotinylated amplicon is quantitated by fluorescence detection with a 532 nm laser. The multiplex assay is specific and fast; species that differ by 1 nucleotide often can be discriminated and the assay can be performed, after amplification, in less than 50 min in a 96-well format, with as many as 100 different species-specific probes per well. The advantage of this method for clinical, food quality and ecology laboratories is that multiple species can be identified quickly from multiple samples.

Luminex technology was employed by Diaz and Fell (2004) to develop a direct hybridization assay for high-throughput detection of *Trichosporon* spp. The assay used a set of 48 species-specific probes and 3 sets of primers, which were designed to amplify 3 different target regions of the rRNA gene: D1/D2 region, ITS and IGS. The assay was specific and enabled detection of 10^2 genome copies. This report, which was the first to adapt the technology for the detection of pathogenic yeasts, was expanded to an eight-plex hybridization array for the detection of the varieties and genotypes within the *Cr. neoformans* species complex (Diaz et al. 2005). The method, which employed a direct hybridization assay format, allowed discrimination of 1 bp mismatch with no apparent cross-reactivity, permitted the detection of 10^1 to 10^3 genome copies and allowed simultaneous detection of

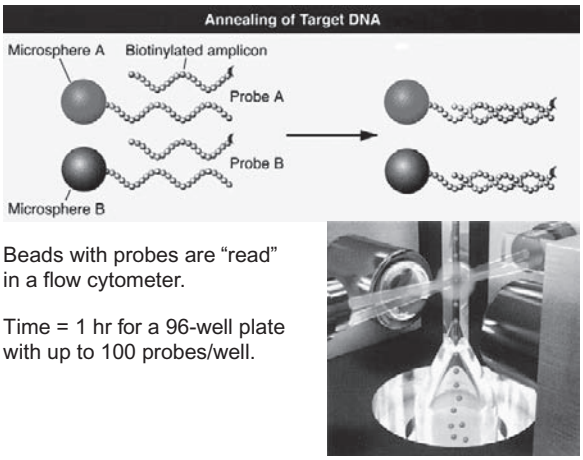


FIGURE 10.8 Overview of the Luminex flow cytometer system for rapid detection of species using species-specific oligonucleotides in a 96-well microtiter plate. See text for discussion. Figure from Diaz (2007)

multiple target sequences. Also the assay can be carried out directly with yeast cells or from isolated DNA. The described assay format was validated with a collection of environmental and clinical isolates (Bovers et al. 2007). The suspension array correctly identified the isolates at species and subspecies level. The results confirmed the identification of hybrid isolates which, according to flow cytometric profiles and cloning experiments, were classified as diploids or partial diploids. These hybrid isolates, which were found to contain two IGS 1 alleles, belonged to serotype AD or BD. Further adaptation of the technology was also documented for the detection of *Malassezia* species (Diaz et al. 2006a). In this particular study the authors designed an array comprising 16 sets of species-specific and multi-species-specific probes to identify recognized and newly emergent species within the genus.

5.7. Summary

The molecular detection methods just discussed have provided some remarkable capabilities for yeast identification, but a number of factors affect detection and quantitation. These include:

1. cellular copy number of the gene to be used,
2. whether the gene is sufficiently conserved to be PCR amplified by "universal" primers that will detect all species of interest,
3. efficiency of DNA extraction from cells in the sample,
4. efficiency of DNA recovery from the sample,
5. sample components that may interfere with DNA recovery or PCR amplification, and
6. level of cell population detectable.

In summary, rapid detection, accurate identification and quantitation of yeasts is now possible through use of a variety of molecular methods. Increased application of these methods will bring a greater degree of clarity to all questions in yeast microbiology, which previously was not possible when yeasts were identified from phenotype.

Chapter 11

Genome Sequences of Saccharomycotina: Resources and Applications in Phylogenomics

Elżbieta Rozpędowska, Jure Piškur and Kenneth H. Wolfe

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1. SUMMARY OF THE SEQUENCED YEAST GENOMES

Saccharomyces cerevisiae was the first yeast species, and indeed the first eukaryote, to have its complete genome sequenced. That milestone was achieved in 1996 by an international team of more than 600 scientists (Goffeau et al. 1996, 1997). In the years since then, the costs and technical difficulty of sequencing genomes have reduced dramatically, and at the time of writing (May 2008) more than 20 yeasts in the subphylum Saccharomycotina have had their genomes extensively sequenced and are publicly available (Table 11.1). This wealth of comparative genomics information substantially exceeds what is currently available for animals or plants, making the yeasts a model system for studying eukaryotic genome evolution (Piskur and Langkjaer 2004, Wolfe 2006). In this chapter we review the data that are currently available in yeast (Saccharomycotina) comparative genomics, and discuss how taxonomists can access and make use of these data.

1.1. Sequencing Strategies

Genomes can be sequenced to various levels of completion. It is relatively easy and inexpensive to obtain the sequence of the first 90% of a yeast genome, much harder to obtain the next 9% and almost impossible to obtain the final 1%. The "gold standard" is a sequence that spans every chromosome from telomere to telomere, with no gaps or ambiguities. The genome sequence of *S. cerevisiae* comes close to meeting this standard, but even for this species it has proved impossible (with current technology) to determine the complete sequence of the rDNA locus. This is a region of more than 1 million base pairs consisting of about 150 virtually identical copies of a 9-kilobase repeating unit that contains the ribosomal RNA (rRNA) genes (Ganley and Kobayashi 2007, Johnston et al. 1997). Some other Saccharomycotina genomes, such as those sequenced by the Génolevures program (Dujon et al. 2004) and the *Eremothecium (Ashbya) gossypii* genome (Dietrich et al. 2004), have also been finished to this standard. The term "finishing" refers to the process of designing strategies to close the remaining gaps in a genome sequence, a process that is not completely automated and involves considerable human effort.

An alternative strategy in genomics is whole-genome shotgun (WGS) sequencing without further finishing. This strategy saves much time and expense, but loses out in terms of the completeness of the information obtained. The completeness of a WGS project is often expressed as a coverage number such as 8× or 3× (Table 11.1). These numbers refer to the ratio of the number of nucleotides of raw sequence data collected to the estimated size of the genome; so 120 million base pairs (Mb) of raw data from a genome of 12 Mb in size corresponds to 10× coverage. The shotgun sequencing process involves "assembling" the raw data, by finding overlaps between individual sequence reads of random fragments of genomic DNA, in

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TABLE 11.1 Available Genome Sequence Data from Saccharomycotina Species (situation in early 2008)

Species	Strain	Coverage[a]	GenBank Annotated[b]	GenBank Unannotated[b]	Number of Contigs	Internet Site for Annotation[c]	Clade[d]	Reference/Genome Center
Saccharomyces cerevisiae	S288C	Complete	NC_001398–NC_001148		16	SGD	1	(Goffeau et al. 1996, 1997)
Saccharomyces cerevisiae	YJM789	10×		AAFW00000000	150	J. Stajich	1	(Gu et al. 2005)
Saccharomyces cerevisiae	RM11-1a	10×		AAEG00000000	115	Broad Inst.; J. Stajich	1	(Ruderfer et al. 2006)
Saccharomyces paradoxus	NRRL Y-17217	7.7×		AABY00000000	832	SGD FTP site; J. Stajich	1	(Kellis et al. 2003)
Saccharomyces mikatae	IFO 1815	5.9×		AABZ00000000	1648	SGD FTP site; J. Stajich	1	(Kellis et al. 2003)
Saccharomyces mikatae	IFO 1815	2.8×		AACH00000000	2808	SGD FTP site	1	(Cliften et al. 2003)
Saccharomyces kudriavzevii	IFO 1802	3.4×		AACI00000000	2029	SGD FTP site; J. Stajich	1	(Cliften et al. 2003)
Saccharomyces uvarum[e]	MCYC 623	6.4×		AACA00000000	1098	SGD FTP site	1	(Kellis et al. 2003)
Saccharomyces uvarum[e]	MCYC 623	2.9× + 6.4×		AACG00000000[f]	586	SGD FTP site; J. Stajich		(Cliften et al. 2003, Kellis et al. 2003)
Kazachstania exigua (= *Saccharomyces exiguus*)	CBS 379	GSS (0.2×)		AL407377–AL409955			2	(Bon et al. 2000)
Kazachstania servazzii (= *Saccharomyces servazzii*)	CBS 4311	GSS (0.2×)		AL402279–AL404848			2	(Casaregola et al. 2000)
Naumovozyma castellii (= *Saccharomyces castellii*)	NRRL Y-12630	3.9×		AACF00000000	570	SGD FTP site; YGOB site; J. Stajich	3	(Cliften et al. 2006)
Candida glabrata	CBS 138	Complete	NC_005967–NC_006036		13	Génolevures	4	(Dujon et al. 2004)
Nakaseomyces delphensis (= *Kluyveromyces delphensis*)	CBS 2170	GSS (0.4×)		BZ299346–BZ305583			4	(Wong et al. 2003)
Vanderwaltozyma polyspora (= *Kluyveromyces polysporus*)	DSMZ 70294	7.8×	DS480378–DS480658		281		6	(Scannell et al. 2007)
Zygosaccharomyces rouxii	CBS 732	GSS (0.4×)		AL392443–AL397138			7	(de Montigny et al. 2000a)
Lachancea waltii (= *Kluyveromyces waltii*)	NCYC 2644	8×		AADM00000000	713	*K. waltii* site at MIT	10	(Kellis et al. 2004)
Lachancea thermotolerans (= *Kluyveromyces thermotolerans*)	CBS 6340	GSS (0.2×)		AL419725–AL421896			10	(Malpertuy et al. 2000)
Lachancea kluyveri (= *Saccharomyces kluyveri*)	NRRL Y-12651	3.6×		AACE03000000[g]	30	SGD FTP site; J. Stajich	10	(Cliften et al. 2003)

Kluyveromyces lactis	NRRL Y-1140	Complete	NC_006037–NC_006042		6	Génolevures	11	(Dujon et al. 2004)
Kluyveromyces marxianus	CBS 712	GSS (0.2×)		AL424030–AL424880			11	(Llorente et al. 2000)
Eremothecium gossypii (= *Ashbya gossypii*)	ATCC 10895	Complete	NC_005782–NC_005788		7	AGD	12	(Dietrich et al. 2004)
Candida albicans	SC5314	7.1×	AACQ00000000		413		N/A	(Jones et al. 2004)
Candida albicans	WO-1	10×		AAFO00000000	86	Broad Inst.	N/A	MIT FGI
Candida dubliniensis	CD36	8×		(Sanger Institute website)		J. Stajich	N/A	Sanger Institute
Candida tropicalis	MYA-3404	10×		AAFN00000000	145	Broad Inst.; J. Stajich	N/A	MIT FGI
Candida parapsilosis	CDC isolate 317	9.2×		(Sanger Institute website)	143		N/A	Sanger Institute
Lodderomyces elongisporus	NRRL YB-4239	8.7×		AAPO00000000	145	Broad Inst.	N/A	MIT FGI
Meyerozyma (= *Pichia*) *guilliermondii* (anamorph *Candida guilliermondii*)	ATCC 6260	12×		AAFM00000000	71	Broad Inst.; J. Stajich	N/A	MIT FGI
Clavispora lusitaniae (= *Candida lusitaniae*)	ATCC 42720	9×		AAFT00000000	88	Broad Inst.; J. Stajich	N/A	MIT FGI
Debaryomyces hansenii	CBS 767	Complete	NC_006043–NC_006049		7	Génolevures	N/A	(Dujon et al. 2004)
Dekkera bruxellensis	CBS 2499	GSS (0.4×)		EI011584–EI026443			N/A	(Woolfit et al. 2007)
Ogataea polymorpha (= *Hansenula polymorpha*)	CBS 4732	GSS (0.4×)		AL430961–AL436044			N/A	(Blandin et al. 2000)
Millerozyma farinosa (= *Pichia sorbitophila*)	CBS 7064	GSS (0.4×)		AL414896–AL419724			N/A	(de Montigny et al. 2000b)
Scheffersomyces stipitis (= *Pichia stipitis*)	CBS 6054	Complete		(JGI website)	9	JGI website	N/A	Joint Genome Institute
Yarrowia lipolytica	CLIB 122	Complete	NC_006067–NC_006072		6	Génolevures	N/A	(Dujon et al. 2004)

[a] *Coverage is expressed as "complete", or as a fold coverage for WGS projects (data from http://www.ncbi.nlm.nih.gov/genomes/leuks.cgi) and GSS projects.*
[b] *Annotated sequences are included in the NR (nonredundant) database on the NCBI BLAST search website (Table 11.2), and proteins encoded by these sequences are included in the protein sequence databases. Unannotated sequences are not included in the NR (nonredundant) database on the NCBI BLAST search website. Instead, they are included in the WGS (Whole Genome Shotgun) or GSS (Genome Survey Sequencing) databases. Proteins encoded by these sequences do not appear in the protein sequence databases but can be found using TBLASTN searches.*
[c] *See Table 11.2 for Internet URLs.*
[d] *Clade number in Kurtzman and Robnett (2003) for species in the 'Saccharomyces complex' (Figure 11.1).*
[e] *Strain MCYC 623 (= CBS 7001 ex S. abuliensis Santa Maria) and its spore clone 623-6c which were sequenced by Cliften et al. (2003) and Kellis et al. (2003) are S. uvarum (Beijerinck) and not S. bayanus as they were called by the sequencing groups (Nguyen and Gaillardin 2005).*
[f] *GenBank accession number AACG00000000 is a composite assembly of the S. uvarum MCYC 623 genome, assembled by combining data from Cliften et al. (2003) and Kellis et al. (2003).*
[g] *The L. kluyveri data in GenBank accession number AACE03000000 has been updated since the original publication by Cliften et al. (2003), and the number of contigs has been reduced from 2381 to 30.*

order to form larger "contigs" of contiguous genomic sequence data. The higher the level of coverage, the larger the contigs are expected to be. For a yeast genome of around 12 Mb, 8×–10× coverage should result in many contigs that are hundred of kilobases long. Typically, such WGS projects will have difficulty assembling the sequences of regions that involve copies of repeated elements that are large and highly similar – such as Ty retroelements – and contigs may terminate at such repeats. It is not cost-effective to pursue a WGS strategy to coverage higher than about 10×, because at this level there should be relatively few remaining gaps in the genome. It is generally more efficient to switch to a directed finishing strategy than to continue sequencing random fragments. However, strategies of lower-coverage WGS are often used. Coverage of 3×–4×, as used by Cliften et al. (2003), detects about 80–90% of the genes in a genome, but the contigs are small (tens of kilobases) and many genes are only partially sequenced.

Very low coverage (0.2×–0.4×) WGS sequencing has been used to gain a preliminary glimpse of the genomes of many other yeast species (Table 11.1). This strategy is called Genome Survey Sequencing (GSS) or Random Sequence Tag (RST) sequencing. GSS data can often be assembled to obtain contigs that correspond to a consensus sequence of the rDNA repeat unit and any Ty-like elements (Neuveglise et al. 2002). GSS data can also be used (in conjunction with complete genome sequences from other species) to produce multi-gene phylogenies (Woolfit et al. 2007). It is important to note however, that GSS data, or even 3×–4× WGS data, do not allow firm conclusions to be drawn about whether a particular gene is absent from a genome.

Lastly, "next-generation" DNA sequencing, based on technologies other than the conventional Sanger method, seems poised to alter the landscape of fungal genomics dramatically over the next few years. These new technologies generate individual DNA sequencing reads that are much cheaper than Sanger sequencing, but also much shorter and more error-prone (Schuster 2008). Most of the applications of these technologies that have been published to date have been in "resequencing" projects, where data from additional strains or isolates are overlaid onto a reference (Sanger) genome sequence from the same species, allowing within-species polymorphism to be studied. The use of next-generation technology for *de novo* sequencing (i.e., where there is no reference sequence) was hampered by the short read lengths, but this obstacle has recently been overcome by the development of sequence-assembly software designed specifically for this purpose. Butler et al. (2008) recently reported software with the potential to assemble a yeast genome sequence almost completely from reads that are just 35 bp long, provided that the reads come in pairs from nearby regions of the genome.

1.2. Annotated and Unannotated Genomes

The process of identifying genes (and other functional elements) in a genome sequence is called annotation. The genome sequence of the *S. cerevisiae* laboratory strain S288c is one of the most comprehensively and accurately annotated genome sequences in existence. Curation of this annotation, and of any revisions to the nucleotide sequence (Fisk et al. 2006), is coordinated by the *Saccharomyces* Genome Database (SGD; Table 11.2). Protein-coding genes in *S. cerevisiae* have been assigned "systematic" names based on their locations in the genome, and 79% of them currently also have a "genetic" name based on an experimental result such as a mutant phenotype. For example, the gene for the major isoform of cytochrome *c* has the genetic name *CYC1* and the systematic name *YJR048W*. Genetic names are chosen by the laboratory that characterized the gene's function, usually consist of three letters followed by a number, and must have been described in a scientific publication in order to be valid (Fisk et al. 2006). The systematic nomenclature was introduced when the *S. cerevisiae* genome was sequenced and many completely uncharacterized genes were discovered. The cytochrome *c* gene's systematic name shows that it is a yeast gene (*Y*), located on chromosome X (*J*, the tenth letter of the alphabet), on the right arm of the chromosome (*R*), and it is the 48th gene on that arm, counting outwards from the centromere. The *W* indicates its transcriptional orientation: *W* ("Watson strand") genes are transcribed towards the chromosome's right telomere, and *C* ("Crick strand") genes are transcribed towards the left telomere.

A similar systematic nomenclature was used for genes in the *E. gossypii* genome (Dietrich et al. 2004); for example its cytochrome *c* gene is called *AFR360W*. The Génolevures project (Dujon et al. 2004, Sherman et al. 2006) used a different but still systematic approach to gene nomenclature for the four species it sequenced (Table 11.1): the *Kluyveromyces lactis* cytochrome *c* gene is called *KLLA0F16929g*, indicating a species acronym (*KLLA*), chromosome (*F*) and sequential gene number (16929).

Annotation of the *Candida albicans* (strain SC5314) genome has proved difficult, because the genome is diploid and there are many sequence differences between the alleles. The genome was sequenced by a WGS strategy that resulted in an assembly (called Assembly 19) that included pairs of allelic contigs for most of the

TABLE 11.2 Internet URLs for Saccharomycotina Yeast Genomics Resources

Resource	URL
Saccharomyces Genome Database (SGD)	http://www.yeastgenome.org/
Candida genome database (CGD)	http://www.candidagenome.org/
Comprehensive Yeast Genome Database (CYGD)	http://mips.gsf.de/genre/proj/yeast/
Génolevures database	http://www.genolevures.org
Ashbya Genome Database (AGD)	http://agd.vital-it.ch/
Yeast Gene Order Browser (YGOB)	http://wolfe.gen.tcd.ie/ygob/
GenBank database	http://www.ncbi.nlm.nih.gov/Genbank/
NCBI BLAST Server	http://www.ncbi.nlm.nih.gov/blast/
NCBI ORF Finder	http://www.ncbi.nlm.nih.gov/gorf/gorf.html
SGD FTP site	ftp://genome-ftp.stanford.edu/pub/yeast/sequence/fungal_genomes/
K. waltii site at MIT	http://www.broad.mit.edu/seq/YeastDuplication/
Broad Institute FGI	http://www.broad.mit.edu/annotation/fgi/
Jason Stajich's webpages	http://fungalgenomes.org
Sanger Institute website	http://www.sanger.ac.uk/Projects/Fungi/
JGI website	http://genome.jgi-psf.org

genome. The group at Stanford University (Jones et al. 2004) that sequenced this genome used a convention for contig numbering whereby allelic contigs have numbers that are 10,000 apart. For example, the two allelic cytochrome *c* genes are located on contigs Ctg19-10125 and Ctg19-20125. These two genes are named CaO19.1770 and CaO19.9339, where CaO19 means a *C. albicans* open reading frame in Assembly 19 (these are also called "orf19" names, for example orf19.1770). The numbers after the decimal point in these gene names are arbitrary and do not indicate the allelic relationship or the contig numbers. Several modifications to the annotation of the *C. albicans* SC5314 genome have been produced (e.g., Braun et al. 2005, d'Enfert et al. 2005) and the nomenclature conventions are summarized in Arnaud et al. (2007). A WGS sequence of a second *C. albicans* strain (WO-1) is also now available (Table 11.1).

Unfortunately, many of the other sequenced yeast genomes are not available in an annotated form through the GenBank nucleotide sequence database, although annotations for many of them are available elsewhere on the Internet (Tables 11.1 and 11.2). Yeast genome sequences in GenBank are placed in either the NR (non-redundant) or the WGS (whole-genome shotgun) divisions of the database. Sequences in the NR division are usually annotated (i.e., the locations of protein-coding genes within these sequences are indicated), but those in the WGS division usually are not. Consequently, the proteins encoded by sequences in the WGS division are not present in the protein sequence databases. This is a major flaw in the way that yeast sequences are currently presented in GenBank. Researchers who are interested in finding a particular gene in a particular genome can work around the problem by using a TBLASTN search at the NCBI BLAST website. Here they can locate the relevant contig in the WGS database, followed by using NCBI's ORF Finder to find the open reading frame corresponding to the gene (assuming that it has no introns; see Table 11.2 for URLs for these resources). Researchers who wish to download complete sets of proteins or genes from a genome are referred to the species-specific annotation sources listed in Table 11.1.

2. ONLINE RESOURCES FOR ACCESSING THE DATA

Internet URLs for some databases, both species-specific and comparative, that are of relevance to genome evolutionary studies are listed in Table 11.2.

***Saccharomyces* Genome Database** (SGD; Fisk et al. 2006, Nash et al. 2007) is a central website that is heavily used by the *S. cerevisiae* genetics and molecular biology community. It hosts a wealth of resources, including a page for each gene in the genome summarizing what is known about the gene, a list of the relevant journal articles, and links to other databases. SGD curates the annotation of the *S. cerevisiae* genome, and files containing up-to-date versions of the annotation and chromosome sequences can be downloaded from SGD's FTP site. The sequences and annotations of *Saccharomyces sensu stricto* species from Cliften et al. (2003) and Kellis et al. (2003) are distributed through SGD's FTP site (Table 11.2). SGD also hosts a Synteny Viewer that allows users to visually compare orthologous regions in the genomes of the *sensu stricto* species, using data from Kellis et al. (2003), and alignments of sequences among *Saccharomyces sensu stricto* species.

***Candida* Genome Database** (CGD; Arnaud et al. 2007) is a bioinformatics resource for *Candida albicans* data, closely modeled on SGD.

Comprehensive Yeast Genome Database at MIPS (Munich Information site for Protein Sequences; Guldener et al. 2005) also curates and distributes annotation and information about the *S. cerevisiae* genome. Widely-used information from the MIPS site includes a classification of *S. cerevisiae* genes by functional category, a protein–protein interaction database, archived data from high-throughput experiments, and curated information on mRNA splicing and particular protein families such as transporters and transcription factors.

Génolevures Database (Sherman et al. 2006) provides resources to support the genome sequences of the *K. lactis*, *C. glabrata*, *Debaryomyces hansenii* and *Yarrowia lipolytica* genomes (Dujon et al. 2004). The site distributes current annotation and sequences for each of these genomes. It also provides a browser for viewing genomic regions in a single species, with links to orthologous genes in other genomes sequenced by the Génolevures project, as well as to *S. cerevisiae*. It also distributes curated information on protein families in yeast species.

***Ashbya* Genome Database** (AGD) (Gattiker et al. 2007) distributes current annotation and a visual interface to the *E. gossypii* genome sequence. This site includes a Synteny browser that displays orthologous regions from the *S. cerevisiae* and *E. gossypii* genomes. Microarray data on gene expression in *E. gossypii* has recently become available through this site.

Yeast Gene Order Browser (Byrne and Wolfe 2005) provides an interface for comparing the order of homologous genes along chromosomes among species that underwent whole-genome duplication (*S. cerevisiae*, *Naumovozyma castellii*, *C. glabrata* and *Vanderwaltozyma polyspora*) and some that did not (*K. lactis*, *Lachancea waltii*, *L. kluyveri* and *E. gossypii*).

Jason Stajich's Webpages (Table 11.2) provide access to annotations of many of the sequenced genomes of yeasts and other fungi, in a uniform and convenient format.

3. GENE LOSSES, GAINS AND DUPLICATIONS

Genome sequencing projects have revealed that the Saccharomycotina species share a large common core of genes. Even though the sequences of these genes can, in some cases, be highly divergent, it is usually the case that a gene in one species will have an orthologue in another. In addition, the order of genes along the chromosomes is relatively well conserved among species (Byrne and Wolfe 2005). For example, the *S. cerevisiae* and *E. gossypii* genomes share 4,281 genes that are orthologous and syntenic (Dietrich et al. 2004).

Morphological or physiological differences among species can be the result of the gain or loss of genes, or are due to changes in gene regulation. As yet, we know relatively little about the evolution of gene regulation, although exciting progress has been made recently with particular regulatory pathways in yeasts (Martchenko et al. 2007, Tsong et al. 2006, Tuch et al. 2008). In contrast, evolutionary changes that have resulted in gene losses or gains can be documented more readily after genome sequencing. In many cases these changes in gene content correlate with metabolic differences among species (Table 11.3).

A major cause of differences in gene content and gene order among species is the whole-genome duplication (WGD) event that occurred during the evolution of one clade of Saccharomycotina (Figure 11.1). This event appears to have increased the number of chromosomes from 8 to 16. It transiently doubled the number of genes (from about 5000 to about 10,000), but one copy of most of these duplicated genes was lost quite quickly after this event, leaving the current *S. cerevisiae* genome with about 5500 genes, of which 1,102 are members of 551 duplicated gene pairs formed by the WGD event (Byrne and Wolfe 2005). The impact of the WGD on genome evolution has been recently reviewed elsewhere (Montcalm and Wolfe 2006, Wolfe 2006). The primary consequence of this process of genome duplication followed by extensive gene loss is the existence, in all the "post-WGD" species, of pairs of sister genomic

TABLE 11.3 Some Genes Gained and Lost During Saccharomycotina evolution

Gene(s)	Function	Gained/Lost	Species[a]	Reference
URA1	Uracil synthesis	Gained	Ancestor of clades 1−11	(Gojkovic et al. 2004, Hall et al. 2005)
HO	Endonuclease for mating-type switching	Gained	Ancestor of clades 1−7	(Butler et al. 2004)
DbHAD1	Adenyl deaminase	Gained	*Dekkera bruxellensis*	(Woolfit et al. 2007)
URA9	Uracil synthesis	Lost	*S. cerevisiae* and others	(Gojkovic et al. 2004, Hall et al. 2005)
PYD2 and PYD3	Uracil catabolism	Lost	Ancestor of clades 1−6	(Gojkovic et al. 2001)
7 *GAL* genes	Galactose catabolism	Lost	*S. kudriavzevii, C. glabrata, E. gossypii, L. waltii*	(Hittinger et al. 2004)
5 *BNA* genes	Nicotinic acid synthesis	Lost	*C. glabrata*	(Domergue et al. 2005)
6 Dynein/dynactin components	Mitotic spindle positioning	Lost	*V. polyspora*	(Scannell et al. 2007)
MATa2 gene	Positive regulator of a-specific genes	Lost	Ancestor of clades 1−6	(Tsong et al. 2006)
6 *DAL* genes	Allantoin catabolism	Lost	*C. glabrata, V. polyspora*	(Dujon et al. 2004, Scannell et al. 2007)
5 *ZMM* genes[b]	Synaptonemal complex proteins	Lost	*E. gossypii*	(Dietrich et al. 2004)

[a]*Clade numbers as in Kurtzman and Robnett (2003) for species in the 'Saccharomyces complex' (Figure 11.1).*
[b]*Five genes (ZIP1, ZIP2, ZIP3, MER3, MSH5) involved in meiosis and the synaptonemal complex. See Borner et al. (2004).*

regions that both contain subsets of the genes that are present in the single equivalent genomic region of any species that did not undergo the WGD.

The WGD also has important consequences for molecular systematics within the Saccharomycotina, for two reasons. First, after the WGD, many gene copies were subsequently lost, but the process of gene loss occurred simultaneously with lineage-splitting (Scannell et al. 2006). Consequently, some loci have undergone reciprocal gene loss, where the single copy of a gene that has been retained in one species is a paralogue, not an orthologue, of the single copy that has been retained in another species (Figure 11.2). Consequently, the divergence time between the remaining genes corresponds to the date of the WGD, and not to the time of divergence between the species. Secondly, gene duplication typically results in the acceleration of evolutionary rates. Some loci that have been retained as duplicates following the WGD show rates of sequence evolution that are both highly accelerated and highly asymmetric, with one gene copy evolving much faster than the other (Byrne and Wolfe 2007, Scannell and Wolfe 2008). These changes in rate can lead to incorrect inferences of phylogenetic history (Fares et al. 2006).

4. WHOLE-GENOME PHYLOGENETIC ANALYSIS

Comparison of gene sequences originating from different organisms has provided a useful tool to determine the phylogenetic relationships among them. However, this approach has some limitations (Petersen et al. 2000). One of the main questions puzzling yeast systematics researchers is how many sequences need to be analyzed to obtain reliable results. In the 1990s, fungal molecular phylogeny studies were limited by two factors: only a small number of genes had been sequenced, and from a small number of species. However, with the advent of genome projects over the past decade, we now have large numbers of gene sequences from a few species, both in the Saccharomycotina (Table 11.1) and more broadly among fungi (Fitzpatrick et al. 2006, Galagan et al. 2005b, Sunnerhagen and Piskur 2006). These data have helped to reconstruct the evolutionary and phylogenetic relationships among yeasts, and provided a background for the development of general phylogenetic tools applicable to other organisms.

4.1. Single Gene Sequences Versus Whole-Genome Sequences

The majority of phylogenetic studies have been performed on ribosomal DNA sequences, often using only a single gene or a very few genes (Petersen et al. 2000). The primary advantages of rDNA in phylogenetic studies are its universal presence in all taxa, and the ease with which it can be accessed for sequencing. A further advantage is that different rDNA gene regions with different evolutionary rates can be chosen as appropriate to address phylogenetic questions of differing depths; the 18S rRNA gene has a relatively slow rate and has been used in studies of the whole kingdom Fungi (e.g., Berbee and Taylor 1993), whereas the internal transcribed sequences (ITS) between the 18S and 26S RNA genes have a much faster rate and typically provide much better resolution within a genus than would the 18S RNA gene itself (e.g., Solieri et al. 2007). The D1/D2 domain of the 26S rRNA gene has an intermediate rate and has been used to great effect within the Saccharomycotina, initially on its own and later as one component of a multigene set (Kurtzman and Robnett 1998a, 2003).

In general, analysis of genes that are involved in processes that are vital to all organisms, e.g., components of the DNA replication, transcription or translation apparatus (such as rRNA) results in more robust phylogenetic reconstruction than does analysis of genes with more peripheral functions. However, it is very risky to use only one or a small number of genes for a single biochemical pathway. A single gene may not reflect the evolutionary history of the entire organism. For example, Figure 11.3 shows an example of three phylogenetic trees that attempt to place *Dekkera bruxellensis* among other yeasts, each based on a different single gene that is involved in carbon metabolism. As can be seen, the three genes yield three different tree topologies, making it impossible to reach a conclusion about the true position of *D. bruxellensis* from these data. Similarly,

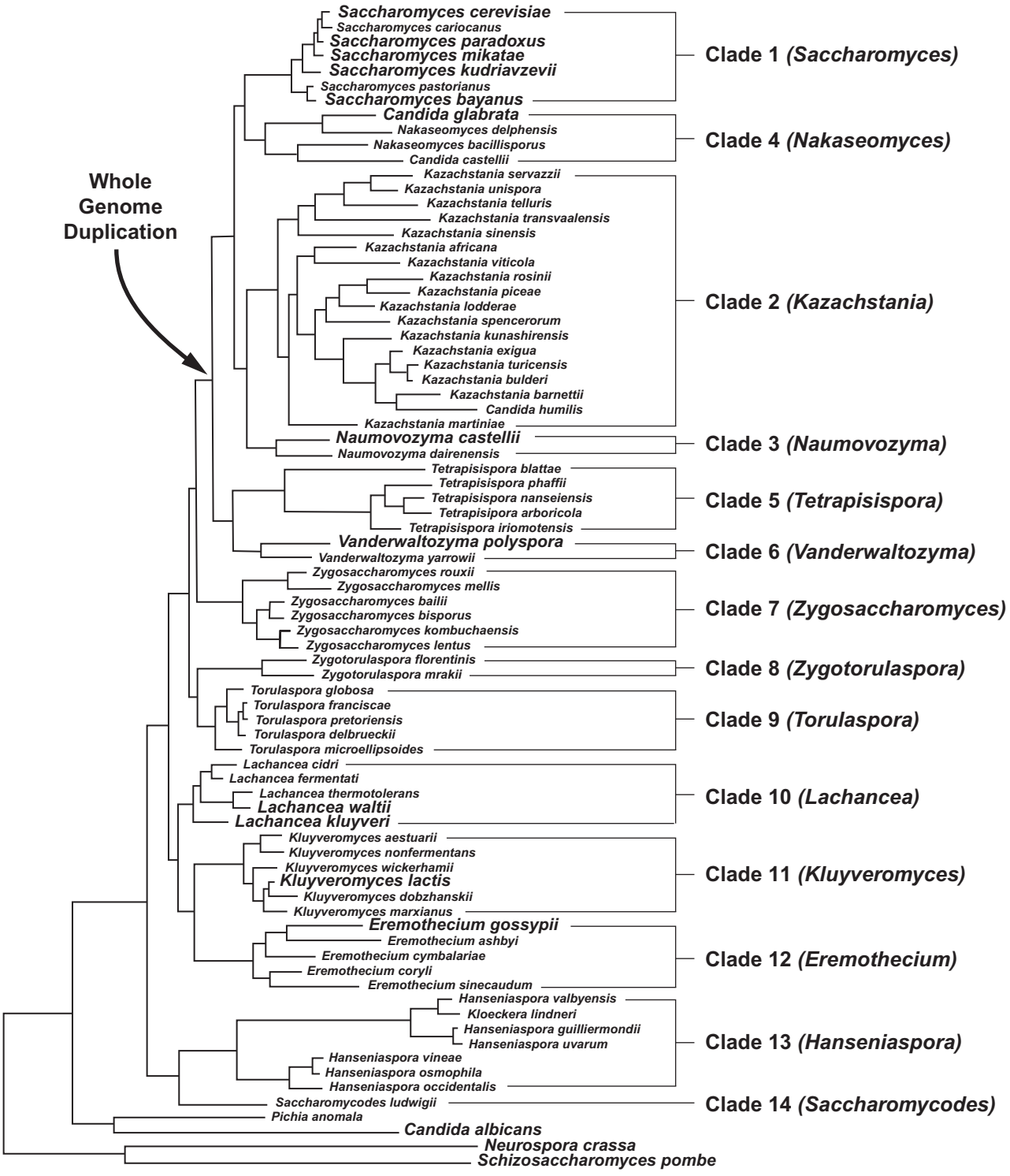


FIGURE 11.1 Phylogenetic tree of 14 clades in the "*Saccharomyces* complex". Species named in larger font are those for which complete or near-complete genome sequences are available (Table 11.1). The tree topology is from Hedtke et al.'s (2006) maximum likelihood analysis of eight genes, and differs slightly from Kurtzman and Robnett's maximum parsimony tree for the same dataset (Kurtzman 2003, Kurtzman and Robnett 2003). Clade numbering and revised genus names are from Kurtzman (2003).

Kuramae et al. (2006a) found that different genes gave conflicting, but individually well supported, placements of *Schizosaccharomyces pombe* within the tree of fungi.

Contradictory topologies could be due to the different evolutionary histories of individual sequences. Genes can, for example, be duplicated or horizontally transferred between organisms (Hall et al. 2005, Liti et al. 2006, Petersen et al. 2000, Woolfit et al. 2007), or the function of the corresponding products may have changed. Incongruence in phylogenetic analysis can also result from analytical factors. These include taxon sampling, choice of optimality criteria, or choice of an

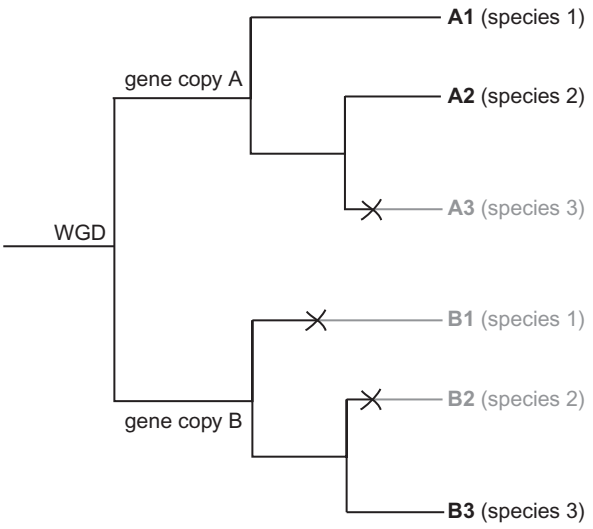


FIGURE 11.2 The process of reciprocal gene loss after whole-genome duplication (WGD). In this hypothetical example, genes A and B were formed by duplication in the WGD event. Species 1, 2 and 3 diverged after the WGD, and species 1 is an outgroup to species 2 and 3. Each species has retained only one member of the duplicated gene pair (X symbols and grey branches represent loss of a gene). The three surviving genes are A1, A2 and B3. A phylogenetic tree drawn from these three sequences under the assumption that they were orthologues would incorrectly show species 3 (gene B3) as an outgroup to species 1 and 2 (genes A1 and A2), and would overestimate the date of divergence between species 3 and the other two species.

incorrect model of sequence evolution (Delsuc et al. 2005, Rokas et al. 2003, Soltis et al. 2004). Moreover, single genes contain a limited number of nucleotide or amino acid sites, and therefore the resolution can be low. Using larger sets of genes tends to eliminate the incongruence in phylogenetic studies, as discussed below, but larger sets can also cause phylogenetic analyses to converge onto the wrong topology.

4.2. Multigene Concatenation

Concatenation of genes increases resolution and helps to resolve problematic nodes. Multigene phylogenetic analyses of data concatenated from several genes from a set of taxa, sequenced by polymerase chain reaction (PCR), have been used for several years (e.g., James et al. 2006, Kurtzman and Robnett 2003). Concatenation of much larger numbers of genes, obtained from genome projects, also holds much promise (Ciccarelli et al. 2006). The concatenation approach has the advantage of giving comparable branch lengths across the tree – because the set of genes is the same for the whole analysis – unlike supertree analysis (Fitzpatrick et al. 2006). Analysis of whole genomes also tends to overcome the problem of incorrect orthology annotation; even wrongly annotated genes will be "buffered" in the analysis if they are relatively rare, and stochastic error disappears when more genes are included in the analysis (Jeffroy et al. 2006). However, despite all these advantages, genome-wide concatenation poses a serious problem; namely, systematic error will not disappear with additional data (Jeffroy et al. 2006, Phillips et al. 2004). As the length of the sequences that are analyzed increases, the accumulation of errors may lead to strong support for a false inference (Delsuc et al. 2005, Fitzpatrick et al. 2006). Until the advent of whole-genome phylogenies, bootstrapping was widely assumed to indicate the degree of statistical support for a particular branch in a tree. In fact, the bootstrap value of a branch is merely an estimate of the probability that, if we had infinitely long sequences similar in type to the available data, the branch will continue to be found. Because genome sequences are large, trees derived from them will tend to have strong bootstrap support – but this does not necessarily mean that they are correct (Delsuc et al. 2005, Phillips et al. 2004). Jeffroy et al. (2006) comment that increasing the length of sequence analyzed tends to eliminate stochastic error (due to sampling of sites), but does not remove systematic errors such as those caused by nucleotide composition biases.

Genome-scale multigene phylogenetic analyses require automated approaches for identifying orthologous genes suitable for inclusion in a concatenated sequence alignment. This alignment is then used as the starting point for phylogenetic analysis. This task was first achieved in 2006 by two groups. Robbertse et al. (2006) concatenated 781 orthologous protein sets from 17 fungal species, while Kuramae et al. (2006b) used a concatenation of 531 proteins held in common by 21 fungi, with four animal and plant outgroups. Both of these studies used multiple methods of tree reconstruction (likelihood, distance and parsimony), and they both reported robust recovery of the expected clades, almost regardless of the phylogenetic method used. Both studies found monophyletic Saccharomycotina and Pezizomycotina clades. Robbertse et al. (2006) included 10 Pezizomycota genomes and recovered monophyletic Sordariomycete, Leotiomycete and Eurotiomycete clades among these (Figure 11.4). Kuramae et al. (2006b) included more Saccharomycotina genomes and recovered a topology similar to that of Kurtzman and Robnett's (2003) eight-gene analysis, except that *E. gossypii*, *K. lactis* and *L. kluyveri* formed a monophyletic group to the exclusion of the WGD clade (see below).

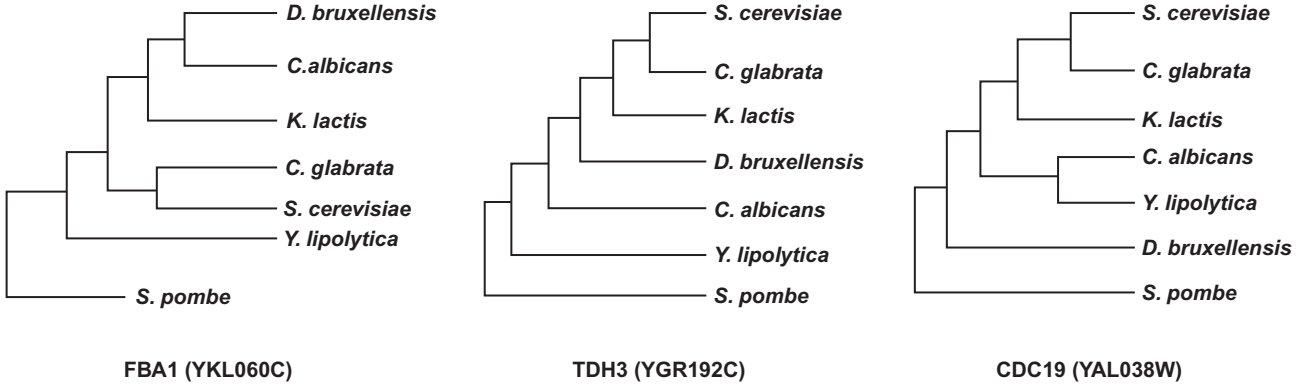


FIGURE 11.3 Single gene phylogenies derived from conserved genes involved in carbon metabolism. Three different genes result in three different tree topologies. All analyses are conducted using the same method, neighbor joining. Note the different positions of *D. bruxellensis*.

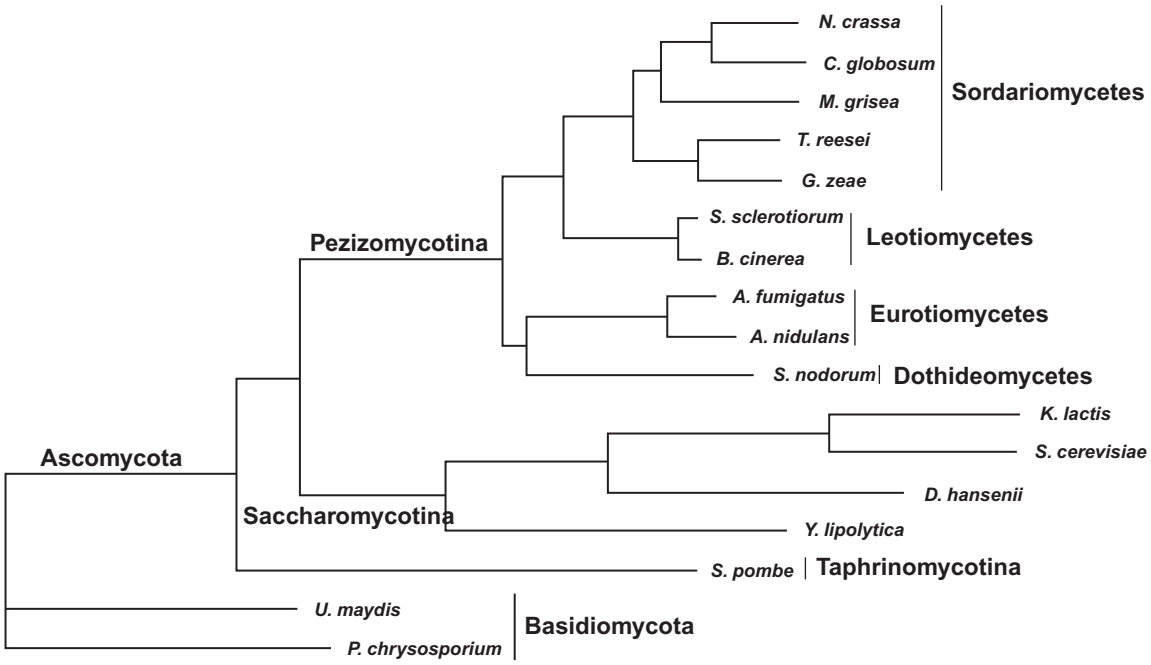


FIGURE 11.4 Phylogenetic relationship among Ascomycota, constructed from concatenated sequences of 781 genes from 17 species (modified from Robbertse et al. 2006). This topology was seen in maximum likelihood and neighbor-joining analyses, but the position of *S. nodorum* was different in maximum parsimony analysis (Robbertse et al. 2006).

4.3. Supertrees

Supertree analysis represents an alternative approach to reconstructing phylogenetic relationships. The input to this analysis is a set of single-gene trees, and the output is one or more phylogenetic trees which show relationships among all the taxa that were represented in the input trees. The set of taxa used for each input tree can overlap entirely or partially with the other input trees. In other words, each input tree must share at least two taxa with another tree used for the same supertree analysis (Fitzpatrick et al. 2006). Because the impact of individual trees on the final topology is limited, and conflicts within the data can be visualized, the supertree technique is becoming more popular. As an illustration of this approach, we recently used supertrees to study the question of the phylogenetic position of *D. bruxellensis*, as introduced above (Woolfit et al. 2007). The 396 single-gene trees indicated the presence of splits in the data, from which three alternative possible topologies could be inferred (Figure 11.5). Our subsequent analysis rejected one of these three topologies, but it was impossible to determine whether topology 1 or 2 represents the true evolutionary history of *D. bruxellensis* (Figure 11.5). Only further sequencing of the *Dekkera* group may help to resolve this problem.

Fitzpatrick et al. (2006) examined protein sequences from 42 sequenced fungal genomes, in order to resolve their phylogeny. In total 4,805 single trees were used for construction of supertrees by several different methods (Figure 11.6). For comparison, they also constructed a tree from a concatenation of the 153 genes that were universally present in all 42 taxa in their analysis. The trees are congruent with each other to high degree. Zygomycota, Basidiomycota and Ascomycota form separate branches. The grouping of Sordariomycetes and Leotiomycetes produced a high bootstrap value, and confirmed the results of Robbertse et al. (2006). Fitzpatrick et al. (2006) were also able to resolve the phylogeny of eight species in the "CTG clade" of Saccharomycotina, which includes *C. albicans*. These species all translate CTG codons as serine instead of leucine (Massey et al. 2003). For the CTG clade, Fitzpatrick et al. (2006) obtained well-resolved trees, that were congruent between supertree and concatenation methods, and which grouped the species into two clades, one sexual (*C. lusitaniae*, *C. guilliermondii*, *D. hansenii*) and one mostly asexual or cryptically sexual (*C. tropicalis*, *C. albicans*, *C. dubliniensis*, *C. parapsilosis* and *Lodderomyces elongisporus*).

Both Fitzpatrick et al. (2006) and Robbertse et al. (2006) found inconsistencies between different methods when studying the phylogenetic position of *Stagonospora nodorum*. The results obtained by the two groups using maximum likelihood analysis of concatenated data contradict each other: Robbertse et al. placed *S. nodorum* as sister to the Eurotiomycetes (Figure 11.4), whereas Fitzpatrick et al.'s tree of concatenated data (not shown) placed it as sister to the Sordariomycetes/Leotiomycetes clade. However, Fitzpatrick et al.'s supertree analyses (Figure 11.6) placed it in the former position, and maximum parsimony analysis by Robbertse et al. placed it in yet another position; outside both Eurotiomycetes and Sordariomycetes/Leotiomycetes. All of these alternative placements received close to 100% bootstrap support, which illustrates that a strong support value does not necessarily mean that the tree is correct (Delsuc et al. 2005).

Another puzzling discrepancy concerns the branching order in the whole-genome duplication (WGD) clade, even though this is one of the best studied groups of Saccharomycotina. The relationship among three major WGD lineages for which we have genome sequences (Clades 1, 3 and 4 in Figure 11.1) is controversial. A placement of *C. glabrata* as an outgroup to *N. castellii* and *S. cerevisiae* has been found in many analyses, including concatenation trees constructed by several methods (Hittinger et al. 2004, Jeffroy et al. 2006), supertree analyses (Fitzpatrick et al. 2006, Figure 11.6), and Kurtzman and Robnett's (2003) multigene parsimony analysis. This topology is sharply contradicted by the patterns of gene loss seen after WGD; the *C. glabrata* and *S. cerevisiae* genomes show far more shared losses of genes (*i.e.*, synapomorphies) than either of these species does with *N. castellii* (Scannell et al. 2006, 2007). A placement of *N. castellii* outside a *C. glabrata*–*S. cerevisiae* clade is also indicated by the pattern of shared rearrangements throughout the genome (J.L. Gordon and K.H. Wolfe, unpublished data), and the same

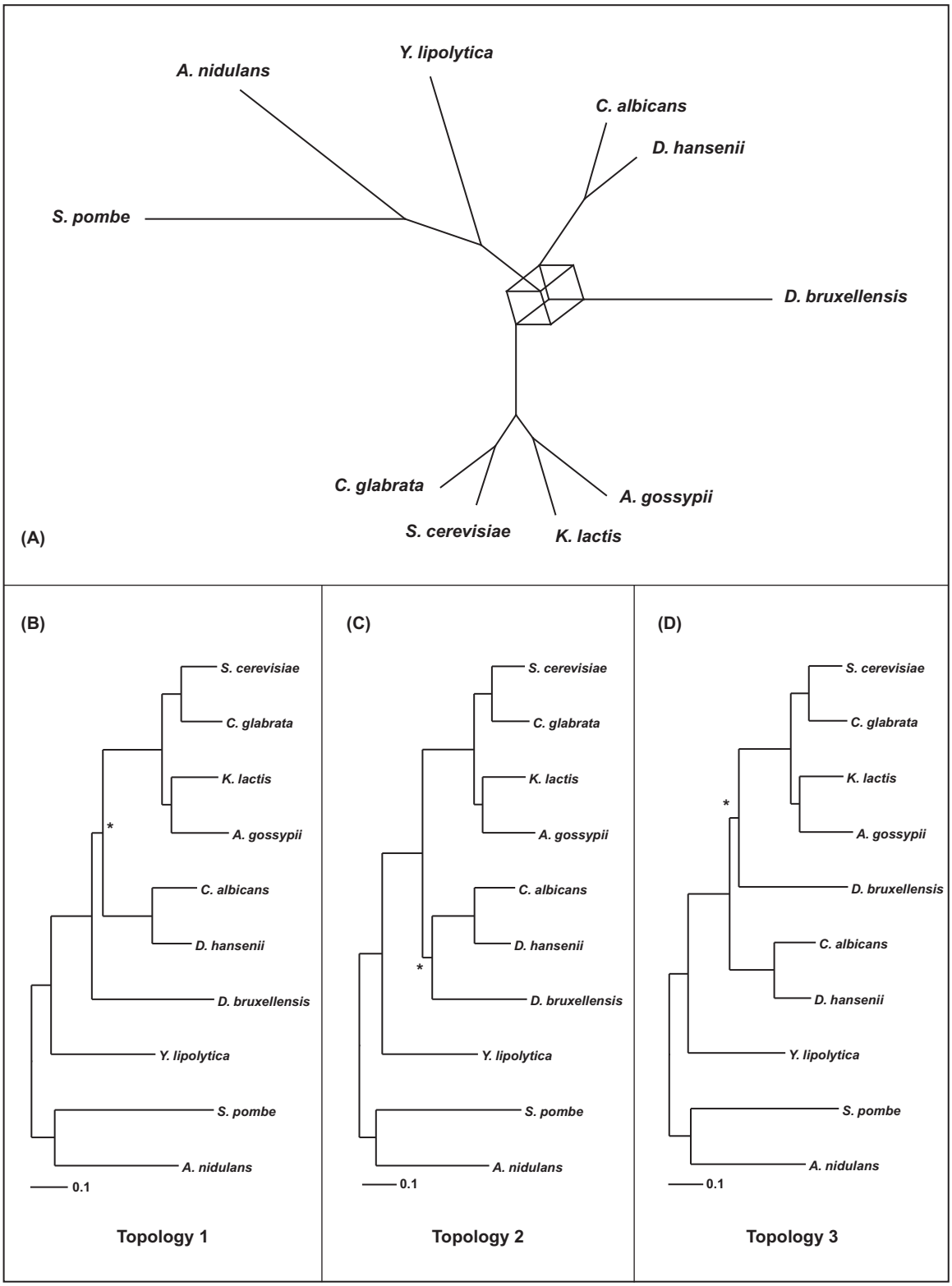


FIGURE 11.5 Phylogenetic position of the wine spoilage yeast *Dekkera bruxellensis*. (A) Phylogeny based on 396 genes showing splits in the data (side lengths in the cube are proportional to the number of individual trees supporting each topology). (B–D) Three topologies of *D. bruxellensis* inferred from the consensus network. Topology 1 was supported by 34% of the genes, topologies 2 and 3 by 27% and 26% of the genes, respectively. The Shimodaira-Hasegawa test was used in order to check whether the phylogenetic data statistically reject any of the topologies. Topology 3 was significantly rejected. Topology 2 fits best to the concatenated data but is not significantly better than Topology 1. From Woolfit et al. (2007).

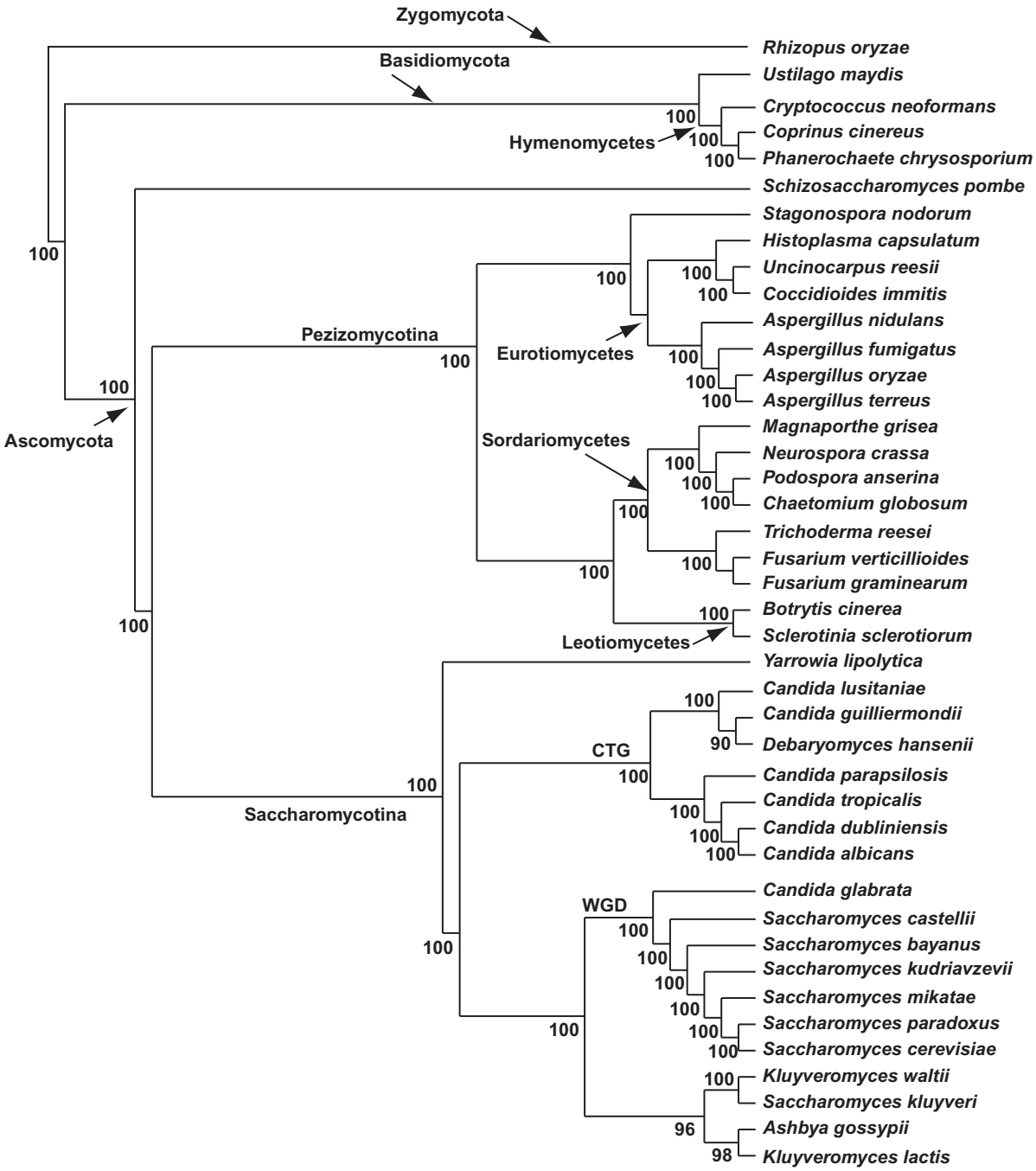


FIGURE 11.6 Supertree of 42 sequenced fungal genomes, derived from 4,805 individual gene trees (from Fitzpatrick et al. 2006). This supertree was produced by the MRP method. The WGD (whole-genome duplication) and CTG (genetic code change) clades of Saccharomycotina are marked.

branching order has been seen in some molecular phylogenies (maximum likelihood analysis of a concatenated set of 153 genes [Fitzpatrick et al. 2006], and maximum likelihood reanalysis of the Kurtzman and Robnett multigene dataset [Hedtke et al. 2006, Figure 11.1]). Scannell et al. (2006) suggested that an unknown artifact was causing misplacement of *C. glabrata* in molecular phylogenies, and showed that this was true for test cases that consisted of mixtures of orthologous and paralogous sequences, where the true phylogeny was known but was not recovered by any molecular phylogenetic method. This disparity between molecular sequence phylogenies and other types of phylogenetic information remains unresolved, and further exploration of this group of species may lead to methodological improvements.

4.4. Multigene Concatenation Versus Supertree Analysis

There exist many examples of incongruence between multigene concatenation-based phylogenies and supertree analyses. Just to mention one example, three groups (Fitzpatrick et al. 2006, Hittinger et al. 2004, Jeffroy et al. 2006) have attempted to use whole-genome data to resolve the phylogenetic relationships among the four species

L. waltii, *L. kluyveri*, *K. lactis* and *E. gossypii* (Clades 10–12 in Figure 11.1), and the placement of the WGD clade (Clades 1–6) relative to these four. Two of the studies even used the same dataset of 106 genes (Hittinger et al. 2004, Jeffroy et al. 2006). The topology (WGD, [(*L. kluyveri*, *L. waltii*), (*K. lactis*, *E. gossypii*)]) is the one most often supported in different studies. It was obtained using a maximum likelihood method on concatenated amino acid sequence data for 153 genes (Fitzpatrick et al. 2006), by using either Bayesian Inference or maximum parsimony on concatenated amino acid data of 106 genes once fast-evolving sites were removed (Jeffroy et al. 2006), and in some supertree approaches (Fitzpatrick et al. 2006). However, a different supertree method used by Fitzpatrick et al. (2006) gave the topology ((*K. lactis*, *E. gossypii*), [WGD, (*L. kluyveri*, *L. waltii*)]). Jeffroy et al. (2006) showed that other trees were obtained if nucleotide data were used instead of amino acid data, and showed that those other trees were likely to be erroneous, due to the large variation in nucleotide composition among these genomes (ranging from 27% G + C at codon third positions in *C. albicans* to 68% in *Y. lipolytica*). Hittinger et al. (2004) used a concatenation of the 106 genes and proposed the topology (WGD, *K. lactis*, [*L. kluyveri*, (*L. waltii*, *E. gossypii*)]), which includes a trichotomy. They commented that they found different placements of *K. lactis* and *E. gossypii* relative to the other species, depending on the phylogenetic method (maximum parsimony versus maximum likelihood) used, and on whether nucleotide or amino acid sequences were considered. From this example one might conclude that in addition to the incongruence among genes, there also exists significant incongruence among methods.

Dutilh et al. (2007) compared several automated approaches to fungal phylogenomics, exploring numerous alternative methods for orthologue identification and multigene phylogenetic reconstruction. They evaluated the performance of different methods according to how well they recovered the nodes of a "gold standard" fungal topology, which was essentially a consensus derived from previously published phylogenetic analyses. This approach strikes us as somewhat circular, and we note that it has the effect of penalizing any method that manages to overcome artifacts existing in the published studies (for example, their "gold standard" tree included the questionable placement of *C. glabrata* outside *N. castellii* and *S. cerevisiae* discussed above). Nevertheless, Dutilh et al.'s work provides a useful systematic overview of different approaches, and emphasizes how they can be categorized (as superalignments, superdistances, or supertrees) in terms of the point in the process at which they make the switch from a phylogenetic to a phylogenomic methodology. One clear conclusion from Dutilh et al.'s study is that methods which are based on the extent of shared gene content do not work well for fungi; they tend to reflect similarity of niche as opposed to shared ancestry.

5. TAXON SAMPLING: MORE GENES OR MORE SPECIES?

What is the minimal number of genes that needs to be analyzed in order to obtain a congruent tree? The answer obviously depends on the particular tree that is in question, but this answer is of little help to scientists who are trying to design PCR-based multigene phylogenetic studies. They would like to know in advance how many genes they should sequence. Rokas et al. (2003) suggested that, for *Saccharomyces* species, the number is 20. They analyzed 106 genes from eight yeast species in Clades 1–11 with *C. albicans* as an outgroup; these species have a divergence time of perhaps 100–150 million years since their separation from a common progenitor. The authors ran sequential phylogenetic analyses (by multiple methods) with concatenations of decreasing numbers of genes. The trees obtained stabilized if 20 or more genes were used in the analysis, whereas lower numbers of genes generated conflicting trees.

Further analysis by Rokas and Carroll (2005), using subsets of a data matrix containing 106 genes from 14 yeast species, suggested that increasing the number of genes has a strong positive effect on phylogenetic accuracy, whereas increasing the number of taxa correlates with a slight decrease in accuracy. They repeated the same procedure on mammalian and angiosperm data matrices and found the same result. In contrast, Brinkmann et al. (2005), Delsuc et al. (2005), Hedtke et al. (2006) and Philippe et al. (2005) all claimed that increasing the number of taxa will help to detect multiple substitutions and, therefore, increase the accuracy of the phylogenetic analysis. Nucleotide sites that are uninformative or homoplasic in analyses of small numbers of taxa can become informative at multiple nodes if more taxa are added (Soltis et al. 2004). Adding more genes also improves the accuracy, but at a much slower rate (Graybeal 1998). In an interesting study that used simulated data for 106 genes and 79 taxa, Hedtke et al. (2006) considered a particular quartet of species that was susceptible to the long-branch attraction artifact. They showed that as the number of genes was increased, the relative branching order of these four species stabilized (i.e., the bootstrap value for the central branch in the four-species subtree increased). However, depending on the number of other taxa included in the analysis, the results either converged onto a correct topology (if 40 taxa were included) or onto an incorrect topology (if only 4 taxa were included). The more other taxa that were included, the higher the bootstrap support that was seen for the true branching order of these four species.

Without a doubt the results of genome projects have accelerated the scope of phylogenetic analyses. It is clear that single-gene phylogenies often have difficulty correctly resolving the relationships among taxa, and that the analysis of much larger datasets holds much promise. For the near future, the question arises: should phylogenetic studies be based on the analysis of complete genome sequences from relatively few taxa, or should we instead use a limited number of genes from many more species?

The importance of taxon sampling has been demonstrated by two recent controversies from other areas of systematics. The first concerns the phylogenetic position of the dicot plant *Amborella trichopoda* in relation to other angiosperms. This concern might seem like a "storm in a teacup" among plant taxonomists, but the issues it raises have broader implications about the value and utility of genome sequences in systematics (Lockhart and Penny 2005). In 1999–2000, several independent multigene phylogenetic studies reached the same conclusion; *Amborella* was a sister taxon to all other angiosperms, and so was an outgroup to both monocots and the remaining dicots (eudicots). Nine such studies, using 1–17 genes each, reported this placement with strong bootstrap values (summarized in Stefanovic et al. 2004). This consensus was shattered when Goremykin et al. (2003) sequenced the complete chloroplast genome of *Amborella,* and reported that a phylogenetic analysis of 61 genes from chloroplast genomes of the 13 other angiosperms then available consistently and with high bootstrap support showed monocots, not *Amborella*, to be the most basal angiosperms. In response, Stefanovic et al. (2004) and Soltis et al. (2004) argued that Goremykin et al.'s study did not include enough taxa, that their use of three fast-evolving grass species as the only representatives of monocots, and their choice of sequence evolution models, all made their conclusion questionable. Further analyses that included more taxa but smaller numbers of genes continued to show *Amborella* as basal (Soltis et al. 2004, Stefanovic et al. 2004), but which of the competing trees is the true one continues to be debated (Lockhart and Penny 2005, Martin et al. 2005).

The second controversy about taxon sampling concerns Rokas et al.'s (2005) analysis of metazoan phylogeny, which used approximately 50 genes from 17 animal species, with fungi as an outgroup. Rokas et al. were unable to resolve most nodes of the phylogenetic

tree of metazoa (despite good resolution of the fungal clade, which had similar levels of sequence divergence), leading them to propose that a rapid radiation of animal lineages had occurred. Their conclusion was criticized by Baurain et al. (2007), who showed that most of the problematic nodes in Rokas et al.'s study could be resolved if three steps were taken:

(i) increase the number of species (to 56 instead of 17);
(ii) replace some fast-evolving taxa with slower-evolving ones; and
(iii) use a better model of sequence evolution. In this way, "nonphylogenetic" signals in the data are minimized, permitting the underlying phylogenetic signal to be detected.

In both of these illustrations, the debate centers on whether an analysis with more nucleotide sites but fewer taxa (i.e., one based on complete genome sequences) is preferable to one with fewer sites but more taxa. In the *Amborella* example the genome-based tree was well resolved but probably incorrect, and increasing the taxon sampling (at the expense of losing some nucleotide sites) changed the topology. In contrast, in the vertebrates example the genome-based tree was poorly resolved, and increasing the taxon sampling added resolution. One positive outcome from these debates has been the increased awareness of the distinction between stochastic and systematic error in phylogenetic analysis (Delsuc et al. 2005), and the realization that analyses based on genome-scale nucleotide datasets are likely to have low incongruence and high bootstrap values because stochastic error has been eliminated, but systematic error can still remain (Phillips et al. 2004). Careful choice of taxa, so as to represent as much diversity within the groups under study as possible, but to avoid taxa that have highly accelerated rates of molecular evolution or biased nucleotide compositions, is very important (Delsuc et al. 2005). The best taxa will not necessarily be those species whose genomes have been sequenced. As Soltis et al. (2004) comment,

> *The systematics community must be careful that we are not blinded by genomics; complete genome data by themselves are not the panacea for phylogeny reconstruction.*

These results show clearly that if more taxa are used for a study, fewer genes can be used. However, the minimum numbers necessary for the analysis cannot be generalized, and will depend on the particular set of species and genes under consideration. For simple phylogenetic problems a few genes and a few taxa are sufficient. For more complicated phylogenetic relationships, an increasing taxon representation improves the accuracy more effectively than increasing the gene number. On the other hand, there is an increasing recognition among the genomics community that the genomes chosen for sequencing should reflect the extant diversity of species, and not solely be focused on species of economic or medical importance (Galagan et al. 2005b). This raises the question of how, if we decide to sequence whole genomes, to select the "best" organisms for sequencing. Future emphasis should be placed on the development of more objective methods for species choice in genome projects, as well as on improved models of sequence evolution.

5.1. Complete Genome Sequence Reports Received too Late for Inclusion in this Chapter

Candida albicans (strain WO-1). *Candida tropicalis*, *Candida parapsilosis*, *Candida guilliermondii*, *Clavispora lusitaniae*, and *Lodderomyces elongisporus* (Butler et al. 2009).

Lachancea kluyveri, *Lachancea thermotolerans*, and *Zygosaccharomyces rouxii* (Souciet et al. 2009).

Komagataella (Pichia) pastoris (de Schutter et al. 2009).

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Chapter 12

Molecular Phylogenetic Reconstruction

Michael Weiß and Markus Göker

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1. INTRODUCTION

Molecular phylogenetic reconstruction has become the decisive tool in systematics and taxonomy, and began to be used for yeasts earlier than in any other eukaryotic group. The approach is straightforward in a discipline of systematic biology where living strains are preserved for each described species, and morphological characters that delimit species are sparse. Today, at least partial rDNA sequences are available for each described yeast species. The first sequenced genome of a eukaryote was that of *Saccharomyces cerevisiae*, and subsequently, more genomes have been sequenced in ascomycetous yeasts than for any other group of eukaryotes, making these organisms the most intensively studied group in phylogenomics.

In the following chapter we give an overview of the principles of the various methods that are now available for molecular phylogenetic reconstruction. Our descriptions are focused on DNA analyses, though phylogenetic analyses of amino acid sequences and other kinds of molecular data are also feasible (see the remarks in section 9).

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This chapter is not a substitute for a detailed textbook treatment of the methods. For more detail, an introductory text is provided by the book by Page and Holmes (1998); a broader introduction into molecular phylogenetics can be found in Swofford et al. (1996); the book by Felsenstein (2004) is a comprehensive overview of the state of the art, which also includes an excellent survey of the history of the rapidly evolving field of molecular phylogenetics.

2. PHYLOGENETIC TREES AND NETWORKS

Phylogenetic hypotheses are most frequently illustrated in tree-shaped graphs, consisting of *nodes* (which represent species), and *branches* (which determine the ancestor relationships). Terminal nodes of a tree (also called the *leaves* or the *tips* of a tree) represent the extant species, from which the molecular sequences were derived; inner nodes represent hypothetical ancestral species. To hypothesize that a group of species forms a monophyletic clade, it is crucial that the tree is *rooted* (e.g., Fig. 12.1); that is, it contains one node which represents the oldest ancestral species involved. However, most of the methods of molecular phylogenetic inference that are used today yield *unrooted* trees (e.g., Fig. 12.2). Unrooted trees are most often rooted by inclusion of one or more *outgroup species* (species that do not belong to the group of interest, e.g., species I in Fig. 12.1) in the phylogenetic analysis. For rooting purposes, outgroup species must be phylogenetically separate from the taxa studied, but ideally the outgroup sequences should not be so distant as to cause problems in sequence alignment. Running molecular phylogenetic analyses with and without outgroup sequences is recommended (Bergsten 2005), in order to become aware of possible artifacts that may be caused by long-branch attraction (see section 5.1).

Each branch of a tree induces a *split* (bipartition) of the set of terminal taxa included in the phylogenetic analysis, and a tree can be completely reconstructed from the set of all possible splits that it induces. A set of splits that can be represented by a tree is called *compatible*. Non-compatible splits can be represented by a generalization of a phylogenetic tree called a *splits network* (Fig. 12.3). In such a network each bunch of parallel branches corresponds to one of the underlying splits (which can be visualized by cutting the network through these branches).

The branching pattern of a tree or phylogenetic network is also referred to as the *topology* of the tree or network. A phylogenetic tree can be viewed as a topology plus information detailing the amount of evolutionary change between the taxa involved. This is usually expressed by assigning weights to the branches (*branch lengths*), which may be done in various ways (see below). The graphical visualization of a tree in this strict sense is called a *phylogram* (Fig. 12.1A), and the graphical representation of a topology is called a *cladogram* (Fig. 12.1B). In a broader sense topologies are also often referred to as trees in the literature. In the following parts of this review we will use "tree" in this relaxed sense.

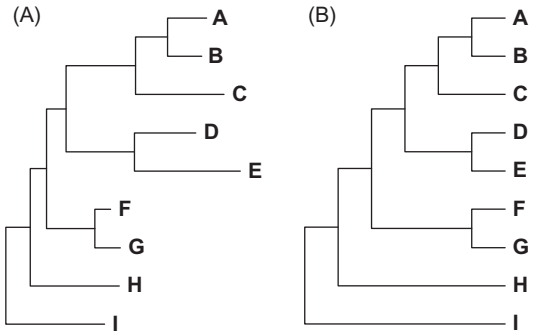


FIGURE 12.1 Rooted trees. (A) Rooted phylogram. (B) Rooted cladogram.

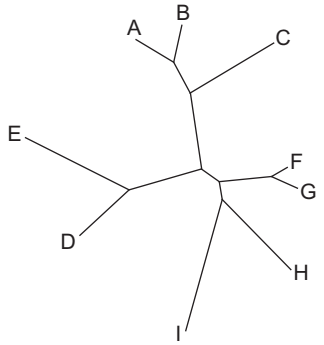


FIGURE 12.2 Unrooted phylogram.

2.1. The Number of Dichotomic Topologies

As the number of terminal nodes (i.e., the number of terminal taxa included in a phylogenetic analysis) increases, the number of possible dichotomic trees increases overexponentially; if n denotes the number of terminal taxa, there are

$$\frac{(2n-3)!}{2^{n-2}(n-2)!}$$

distinct rooted dichotomous topologies (Felsenstein 1978). Thus, for only 10 terminal taxa there are already 34,459,425 topologies, for 20 terminal taxa 8,200,794,532,637,891,559,375, and for 50 taxa ca 2.75292×10^{76} distinct rooted topologies (Felsenstein 2004)! This is a serious problem for phylogenetic reconstruction, since some of the methods commonly employed use optimality criteria to screen the tree space for a best tree. Given the huge number of possible tree topologies, this optimization problem cannot be solved exactly, and heuristic methods have to be employed (see section 8).

2.2. Consensus Trees, Consensus Networks and Supertrees

2.2.1. Consensus Trees and Networks

If some kind of phylogenetic analysis yields multiple trees that all include the same taxon sampling, part of this information can be extracted and visualized in a *consensus tree*. The types most often

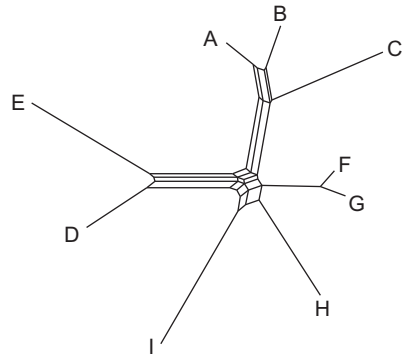


FIGURE 12.3 Splits network. The splits (i.e., the bipartitions of the taxon set) contained in this graph can be retrieved by cutting the graph along parallel edges.

used are the *strict consensus* and the *majority-rule consensus*. A majority-rule consensus tree (Margush and McMorris 1981) includes exactly those groups (bipartitions of the set of taxa, if unrooted trees are considered) that are contained in more than 50 percent of the source trees. There is also a unique p% consensus tree for each percentage $p > 50$, that includes exactly the groups or bipartitions present in more than p percent of the source trees. For $p = 100$, this yields the *strict consensus*, a tree that contains exactly those groups/bipartitions that are present in all source trees.

Principally, branch length information of source trees can also be represented in a consensus tree or network (e.g., using mean values). If this is not an option in the software used, branch lengths can be estimated separately for the consensus topology, with the same optimality criterion that was used for the derivation of the source trees. Lapointe and Cucumel (1997) suggest a procedure in which branch lengths of the original trees are used directly to derive a consensus tree.

A unique p% consensus does not usually exist for percentages $p < 50$, since conflicting bipartitions cannot be integrated into a single tree topology. It is however possible to include compatible groupings with lower frequencies into a majority-rule consensus. Conflicting groupings can be represented in a consensus network (Bandelt 1995, Holland et al. 2004, Huson and Bryant 2006). Fig. 12.4 illustrates the consensus types discussed here.

2.2.2. Supertrees and Supernetworks

The consensus techniques described above cannot be directly applied in cases where the input trees deviate in their taxon samplings (perhaps because some genes in a multi-gene analysis could not be sequenced for all the studied taxa). In this case a *supertree* approach can be used to construct a single tree that is maximally compatible with all the partial input trees (e.g., Bininda-Emonds 2004). The MRP approach (matrix representation with parsimony; Baum 1992, Ragan 1992) is a widely-adopted way of computing a supertree from a set of partial trees. Here, the phylogenetic information of the partial trees is extracted into a 0/1 character matrix, by transforming each split (see above) of a partial tree into one column (assigning 0 to the taxa of one subset and 1 to the taxa of the complementary subset). The empty entries of this matrix (which correspond to the taxa that are not contained in a certain tree) are interpreted as missing data. This character matrix is then analyzed using the maximum parsimony criterion (see section 5) to find an optimal tree for the whole taxon sampling. A generalization of the supertree approach to phylogenetic networks was developed by Huson et al. (2004).

3. ALIGNMENTS

The vast majority of methods for molecular phylogenetic analysis require that a multiple alignment (i.e., an estimate of homologous nucleotides between the sequences) has been constructed from the sequence data. While the sequences are still aligned manually in many phylogenetic studies, several authors have cautioned against this strategy (Gatesy et al. 1993, Giribet et al. 2002; see also Thorne et al. 1991). To align sequence data reproducibly, several methods have been proposed.

The principle of the still most widely used method, ClustalW (Thompson et al. 1997) is as follows. First, the sequences are aligned pairwise. Genetic distances are then calculated from these alignments, and these are used to construct a neighbor-joining tree (see section 4.6). Following the topology of this guide tree from the tips to the backbone, the sequences are subsequently aligned in blocks (*profiles*) until a multiple alignment results. In recent years, a number of alignment algorithms have been developed that considerably outperform ClustalW regarding both speed and accuracy. Examples are MAFFT (Katoh et al. 2002, 2005), MUSCLE (Edgar 2004), and POA (Lee et al. 2002). In some of these approaches (e.g., Edgar 2004, Katoh et al. 2002, 2005) the final multiple alignment results from iterative refinement. Using a novel internal representation of aligned

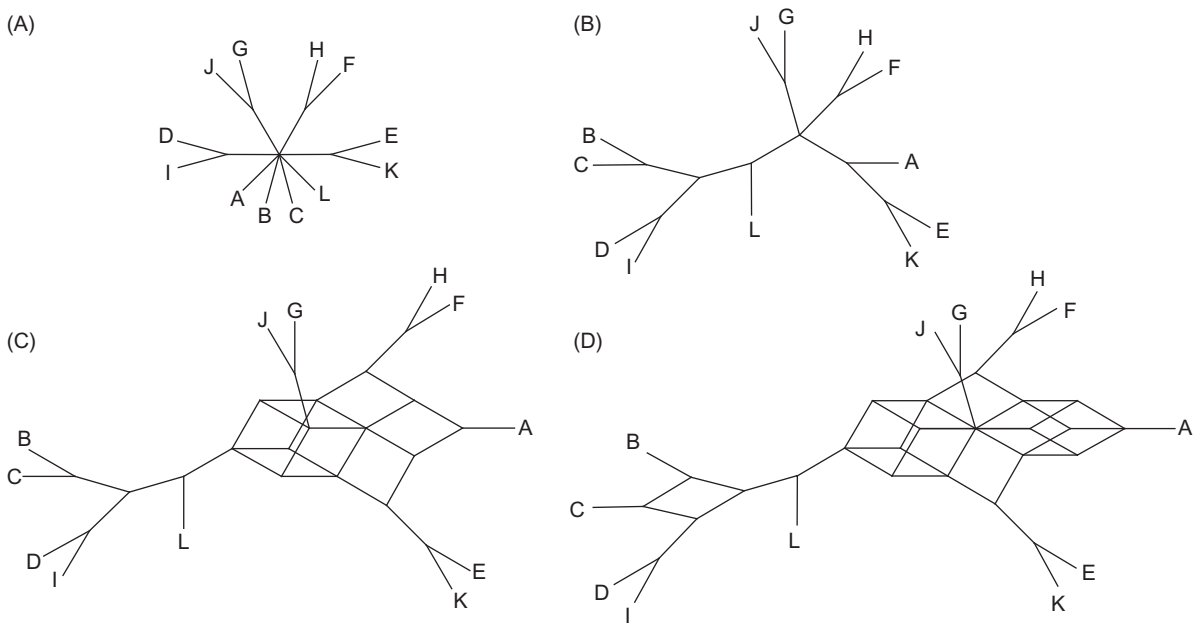


FIGURE 12.4 Consensus trees computed from a set of 1,000 trees resulting from some phylogenetic analysis. (A) Strict consensus: the tree that contains those splits (i.e., bipartitions of the taxon set) that occur in each of the source trees. (B) Majority-rule consensus: the tree that shows all splits that occur in more than 50% of the source trees. (C) Consensus network containing all the splits that occur in more than 20% of the source trees. (D) Consensus network containing all the splits that occur in more than 10% of the source trees. Splits of the consensus networks can be retrieved by cutting along parallel edges.

sequences, POA (Lee et al. 2002) can achieve comparable accuracy by linearly aligning sequences in input order. DIALIGN (Morgenstern et al. 1999) may be preferable if sequences are only locally related (see next passage).

Often much more effort is put into performing phylogenetic analyses on an alignment than into constructing the sequence alignment itself. If variation among sequences is high, an unambiguous whole-length alignment may not be possible; in particular if rDNA sequences are used, since a reading frame which is useful in aligning protein-coding DNA sequences is missing. This is unfortunate, since it has been demonstrated that sequence alignment can have a greater influence on the results of a molecular phylogenetic analysis than the particular tree-building method chosen (e.g., Kemler et al. 2006, Morrison and Ellis 1997).

For difficult alignments, it may thus be appropriate to exclude ambiguously alignable characters. Several methods, which do so in a reproducible or even automated manner, have been proposed (e.g., Castresana 2000, Gatesy et al. 1993, Kemler et al. 2006, Talavera and Castresana 2007); however, valuable information may be discarded if these strategies are followed. Alternatively, several alignments of the same set of sequences – produced by either different software, or different alignment parameters – may be analyzed separately, and the resultant trees then compared. Groups of sequences that are consistently supported by all alignment variants may be considered as being reliably resolved by the data (Lee 2001). Concatenation of the alignment variants has also been proposed as a proper basis for phylogenetic analysis (Wheeler et al. 1995).

	A	B	C	D	E	F
B	0.0519					
C	0.0624	0.0814				
D	0.0536	0.0662	0.0625			
E	0.0558	0.0757	0.0559	0.0187		
F	0.0496	**0.0636**	0.0495	0.0328	0.0400	
G	0.0112	0.0571	0.0664	0.0560	0.0582	0.0507

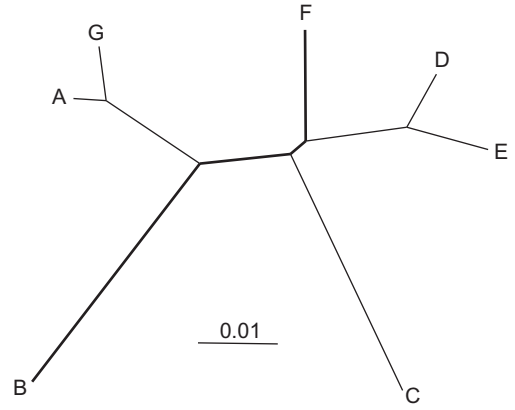


FIGURE 12.5 Principle of distance methods. In a first step, a distance matrix is computed which includes all pairwise distances between the taxa, derived from the data (i.e., an alignment of DNA sequences). Then, a phylogenetic hypothesis is derived by searching for a tree (or a network) that optimally reflects the distance matrix, i.e., a tree in which the path between two taxa in the tree is close to the genetic distance of these taxa.

4. DISTANCE-BASED METHODS

The main principle of distance-based methods for phylogenetic reconstruction is the use of the *genetic distances* that have been derived from the sequence alignment. These distances are usually provided in a distance matrix. They are usually estimates of the number of substitution events per nucleotide that have occurred since two taxa were separated during evolution, and thus indicate the degree of similarity existing between the taxa involved. It is the aim of the distance-based methods of phylogenetic reconstruction to infer a phylogenetic tree that optimally reflects the empirical distances contained in this distance matrix (see Fig. 12.5).

A principal problem with distance-based methods is that the true genetic distance between two taxa is usually unknown. Noise is introduced in the various approaches to estimate these distances from the available empirical data. However, some distance-based methods allow an effective phylogenetic analysis of datasets that include hundreds of taxa, and have reasonable accuracy. Distance-based methods are therefore often applied in the analysis of large datasets. Distance trees may also be good starting points for an exploration of the tree space using other, computationally more expensive methods, such as maximum likelihood.

4.1. Genetic Distances Based on Aligned Sequences

A straightforward approach to estimate genetic distances between two sequences is to use the *p*-distance (also called *Hamming distance*):

$$p = \frac{\text{number of different nucleotides}}{\text{sequence length}}.$$

Nucleotide positions with gaps or uncertain bases (*wobbles*) are excluded. Generally p underestimates the actual number of substitutions that have occurred since the separation of the two species involved. Other genetic distances have been developed in an attempt to account for hidden (multiple) substitutions. The simplest genetic distances are the *Jukes-Cantor distance*

$$d_{JC} = -\frac{3}{4}\ln\left(1 - \frac{4}{3}p\right)$$

(Jukes and Cantor 1969) and the *Kimura two-parameter distance*

$$d_{K2P} = -\frac{1}{2}\ln\left((1 - 2P - Q)\sqrt{1 - 2Q}\right)$$

(Kimura 1980; P and Q denote the proportions of transitions and transversions between the two sequences).

However, using the maximum-likelihood approach, genetic distances can be computed according to any model of DNA substitution (see section 6). A fast method to calculate genetic distances for models allowing substitution rates to vary across alignment sites (following a gamma distribution, see section 6.3.1) was proposed by Guindon and Gascuel (2002). The most commonly used models of DNA substitution assume base frequencies to be constant over time, but there are also approaches which relax this assumption, and allow the base composition to vary at different points on the tree (*logdet* or *paralinear* distances; Lake 1994, Lockhart et al. 1994, Steel 1994).

4.2. Alignment-Free Distances

Genetic distances based on a model of DNA substitution can only be estimated for aligned sequences. Distance estimations are therefore

unreliable when the sequences to be compared are too heterogeneous to align. There are, however, a number of methods for deriving distances from non-aligned sequence data; they are particularly useful for whole-genome data (see section 10). A common approach is to assess the frequencies with which all possible strings of a fixed length (e.g., all possible "words" that can be formed with six nucleotides) occur in each sequence to be compared; these frequency vectors can then be used to define a distance function between the sequences (see, e.g., Vinga and Almeida 2003). It has been shown, by using both simulated and empirical datasets, that the analysis of alignment-free distances results in phylogenetic trees with higher overall reconstruction accuracies if variation of substitution rates within the sequences is high (Höhl and Ragan 2007).

4.3. Cluster Analysis: UPGMA and WPGMA

UPGMA (unweighted pair group method with arithmetic mean; Sokal and Michener 1958) is a straightforward approach to constructing a phylogenetic tree from a distance matrix. It is the only method of phylogenetic reconstruction dealt with in this chapter in which the resulting trees are rooted. UPGMA implicitly assumes a constant substitution rate, over time and phylogenetic lineages (known as the *molecular clock hypothesis*). Since this assumption is often violated, this method is now rarely used.

In a first step, the two terminal taxa with the smallest genetic distance (e.g., taxa *A* and *B*) are clustered together to form a new *operational taxonomic unit* (OTU) *AB*. Next, a new, smaller distance matrix is computed, which includes OTU *AB* instead of taxa *A* and *B*. In this process, means are used to derive distances between the new operational taxonomic unit *AB* and the remaining terminal taxa; this distance is

$$d_{(AB)X} = \tfrac{1}{2}\ (d_{AX} + d_{BX})$$

for any terminal taxon *X*. In a next iteration, again the two taxa with the smallest distance are clustered, and this process is repeated until only two OTUs are left.

In the clustering process, the formula used to compute mean distances is as follows. If C_1, C_2 are clusters including n_1 and n_2 terminal taxa, respectively, that are to be merged into a new OTU C_1C_2, then the mean distance to any other cluster *D* is given by

$$d_{(C_1C_2)D} = \frac{n_1}{n_1+n_2} d_{C_1D} + \frac{n_2}{n_1+n_2} d_{C_2D}$$

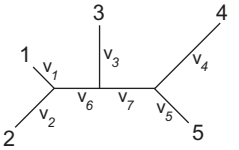
(d_{C_1D} and d_{C_2D} have already been calculated in an earlier clustering step). An alternative method is to use simple means, i.e.,

$$d_{(C_1C_2)D} = \tfrac{1}{2}\ (d_{C_1D} + d_{C_2D}\ );$$

this variant is called the *weighted pair group method* (WPGMA).

4.4. Estimating Branch Lengths

For any topology, branch lengths optimally fitting a given distance matrix can be estimated. This is usually done via a least-squares approach, where the difference between the *phyletic distances* (i.e., the distance between two taxa in the tree) and the genetic distances, as given by the distance matrix, are minimized. Consider the following topology:



Here, the following equations for the phyletic distances e_{ij} hold:

$$\begin{aligned}
e_{12} &= v_1 + v_2 \\
e_{13} &= v_1 + v_3 + v_6 \\
e_{14} &= v_1 + v_4 + v_6 + v_7 \\
e_{15} &= v_1 + v_5 + v_6 + v_7 \\
e_{23} &= v_2 + v_3 + v_6 \\
e_{24} &= v_2 + v_4 + v_6 + v_7 \\
e_{25} &= v_2 + v_5 + v_6 + v_7 \\
e_{34} &= v_3 + v_4 + v_7 \\
e_{35} &= v_3 + v_5 + v_7 \\
e_{45} &= v_4 + v_5
\end{aligned}$$

Using these equations, branch lengths v_i can be determined such that the phyletic distances e_{ij} maximally fit the genetic distances given in the distance matrix. This is usually done via a least-squares approach, as described in the next section. There are several strategies available for dealing with the negative branch lengths, which can occur in this procedure (see the discussion in Swofford et al. 1996).

4.5. Optimality Criteria

Once branch lengths have been estimated for a number of topologies, it is possible to rate these trees according to an optimality criterion. An optimal tree according the chosen criterion is considered as a valid phylogenetic hypothesis given the distance data. The most often used criteria for this purpose are the following.

4.5.1. Cavalli-Sforza and Edwards (1967)

Using this unweighted least-squares approach, the tree is chosen that minimizes

$$\sum_{i<j} (d_{ij} - e_{ij})^2.$$

Again, d_{ij} denotes the empirical genetic distances, and e_{ij} the phyletic distances along the tree which is evaluated.

4.5.2. Fitch and Margoliash (1967)

This weighted least-squares criterion accounts for the relative deviance of the phyletic distances from the empirical genetic distances; the function to be minimized is

$$\sum_{i<j} \left(\frac{d_{ij} - e_{ij}}{d_{ij}} \right)^2.$$

4.5.3. Minimum Evolution

According to this principle (Kidd and Sgaramella-Zonta 1971), unlike the least-squares criteria mentioned above, the tree is chosen in order to minimize the total sum of the branch lengths

$$\sum_i |v_i|.$$

Thus the optimality criterion for the selection of the minimum-evolution tree, indirectly related to the maximum-parsimony criterion, is independent of the distance matrix, unlike the estimation of branch lengths for a given topology.

A general drawback of these methods is that the space of all possible topologies must be explored in order to determine the tree that best fits the data, as in other approaches such as maximum parsimony or maximum likelihood. Since the number of possible topologies increases overexponentially with the number of terminal taxa

involved in the analysis (see section 2.1), heuristic strategies are usually necessary (see section 8).

4.6. Neighbor Joining

Neighbor joining (Saitou and Nei 1987) is a clustering algorithm that greedily optimizes the so-called "balanced minimum evolution" criterion (Gascuel and Steel 2006). If the distance matrix is tree-like, i.e. there is a tree that exactly reflects the distance matrix, then neighbor joining returns that tree. This will not be the case, however, for the vast majority of empirically derived genetic distances. Since neighbor joining is a very fast method (in current algorithms the number of operations is proportional to n^3, where n is the number of sequences) it is widely used for the analysis of large data sets, and has become the most widely used method for constructing phylogenetic trees from distance data (Gascuel and Steel 2006).

According to its original formulation (Saitou and Nei 1987), the procedure starts with a totally unresolved tree (called a *star tree*). A pair of sequences (neighbors) is joined to an OTU to minimize the total branch length of the resulting partially resolved tree. As in UPGMA (see section 4.3), new distances are calculated between the new OTU and the remaining taxa. The process is then iterated until only three taxa/OTUs are left to join. The basis of the procedure is an idea which allows estimation of total branch lengths of star-like trees directly from a distance matrix. Studier and Keppler (1988) have shown that neighbor joining can also be regarded as a modification of UPGMA in which the distances are distorted in a certain way for each clustering step.

4.6.1. Algorithms Related to Neighbor Joining: BIONJ, FASTME, and Neighbor-Net

Since the method was published in 1987, a number of modifications and extensions of neighbor joining have been proposed. In BIONJ (Gascuel 1997), each clustering step minimizes the variance of the new distance matrix. This performs better than neighbor joining for higher substitution rates. FASTME (Desper and Gascuel 2002, 2004) is an algorithm which, like neighbor joining, is based on the balanced minimum evolution criterion, and is able to reconstruct a tree from a distance matrix in time proportional to n^2. Neighbor-net (Bryant and Moulton 2004) is a generalization of the neighbor-joining clustering process. It produces a phylogenetic network rather than a phylogenetic tree. Like neighbor joining, BIONJ, FASTME and neighbor-net return the correct tree if the distance matrix is tree-like.

5. MAXIMUM PARSIMONY

5.1. The Maximum Parsimony Principle

The maximum parsimony criterion is one of the most popular approaches to reconstructing molecular phylogenetic trees. It was originally developed for the cladistic analysis of complex (morphological) characters (Camin and Sokal 1965). For the analysis of multistate unordered characters, such as nucleotides or amino acids, the parsimony algorithm was introduced by Fitch (1971). The objective of this method is to find topologies which explain the distribution of the observed character states (e.g., nucleotides or amino acids in the alignment columns) most parsimoniously. Most parsimonious topologies imply the minimum number of transformation events among all topologies, and thus minimize the number of multiple, independently evolved, character states (*homoplasies*). A search is performed to find the tree topology that requires the smallest number of substitution events to explain the observed alignment. The evaluation principle for one alignment column is illustrated for two different topologies in Fig. 12.6. For each alignment column i the required number s_i of substitution events is determined. The total number of required substitution events for a given topology is then $S = \sum_i s_i$.

Usually a significant number of alignment columns (*parsimony-uninformative sites*) can be neglected in order to obtain the most parsimonious trees, since all possible trees are equally parsimonious for that site. Parsimony-uninformative sites not only include the constant sites, but all alignment columns where only one nucleotide occurs more than once.

Most parsimonious trees are good estimates of the phylogenetic relationships, as long as substitution rates do not vary too much between different branches. If there are long branches in the true phylogeny (as indicative of high substitution rates), then the application of the maximum parsimony criterion may result in phylogenetic trees that cluster the long branches together incorrectly (*long-branch attraction*; Felsenstein 1978b). Similar problems may also occur in probabilistic or distance-based approaches if inappropriate evolutionary models are used; for a review on long-branch attraction, see Bergsten (2005).

5.2. Goodness-of-Fit Indices

There are several approaches to evaluate how well a certain topology explains the given character state matrix in a parsimony framework. For a given topology τ and a column i of an alignment, let

s_i denote the number of substitutions for column i along topology τ,
m_i denote the minimum possible number of substitutions needed in any tree for column i, and
g_i denote the maximum number of substitutions needed in any tree for column i.

Then g_i substitutions are needed in a star "tree". If there are n_i different nucleotides in alignment column i then $m_i = n_i - 1$.

The *consistency index* (Kluge and Farris 1969) for column i is defined as

$$c_i = \frac{m_i}{s_i}.$$

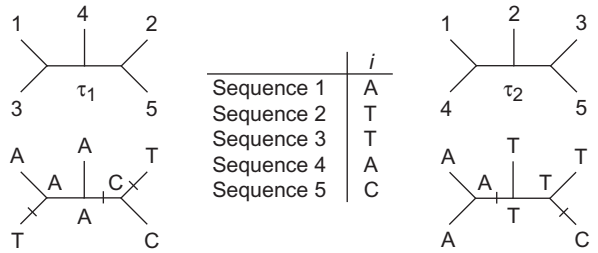


FIGURE 12.6 The maximum parsimony principle. A phylogenetic hypothesis is derived by searching for the tree that minimizes the number of nucleotide changes along its branches. For a given tree, the minimum number of nucleotide changes along its branches is counted for each alignment column by reconstructing nucleotide states of inner nodes (these assignments are often not unique). In the example shown, three nucleotide changes are needed for topology τ_1 to explain the alignment column most parsimoniously; only two changes are needed for topology τ_2. Hence, τ_2 is considered the better hypothesis for the shown alignment column.

Since

$$\frac{m_i}{g_i} \le c_i \le 1$$

there is a lower bound for c_i which depends on the distribution of nucleotides in column *i*. We have $c_i = 1$ if the given topology explains column *i* without homoplasies. If alignment column *i* is *parsimony informative* (i.e., $m_i \neq g_i$) then

$$r_i = \frac{g_i - s_i}{g_i - m_i}$$

is the *retention index* (Farris 1989a). Then $0 \le r_i \le 1$; $r_i = 1$ if there are no homoplasies and $r_i = 0$ for the star topology. The value of r_i can also be used to standardize the consistency index c_i:

$$rc_i = r_i \cdot c_i = \frac{g_i - s_i}{g_i - m_i} \cdot \frac{m_i}{s_i}$$

is the *rescaled consistency index* (Farris 1989b), definable for any parsimony-informative alignment column *i*.

These valuation numbers can be transferred to the total alignment (Farris 1989b):

$$C = \frac{\sum_i m_i}{\sum_i s_i}$$

is the *ensemble consistency index*,

$$R = \frac{\sum_i g_i - \sum_i s_i}{\sum_i g_i - \sum_i m_i}$$

is the *ensemble retention index* (defined if the alignment contains parsimony informative sites), and

$$RC = R \cdot C = \frac{\sum_i g_i - \sum_i s_i}{\sum_i g_i - \sum_i m_i} \cdot \frac{\sum_i m_i}{\sum_i s_i}$$

is the *ensemble rescaled consistency index* (if the alignment contains parsimony informative sites).

The *homoplasy index* is defined as $h_i = 1 - c_i$ for a single column *i* and $H = 1 - C$ for the total alignment.

5.3. Weighted Parsimony

The parsimony principle illustrated above may be extended by assigning different weights to different subsets of the character matrix. If the *i*th character is assigned a weight w_i, then the number to be optimized is

$$S_w = \sum_i w_i s_i$$

(as above, s_i denotes the minimum number of substitution events for character *i*).

In this context, unweighted parsimony is a special case with $w_i = 1$ for all characters. Weighted parsimony is a fundamental part of the *parsimony ratchet* procedure (Nixon 1999; see section 8.2). Iteration of a weighting procedure is known as *successive weighting*. Here, the result of a first unweighted parsimony analysis forms the basis for weighting the alignment columns, e.g., proportionally to their consistency indices ($w_i = c_i$, see above; Farris 1969). The result of a second, weighted parsimony analysis, using these factors, can then be used to iterate the process. If the trees found during this iteration finally stabilize, i.e., they converge to a tree that does not change under repeated iteration, this tree may be used as a phylogenetic hypothesis for the given dataset. However, as there is no natural weighting scheme, weighting in maximum parsimony analysis is debatable.

5.4. Bremer Support (Decay Index)

The parsimony criterion can also be used to derive a measure of support for any branch *v* (i.e., for any split) which is present in all most-parsimonious trees for a given alignment. The *Bremer support* (or *decay index*) b_v (Bremer 1988) is defined as:

$$b_v = \max\{n \mid v \text{ is present in all trees of length} \le S + n\}$$

where *S* is the tree length (i.e., the minimal number of steps) for the most-parsimonious tree(s).

The basic idea is that a branch that is present in several suboptimal trees is considered as more supported than one which collapses in a consensus including non-optimal trees. An efficient way to obtain Bremer support values is to apply *negative constraints*, that is, to forbid the split of interest in a subsequent heuristic search. The support is then calculated as the difference in length between the shortest tree that lacks that split, and the shortest tree that contains that split.

In contrast to bootstrapping and jackknifing (see section 7), the decay index lacks a straightforward statistical interpretation. DeBry (2001) has pointed out that Bremer support values cannot even be compared among branches of the same tree. However, Zander (2004) has obtained minimum values for the decay index which are required for statistically significant support.

Decay indices can also be calculated separately for the distinct subsets of a given alignment partition (e.g., for single genes). This *partitioned Bremer support* (Baker and DeSalle 1997, Baker et al. 1998, Gatesy 2002) can be used to assess whether the support for a node is due to certain alignment regions only.

6. PROBABILISTIC METHODS OF PHYLOGENETIC INFERENCE

During recent years, applications of probability theory and stochastics to molecular phylogenetic reconstruction have become more and more popular. These methods use explicit assumptions (models) about the mechanisms of DNA substitution to derive the probability $P(X|T)$ that the observed alignment *X* (the data) evolved along a certain phylogenetic tree *T*, i.e., under a certain phylogenetic hypothesis. This number is designated the *likelihood* $L(T|X)$ of the phylogenetic tree, given the alignment *X*. The *maximum likelihood principle*, i.e., maximizing the probability of observing the data under a set of hypotheses, is one of the most successful approaches in statistical inference.

6.1. Models of DNA Substitution

The most frequently used models of DNA substitution can be represented by a substitution matrix

$$Q = \begin{pmatrix} \cdot & a\pi_C & b\pi_G & c\pi_T \\ a\pi_A & \cdot & d\pi_G & e\pi_T \\ b\pi_A & d\pi_C & \cdot & f\pi_T \\ c\pi_A & e\pi_C & f\pi_G & \cdot \end{pmatrix}.$$

This is known as the *general time-reversible* DNA substitution model (GTR; Lanave et al. 1984). For $i \neq j$, the entry at position *i*, *j* (row *i* and column *j*) describes the instantaneous substitution rate from base *i* to base *j*. The nucleotides are arranged in the order A, C, G, T. Every instantaneous substitution rate from base *i* to base *j* is composed of two components:

(1) a symmetrical basic rate; each substitution $i \to j$ possesses the same basic rate as the substitution $j \to i$;
(2) the (ideal) frequency π_j of nucleotide j.

The diagonal elements of Q are determined in such a way that the entries of each row add to zero. If molecular evolution is simulated under such a model, then nucleotide j eventually reaches an equilibrium frequency π_j (Yang 1994).

Using matrix calculus, the probability with which nucleotide i is substituted by nucleotide j during time t can be determined as

$$P_{ij}(t) = (e^{-Qt})_{ij},$$

the entry at position i, j of the matrix e^{-Qt} . For the entries of Q the important relationships $\pi_i Q_{ij} = \pi_j Q_{ji}$ $(i \neq j)$ hold. This implies the *time reversibility* of the substitution model, which guarantees that the likelihood of a tree can be calculated independently from the position of its root.

For simple models of substitution, the substitution probability can be calculated directly; for instance, using the Jukes-Cantor model gives (see below: $a = b = c = d = e = f = \mu$):

$$P_{ij}(t) = \begin{cases} \frac{1}{4} + \frac{3}{4} e^{-\mu t} & \text{if } i = j \\ \frac{1}{4} - \frac{1}{4} e^{-\mu t} & \text{else.} \end{cases}$$

In concrete calculations of $P_{ij}(t)$, the time t always appears only in the product with the mean substitution rate μ (the average of the non-diagonal elements of Q); see above for the Jukes-Cantor model. Hence $P_{ij}(t)$ does not change if the time is multiplied by a factor r, and at the same time all entries of Q are multiplied by a factor r^{-1}. Thus, Q is usually standardized in such a way that its mean substitution rate is 1; then not the absolute time t but the *relative time* $\mu \cdot t$ is considered, the product of mean substitution rate with time, expressed as the number of substitutions per nucleotide. Thus substitution probabilities along branches in a distance tree can be calculated. However, which distance in time this branch length corresponds to remains undetermined; a long branch may express a high mean substitution rate or equally, a long time interval. The following list shows some sub-models of the general time-reversible substitution model.

	Model	Basic rates	Base frequencies
JC	Jukes and Cantor 1969	$a = b = c = d = e = f$	$\pi_A = \pi_C = \pi_G = \pi_T = 0.25$
F81	Felsenstein 1981	$a = b = c = d = e = f$	no restriction
K2P	Kimura 1980	$a = c = d = f$, $b = e$	$\pi_A = \pi_C = \pi_G = \pi_T = 0.25$
HKY	Hasegawa et al. 1985	$a = c = d = f$, $b = e$	no restriction
K3ST	Kimura 1981	$a = f$, $c = d$, $b = e$	$\pi_A = \pi_C = \pi_G = \pi_T = 0.25$
TrN	Tamura and Nei 1993	$a = c = d = f$	no restriction
SYM	Zharkikh 1994	no restriction	$\pi_A = \pi_C = \pi_G = \pi_T = 0.25$
GTR	Lanave et al. 1984	no restriction	no restriction

K2P and HKY both distinguish between transversions and transitions in the basic rates, TrN distinguishes between transversions, transitions between purines, and transitions between pyrimidines; K3ST distinguishes transitions and two classes of transversions. For an overview and discussion of DNA substitution models, see Huelsenbeck et al. (2004).

6.2. Maximum Likelihood

The statistical principle of maximum likelihood estimation is to estimate unknown parameters of the probability model in such a way that the actually observed data gain maximum probability. This principle was first discussed as a possible method of molecular phylogenetic reconstruction in a milestone paper by Edwards and Cavalli-Sforza (1964). The computational basis for the application of this approach to molecular phylogenetics was then laid by Felsenstein (1981). Here, the observed data are given by the sequence alignment; the unknown parameters of the probability model comprise the unknown true phylogeny of the given taxa (i.e., the topology and all branch lengths of the true tree). They may also include the DNA substitution model. It can be shown that maximum likelihood is a *consistent* method of phylogenetic reconstruction (Felsenstein 1973; see the discussion in Felsenstein 2004); if the correct model of DNA substitution is used, then the probability of inferring the correct tree approaches one as the length of the DNA sequences increases to infinity. This has also been illustrated in simulation studies (e.g., Huelsenbeck et al. 1996).

For a phylogenetic tree $T = (\tau, v_1, v_2, \ldots)$, i.e., for a topology τ, together with branch lengths $v_1, v_2, \ldots$, the likelihood $L(T|X)$ given the alignment X is defined as the probability $P(X|T)$ that the alignment X evolved along T. Let x_j denote alignment column j and $P(x_j|T)$ be the probability that column x_j evolved along T; then

$$L(T|X) = P(X|T) = \prod_j P(x_j|T)$$

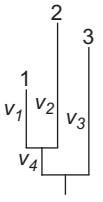
if we assume that the alignment columns evolve independently from each other. It is the objective of maximum likelihood estimation to find a tree T for which $L(T|X)$ is maximized.

Example

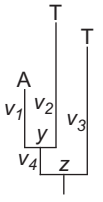
The calculation of the probability $P(x_j|T)$ that an alignment column

$$x_j = \begin{pmatrix} \text{A} \\ \text{T} \\ \text{T} \end{pmatrix}$$

evolved under a tree T



may be illustrated as follows. First, the nucleotides in the alignment column are mapped to the terminal nodes of the tree. Let y and z denote the nucleotides at the inner nodes.



Since y and z are not known, all possible nucleotide combinations at the inner nodes must principally be considered; hence

$$P(x_j|T) = \sum_y \sum_z \pi_z P_{zy}(v_4) P_{yA}(v_1) P_{yT}(v_2) P_{zT}(v_3),$$

where $P_{ij}(v)$ denotes the probability that nucleotide i was substituted by nucleotide j along a branch of length v (this depends on the model of DNA substitution used); π_i is the equilibrium frequency of nucleotide i. The sum extends over all possible assignments of nucleotides to the inner nodes y and z. If a time-reversible model of DNA substitution is used, then this calculation is independent of the particular rooting of the tree.

The fact that principally all possible combinations of nucleotides of inner nodes have to be considered in calculating likelihood values explains why this method is computationally so expensive. As in all methods that use optimality criteria to find trees that best fit the given data, maximum likelihood trees cannot usually be determined exactly, instead heuristic methods of inference have to be used (see section 8). Since very fast heuristics have recently become available (e.g., Guindon and Gascuel 2003, Jobb et al. 2004, Minh et al. 2005, Stamatakis 2006, Whelan 2007, Zwickl 2006), maximum likelihood trees are now being computed for reasonably large taxon numbers.

6.3. DNA Substitution Models: Accounting for Rate Heterogeneity

Any substitution model represented by an instantaneous substitution matrix Q (see section 6.1) can be combined with two refinements for likelihood calculations of phylogenetic trees; gamma-modeled rate heterogeneity across alignment sites, and the model of invariant sites.

6.3.1. Gamma-Distributed Substitution Rates

This approach implements substitution rates that vary across alignment columns. Let x_i represent column i of the alignment X and $T = (\tau, v_1, v_2, \ldots)$ a tree (i.e., a topology τ with branch lengths $(v_1, v_2, \ldots)$; then the likelihood

$$L(T|x_i) = P(x_i|T)$$

of T for column x_i under the chosen substitution model depends on the particular branch lengths $v_1, v_2, \ldots$ of the tree. Replacing branch lengths v_i by $r \cdot v_i$ for a factor $r > 0$ yields a function $P(x_i|T, r)$ of r. By varying r, different mean substitution rates can be simulated. If the variable r is considered as a random variable with some known distribution, it can then be eliminated by integration (i.e., by switching to the expectation value).

A gamma-distributed rate factor r may be used for this purpose (Yang 1993). By varying the form parameter α of the gamma distribution, a wide range of rate variations can be implemented; small α values simulate a high variation of substitution rates, while a constant substitution rate is approximated when α tends to infinity. For a given shape parameter α of the gamma distribution the expectation value

$$L_\alpha(T|x_i) = E_\alpha(P(x_i|T, r)) = \int_0^\infty P(x_i|T, r)\ \ \Gamma_\alpha(r)\ \ dr$$

(where Γ_α is the density function of the gamma distribution with form parameter α) is independent of the rate r. Hence, for the total alignment X,

$$L_\alpha(T|X) = \prod_i L_\alpha(T|x_i)$$

is the likelihood of T under a model of gamma-distributed substitution rates.

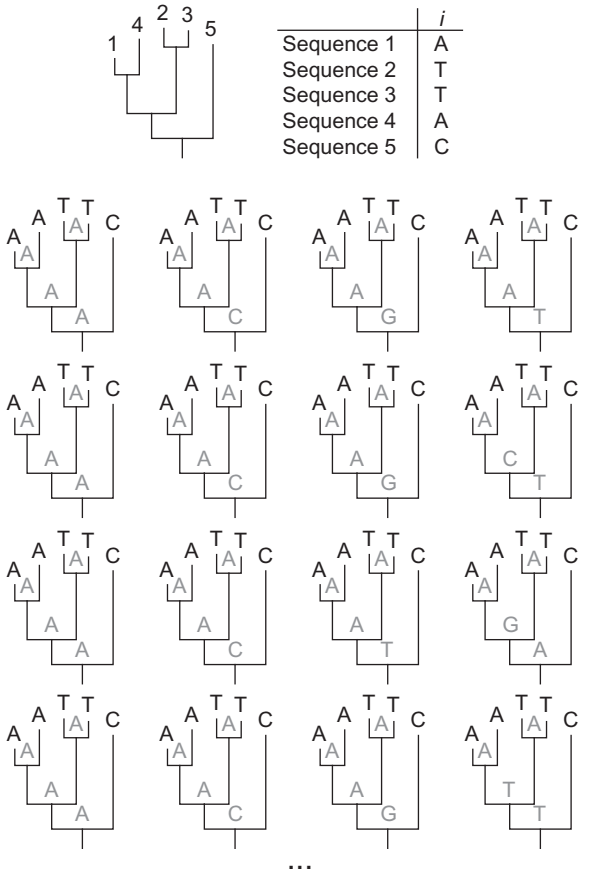


FIGURE 12.7 The maximum likelihood principle. A phylogenetic hypothesis is derived by searching for the tree that maximizes the probability to observe the data, i.e., the probability that the alignment evolved under this tree (= the likelihood of the tree). Principally, for each alignment column all possible combinations of nucleotide states of the inner nodes have to be considered in computing the probability that an alignment column has evolved under this tree. The probability that the total alignment evolved under the tree is the product over the probabilities for each column.

Using maximum likelihood estimation, the parameter α can be chosen in such a way that $L_\alpha(T|X)$ is maximized. For practical computation, the gamma distribution is most often approximated by a step function that uses a specified number of rate classes.

6.3.2. Invariant Sites

In this approach (Hasegawa et al. 1987), a certain percentage of nucleotide sites are considered as invariant (e.g., due to functional constraints); in other words, substitution events are ruled out for these sites. For these sites, a substitution model defined by $P_{ii}(t) = 1$ and $P_{ij}(t) = 0$ $(i \neq j)$ can be used. The percentage I of invariable alignment positions is a parameter that can be optimized using maximum likelihood estimation.

6.4. Choosing an Optimal DNA Substitution Model

In the application of likelihood-based methods in phylogenetic inference, it may be useful to select a DNA substitution model that best fits the data (e.g., Sullivan and Swofford 1997, Whelan et al. 2001).

To do so, two methods are widely used; likelihood ratio tests, and the Akaike information criterion. Both methods are based on comparisons of likelihood values, as discussed below.

6.4.1. Likelihood Ratio Tests

A likelihood ratio test is a common statistical approach to decide which of two nested models should be used to describe the observed data. An illustration of the principle of this procedure in its application to model testing in molecular phylogenetics (Posada and Crandall 1998) is given here.

Let X be a DNA alignment, T a phylogenetic tree, and M_0 (null model) and M_1 (alternative model) be two DNA substitution models that are nested (i.e., $M_0 \subseteq M_1$; the null model is a special case of the alternative model, any set of parameters of M_0 is also contained in M_1). If the null model M_0 is the true model, then the test statistic

$$-2\ln\frac{\max_{\mathbf{a}\in M_0}(P(X|T,\mathbf{a}))}{\max_{\mathbf{a}\in M_1}(P(X|T,\mathbf{a}))} = 2\left(\ln\max_{\mathbf{a}\in M_1}(P(X|T,\mathbf{a})) - \ln\max_{\mathbf{a}\in M_0}(P(X|T,\mathbf{a}))\right)$$

should be approximately χ^2 distributed.

The number of degrees of freedom of this χ^2 distribution should equal the difference between the number of the free parameters of M_1 (the more complex model) and those of M_0 (the simpler model). Examples of nested DNA substitution models are the Jukes-Cantor model (as the null model) and the Kimura 2-parameter model (as the alternative model).

To perform this test for a given DNA alignment, a neighbor-joining tree (see section 4.6) is first computed using Jukes-Cantor distances. This guide tree is subsequently used to test alternative models of DNA substitution using the test statistic given above. These tests are performed stepwise, starting with the simple models and proceeding to the most complex. In each step, one tests whether the respective null model is to be retained or significantly rejected (in this case, the alternative model is accepted). In the latter case, the accepted alternative model then becomes the null model of the next test.

Unfortunately, the choice of model may depend on the model hierarchy that is employed (Posada and Crandall 2001); a different model may be chosen if the likelihood ratio test follows a different model hierarchy. Furthermore, there is the general problem that it is unclear to which degree χ^2 distributions are valid approximations of the likelihood ratio statistic defined above (Goldman and Whelan 2000). These are two of the reasons why a different approach to model testing has been advocated (Posada and Buckley 2004).

6.4.2. Akaike Information Criterion (AIC)

In this approach (Akaike 1974), the statistic

$$\mathrm{AIC}_M = -2\left(\ln\max_{\mathbf{a}\in M}(P(X|T,\mathbf{a})) - k\right)$$

is calculated for the models M to be compared, where k denotes the number of free parameters of M. This number estimates the amount of information that is lost when the model M is used to approximate reality. The model with the lowest AIC_M is considered the one best fitting the data. Besides theoretical arguments, the AIC has the advantage that models need not be nested in order to be compared.

There are other promising approaches to model testing (see Huelsenbeck et al. 2004, Minin et al. 2003), e.g. using the Bayesian information criterion (BIC; Schwarz 1978). In a Bayesian context (see below), an alternative proposal is to use the most complex substitution model available (Huelsenbeck and Rannala 2004).

6.5. Bayesian Analysis

If $T=(\tau, v_1, v_2,\ldots)$ is a phylogenetic tree (i.e., a topology τ together with branch lengths $v_1, v_2,\ldots$), then one can calculate the probability $P(X|T)$ that alignment X evolved under the tree T using a DNA substitution model, as outlined above (section 6.2). In the context of phylogenetic reconstruction, however, it would be particularly interesting to be able to calculate a different conditional probability, namely $p(\tau|X)$, the probability that the topology τ describes the true phylogenetic relationships for the analyzed taxa, given the observed data (i.e., the alignment X).

The straightforward and well-known Bayes' formula (named after Thomas Bayes, 1702−1761) yields

$$P(\tau|X) = \frac{P(X|\tau)\cdot P(\tau)}{\sum_{i=1}^{B(n)} P(X|\tau_i)\cdot P(\tau_i)}.$$

If a time-reversible model of DNA substitution is used, then this sum extends over all $B(n)=\frac{(2n-5)!}{2^{n-3}(n-3)!}$ unrooted dichotomous topologies that are possible for a given set of n taxa (see section 2.1). $P(\tau_i)$ is the prior probability of topology τ_i. If all possible topologies are considered as a priori equally probable, then we have for the prior probabilities $P(\tau)=P(\tau_i)=(B(n))^{-1}$. Hence $P(\tau|X)$ is, in principle, computable if the number of taxa involved is moderate.

However, to calculate $P(X|\tau)$ it would be necessary to integrate $P(X|\tau, v_1, v_2,\ldots)$ over all possible branch lengths $v_1, v_2, \ldots$. As there is no analytical way to do so, $P(\tau|X)$ cannot be calculated by using Bayes' formula. However, an analytically inaccessible probability distribution can, be numerically approximated by using stochastic processes that have the desired distribution as their equilibrium distribution. The most common approach to such problems uses the Markov Chain Monte Carlo (MCMC) method, with the Metropolis-Hastings algorithm (Hastings 1970, Metropolis et al. 1953). Several authors have introduced Bayesian MCMC into phylogenetics (Li et al. 2000, Mau and Newton 1997, Yang and Rannala 1997); in the following section we describe the method developed by Huelsenbeck and Ronquist (2001).

Here, MCMC is used to generate a sequence of phylogenetic trees which, after the process has become stationary, can be considered as samples drawn from the analytically inaccessible probability space of phylogenetic trees for a given alignment. This sequence of trees is a *Markov chain*, i.e., each of the trees depends only on its immediate precursor in the sequence, not on earlier trees. The chain starts with a random tree T_0. If the trees T_0, T_1,..., T_n have already been constructed, then a tree T_n' is built by performing random transformations (e.g., by branch swapping or random transformation of branch lengths) on tree T_n. After this, a decision number ρ_n is calculated, the value of which depends on the likelihood values $L(T_n|X)$ and $L(T_n'|X)$. Finally, a decision number ρ between 0 and 1 is randomly generated; if $\rho_n \geq \rho$ then T_n' is chosen as the next tree T_{n+1} (tree "*generation*") of the chain, otherwise T_n is subjected to a new random transformation.

The likelihood values of the trees sampled in the Markov chain will eventually reach a stationary stage (Fig. 12.8). The trees generated during this stage are sampled to estimate the *posterior probabilities*. For this purpose, trees are regularly drawn (e.g., from every 10th or 100th tree generation) after stationarity is reached. If a sufficiently large number of tree generations has been sampled, then the percentage of trees with topology τ in this sample should be an approximation of the posterior probability $p(\tau|X)$. In the same way the percentage of sampled trees in which a certain group of taxa is

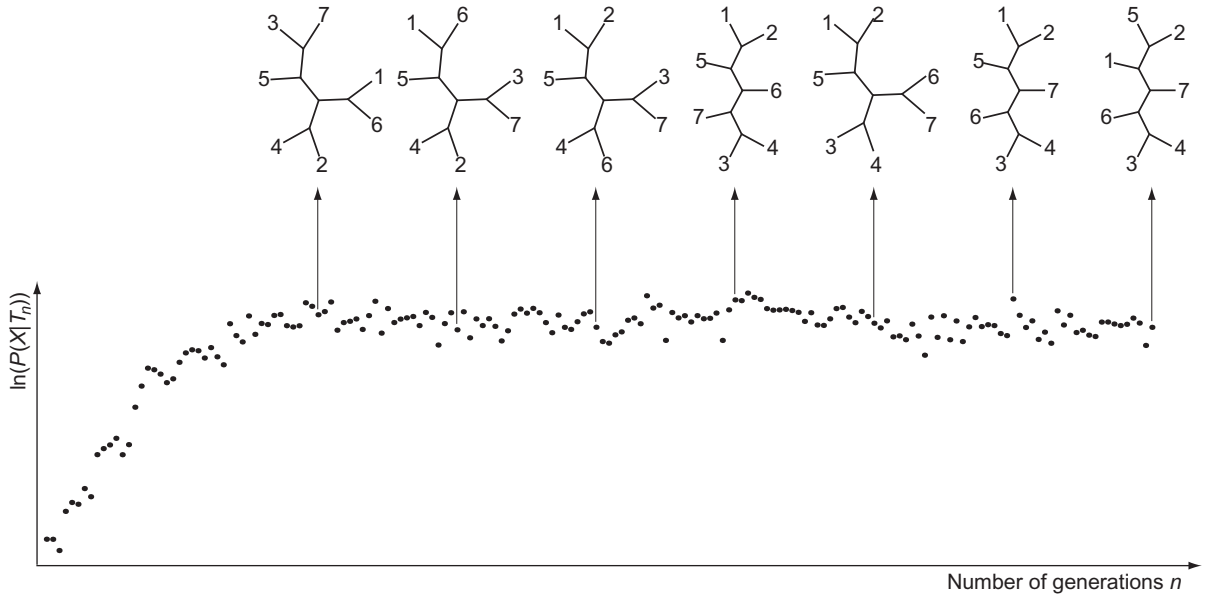


FIGURE 12.8 Principle of the Markov Chain Monte Carlo (MCMC) approach to derive phylogenetic hypotheses: likelihood plot of the generated trees. For a given alignment, a series of phylogenetic trees is generated by a stochastic process; these trees are stored at a certain frequency. The percentage with which a group of taxa occurs in the stored trees that were produced after the process has reached stationarity, is taken as an estimate of the probability that this group is present in the (unknown) true tree. Taken from M. Weiß (2010) *Molecular phylogenetic Reconstruction.* Course manual, University of Tübingen (http://www.orgbot.uni-tuebingen.de/people/tiki-index.php?page=mweiss).

present (the MCMC support value) is an approximation of the probability (under the observed data, i.e., the alignment) that this group is monophyletic.

Parameters of the underlying DNA substitution model may be fixed in the stochastic process, but usually as well undergo random transformations, which are accepted or rejected at each stage of the Markov chain. Thus, each generation in the chain includes a tree and a vector describing the model parameters. This is a way of dealing with uncertainties concerning the model parameters. After the MCMC analyses, confidence intervals can be calculated for any parameter sampled during the process.

Until recently, Bayesian MCMC analyses were much faster than bootstrapped maximum likelihood analyses for larger datasets. This, together with the recent availability of software implementations (e.g., Huelsenbeck and Ronquist 2001), may explain the increasing popularity of MCMC during the past years. However, there has been considerable discussion of how useful MCMC branch support values actually are in evaluating the probability of a clade being present in the true tree. Studies based on simulations and phylogenomic datasets (where the true tree may be derived with some confidence; see section 10) suggest that bootstrap values (see section 7) are generally more conservative estimators for the probability that a group is monophyletic given the data than MCMC support values, which tend to overestimate the posterior probabilities (e.g., Cummings et al. 2003, Simmons et al. 2004, Taylor and Piel 2004, but see also Yang and Rannala 2005). MCMC support values may be particularly problematic when insufficiently complex substitution models are used (Erixon et al. 2003, Suzuki et al. 2002).

There are also some problems connected with the principles of Bayesian MCMC. One such issue is the need to use priors (i.e., unconditional probability distributions) on trees and the model parameters to be sampled during MCMC. These are needed in the decision processes in MCMC, but though they may have significant influence on the outcome on a phylogenetic analysis (e.g., Pickett and Randle 2005, Yang and Rannala 2005, Zwickl and Holder 2004), there is no natural way of choosing them. Another problem is that there is no way to decide when an MCMC process has reached stationarity. Independent runs of MCMC on the same dataset may become stationary at quite different stages of the processes (Soltis et al. 2007), which may particularly affect MCMC analyses of large datasets.

7. BOOTSTRAP AND JACKKNIFE

Bootstrapping and jackknifing are statistical methods to evaluate and distinguish the confidence of partial hypotheses ("*branch support*") that are contained in a phylogenetic tree and have become a standard in molecular phylogenetic analyses.

7.1. Non-Parametric Bootstrapping

Non-parametric bootstrapping (or simply "the bootstrap") was developed by Efron (1979) as a general statistical method for estimating the parameters of an unknown probability distribution by resampling from an existing sample that was drawn from this distribution. The method was transferred to phylogenetic reconstruction by Felsenstein (1985).

Within molecular phylogenetics it works as follows (see Fig. 12.9). From an alignment of length *n*, columns are randomly drawn with replacement *n* times. The drawn columns are arranged in a new dataset, a bootstrapped alignment of length *n*. From this bootstrapped alignment, a phylogenetic tree is constructed by following the same method of phylogenetic analysis as was used for the analysis of the original alignment. This process of constructing bootstrap alignments and bootstrap trees is repeated a large number (e.g., 1000) of times, and the resulting trees are stored. The percentage with which a certain bipartition of the taxon set is present in the bootstrap trees (the *bootstrap value*) can be taken as a measure of how homogeneously this bipartition of sequences (i.e., the respective branch in the underlying topology) is supported by the data. Bootstrap values are often summarized by constructing the majority-rule consensus (see section 2.2.2) from the bootstrap trees.

Suppose genomes of the taxon set are available and a super-alignment could be constructed from them (which is of course not possible using real genomes, see section 10). The original alignment can be seen as the result of a random draw of n columns from that super-alignment. Additional (original) datasets can be interpreted as generated in the same way, and their phylogenetic analysis would be a natural way to infer clade support. The bootstrap can be seen as a transfer of this (hypothetical) way of generating additional datasets to the "real world", i.e., by using the limited empirical data that are at hand instead of a hypothetical genomic super-alignment to deduce clade support.

A theoretical prerequisite for non-parametrical bootstrapping to work for alignments is that the alignment sites should be independent of each other. This assumption may be incorrect (e.g., in portions of rRNA genes coding for stem regions), and variants of the bootstrap have been developed to cope with this problem (e.g., Künsch 1989).

Bootstrap values are often interpreted as probabilities that respective groups of taxa are present in the true phylogeny, i.e., interpreting them in the same way as posterior probabilities (see above). However, it has been shown that support values inferred from non-parametric bootstrapping tend to underestimate the probabilities that groups of taxa are present in the true tree (e.g., Hillis and Bull 1993, Li and Zharkikh 1996; see also the discussion of posterior probabilities inferred from MCMC versus bootstrap values above).

7.2. Parametric Bootstrapping

In a probabilistic context, there is an alternative way of generating replicate alignments from given data by computer simulation. This approach (Efron 1985) is model-based, and hence is commonly referred to as *parametric bootstrapping*. In its first step, a model of DNA substitution and a phylogenetic tree T are estimated from the original alignment X.

Using this model, replicate alignments X_i are generated, i.e., sequences are simulated along T. Subsequently, phylogenetic trees T_i are computed for each of the alignments X_i, and branch support values are derived (as in non-parametric bootstrapping) by computing the percentage with which a certain branch occurs in the set of generated trees T_i.

Support values derived by parametric bootstrapping depend to a large extent on the model estimated from the original alignment. For this reason the method can be used for testing the model inferred from the original alignment as a null hypothesis (Goldman 1993).

7.3. The Jackknife

The jackknife is a resampling method closely related to non-parametric bootstrapping. It works by randomly deleting a certain percentage of columns from the original alignment. Usually 50 per cent of the columns are deleted (*delete-half jackknife*; Felsenstein 1985), which is equivalent to drawing $n/2$ columns from the original alignment of length n without replacement. Models deleting different percentages of columns have also been proposed (Farris et al. 1996). As in non-parametric bootstrapping, the resampling is iterated, trees are computed from the jackknife alignments, and branch-support values are derived as the percentage with which a certain branch is present in the jackknife topologies. Branch support values derived by the delete-half jackknife seem to be closer to bootstrap values if a conflicting signal is present in the original dataset (see the discussion in Felsenstein 2004).

8. HEURISTIC SEARCHING STRATEGIES

Exploring all possible topologies for a given set of n terminal taxa in order to select the tree that best fits the data according to some optimality criterion (e.g., minimium evolution, maximum parsimony, or maximum likelihood) is feasible only when n is small, since the number of possible topologies increases overexponentially with n (see section 2.1). Heuristic approaches will produce locally optimal trees. However, there is no guarantee of whether these trees are the best trees from a global perspective. If the same trees are repeatedly found in several runs of some kind of random-dependent heuristic analysis (see below), then there is a reason to believe that these trees are in fact the best trees globally.

8.1. "Hill-Climbing"

The most popular heuristic search strategy is to explore the tree space locally, according to some optimality criterion. This typically involves the following steps:

1. Initiate the process by choosing a starting tree.
2. Apply some transformation to the current tree.
3. If the transformed tree is better according to the chosen optimality criterion, substitute the transformed tree for the current tree; if not, apply another transformation to the current tree.
4. If the current tree cannot be transformed into a better tree, store the current tree, which is a locally optimal tree.

The starting tree may be one found by some alternative method of phylogenetic reconstruction, such as neighbor joining, or may be a random tree.

Another often-used approach is to arrange the sequences in random order, build a tree with the first three, and then add the remaining sequences by inserting the $n+1$th sequence into the current tree of n sequences at the best position according to the optimality criterion used.

A popular topological transformation that may be applied during the process is *tree bisection and reconnection* (TBR; Swofford et al. 1996), in which the current tree is cut along a branch into two subtrees, which are subsequently glued together in a different way. If the starting tree is a random tree, or is generated by adding sequences in random order, steps 1–4 above may be repeated using a new starting tree. Many recent improvements in maximum likelihood and maximum parsimony hill-climbing have come from algorithms that first apply fast and approximate scoring functions to the candidate trees obtained by topological transformation, and then fully optimize only the most promising candidate trees, according to the scoring function (e.g., Hordijk and Gascuel 2005).

This "hill-climbing" approach does not allow "valleys" in the tree space to be crossed, in order to reach better trees, since transformed trees are only accepted if they are better than the current tree. However, it has been observed that "islands" containing "good" trees are often close to each other with respect to the number of topological transformations that have to be performed on trees of one island to get to trees of another island. Therefore, many fast hill-climbing algorithms consider candidate trees only if their topological distance from the current tree is below a certain threshold (e.g., Stamatakis 2006).

8.2. Ratchet Analysis

In this approach, introduced by Nixon (1999) in maximum parsimony analysis of DNA data, the hill-climbing principle described

(A)

	01	02	03	04	05	06	07	08	09	10	11	12	13	14	15	16	17	18	19	20
Sequence 1	T	G	T	C	C	A	A	–	T	T	C	C	T	G	G	C	C	A	G	A
Sequence 2	A	G	T	A	C	A	A	–	A	A	T	C	T	T	G	G	T	A	T	T
Sequence 3	A	G	T	C	C	A	A	T	T	A	T	C	T	T	G	A	T	A	G	T
Sequence 4	A	G	T	G	C	A	A	T	A	C	C	C	A	T	G	T	G	A	C	G
Sequence 5	A	G	T	G	C	A	A	T	T	C	C	C	T	–	G	G	G	A	C	G

(B)

	02	03	03	04	04	07	08	09	10	11	11	11	13	13	15	16	16	17	19	19
Sequence 1	G	T	T	C	C	A	–	T	T	C	C	C	T	T	G	C	C	C	G	G
Sequence 2	G	T	T	A	A	A	–	A	A	T	T	T	T	T	G	G	G	T	T	T
Sequence 3	G	T	T	C	C	A	T	T	A	T	T	T	T	T	G	A	A	T	G	G
Sequence 4	G	T	T	G	G	A	T	A	C	C	C	C	A	A	G	T	T	G	C	C
Sequence 5	G	T	T	G	G	A	T	T	C	C	C	C	T	T	G	G	G	G	C	C

(C)

	02	03	06	07	09	12	13	16	18	19
Sequence 1	G	T	A	A	T	C	T	C	A	G
Sequence 2	G	T	A	A	A	C	T	G	A	T
Sequence 3	G	T	A	A	T	C	T	A	A	G
Sequence 4	G	T	A	A	A	C	A	T	A	C
Sequence 5	G	T	A	A	T	C	T	G	A	C

FIGURE 12.9 Principle of (non-parametric) bootstrapping and the jackknife. (A) Original alignment. (B) Alignment produced in some bootstrap replicate, assembled from columns that were drawn randomly from the original alignment. (C) Alignment produced in some jackknife replicate by randomly deleting 50% of the original alignment columns. Phylogenetic trees are derived from each bootstrap/jackknife alignment; the bootstrap/jackknife value is the percentage with which a branch (i.e., the respective bipartition of the taxon set) occurs in these bootstrap/jackknife trees.

above is combined with heuristic searches using weighted parsimony. Here, random weights are assigned to some percentage of alignment sites. Hill-climbing using this random weighting scheme is equivalent to searching in a distorted tree landscape in which valleys in the unweighted landscape may have been converted into hill slopes, thus allowing exploration of tree islands that were unaccessible in the unweighted tree landscape. After a locally optimal tree in the distorted tree landscape has been found, this tree is used as the starting tree in a new round of unweighted hill-climbing. This subsequent use of unweighted and weighted searches is repeated several times, finished by a final round of unweighted hill-climbing. Ratchet analysis and other algorithmic improvements (e.g., Goloboff 1999) are implemented in the fast parsimony program TNT (see Table 12.1).

8.3. Heuristic Searches Using Genetic Algorithms

More recently, genetic algorithms have been suggested for the maximum-likelihood criterion (Lemmon and Milinkovitch 2002, Zwickl 2006). We will illustrate the principle given by Lemmon and Milinkovitch (2002). In their approach, a synchronous evolution of populations of phylogenetic trees is simulated, during which the trees of each generation are subjected to mutation events with subsequent selection governed by the maximum-likelihood principle. In this process the populations are linked by a "consensus-pruning" principle: those parts of the trees conserved to a high degree across the current populations have lower mutation probabilities. The process starts with populations of random trees, or with trees obtained by stochastically distorted neighbor-joining.

8.4. Quartet Puzzling

This heuristic approach was originally described for maximum-likelihood analysis (Strimmer and von Haeseler 1996), but can principally be applied to other methods of phylogenetic reconstruction as well. In a first step, all subsets consisting of four sequences (*quartets*) are considered. For each of these sequence quartets an optimal tree is derived and stored. In the next step, the "puzzling procedure", the sequences are arranged in random order. For the first four sequences, the appropriate quartet topology is chosen from the set of stored quartets' trees. If a tree T_n containing n sequences has already been constructed, the $n + 1$th sequence in the list is inserted into T_n in a position that is in conflict with the lowest number of the stored quartet topologies. This process is continued until all sequences are integrated into a final quartet-puzzling topology.

TABLE 12.1 Software that can be Used for Molecular Phylogenetic Reconstruction

Functionality	Title	Homepage	Main features	Availability
Alignment	ClustalW	http://www.ebi.ac.uk/Tools/clustalw/index.html	Outdated; GUI (ClustalX)	Free binaries and source code; web service
Alignment	Dialign	http://dialign.gobics.de/	Accurate	Source code; web service
Alignment	MAFFT	http://align.bmr.kyushu-u.ac.jp/mafft/software/	Fast and accurate	Free binaries and source code; web service
Alignment	MUSCLE	http://www.drive5.com/muscle/	Fast and accurate	Free binaries and source code; web service
Alignment	POA	http://bioinfo.mbi.ucla.edu.poa	Fast and accurate	Source code; web service
Tree reconstruction	BEAST	http://beast.bio.ed.ac.uk/	Bayesian analysis under a molecular clock	Free binaries and source code
Tree reconstruction	FastME	http://atgc.lirmm.fr/fastme/	Very fast distance method	Free binaries and source code; web service
Tree reconstruction	GARLI	http://www.bio.utexas.edu/faculty/antisense/garli/Garli.html	Very fast ML program	Free binaries and source code
Tree reconstruction	IQPNNI	http://www.cibiv.at/software/iqpnni/	Fast ML program	Free binaries and source code
Tree reconstruction	Leaphy	http://www.bioinf.manchester.ac.uk/leaphy/Leaphy.htm	Fast ML program	Free binaries
Tree reconstruction	MEGA	http://www.megasoftware.net/	Distance and MP methods; GUI	Free binaries (Windows only)
Tree reconstruction	MrBayes	http://sourceforge.net/projects/mrbayes/	Bayesian analysis	Free binaries and source code
Tree reconstruction	PAUP*	http://paup.csit.fsu.edu/downl.html	Rich set of methods; GUI for non-Intel-based Mac only	Commercial license
Tree reconstruction	PHYLIP	http://evolution.genetics.washington.edu/phylip/getme.html	Rich set of methods	Free binaries and source code; some functionality as web service
Tree reconstruction	PHYML	http://atgc.lirmm.fr/phyml/	Fast ML program	Free binaries; web service
Tree reconstruction	POY	http://research.amnh.org/scicomp/projects/poy.php	Direct optimization of unaligned sequences	Free binaries and source code
Tree reconstruction	RAxML	http://www.kramer.in.tum.de/exelixis/software.html	Very fast ML program	Free binaries and source code; web service
Tree reconstruction	TNT	http://www.zmuc.dk/public/phylogeny/TNT/	Very fast MP program; GUI for Windows only	Commercial license and free test versions
Tree reconstruction	Treefinder	http://www.treefinder.org/	Fast ML program; GUI	Free binaries
Network reconstruction	SplitsTree	http://www.splitstree.org/	Rich set of methods; GUI	Free binaries
Network reconstruction	T-Rex	http://www.labunix.uqam.ca/~makarenv/trex.html	Constructs reticulation networks; GUI	Free binaries (Windows only); web service
Viewing and editing trees	Dendroscope	http://www-ab.informatik.uni-tuebingen.de/software/dendroscope/welcome.html	Suitable for very large trees; GUI	Free binaries
Viewing and editing trees	FigTree	http://tree.bio.ed.ac.uk/software/figtree	GUI	Free binaries
Viewing and editing trees	Njplot	http://pbil.univ-lyon1.fr/software/njplot.html	GUI	Free binaries and source code
Viewing and editing trees	TreeView	http://darwin.zoology.gla.ac.uk/~rpage/treeviewx/download.html	GUI	Free binaries and source code
Miscellaneous	MacClade	http://macclade.org/	Reconstruction of character evolution; GUI	Commercial license (Mac only)
Miscellaneous	Mesquite	http://mesquiteproject.org/	Testing of various evolutionary hypotheses; GUI	Free binaries; web service
Miscellaneous	Modeltest	http://darwin.uvigo.es/software/modeltest.html	Determines best model in an ML framework	Free binaries and source code; web service
Miscellaneous	PAML	http://abacus.gene.ucl.ac.uk/software/paml.html	Testing of various evolutionary hypotheses	Free binaries and source code

This process of quartet-puzzling of randomly ordered sequences can be iterated. It has been suggested (Strimmer and von Haeseler 1996) that the percentages at which certain groups of sequences appear in the resulting set of quartet-puzzling trees be used as branch support values.

9. PHYLOGENETIC ANALYSIS USING NON-DNA DATA

In our treatment of methods of molecular phylogenetic analysis we have so far assumed that datasets consist of alignable DNA sequences. However, many of the principles described above can also be applied on different types of molecular data.

9.1. Amino Acid Sequences

Alignments of amino acid sequences can be analyzed by using maximum parsimony, distance methods or probabilistic methods explained above. However, since the number of character states increases from four to twenty, an amino acid substitution model is computationally much more expensive than a DNA substitution model. To derive amino acid substitution models, empirical data have been evaluated, e.g., sets of pairs of closely related protein sequences (e.g., Dayhoff et al. 1978, Jones et al. 1992, Whelan and Goldman 2001) or even whole (mitochondrial) genomes (Adachi and Hasegawa 1996). Each of these models can be used for maximum-likelihood or Bayesian analysis of an amino acid alignment. Alternatively, they can be used to derive pairwise distances between the amino acid sequences which subsequently may be evaluated using distance analysis.

9.2. DNA Fragment Banding Patterns

Cloning- or PCR-based techniques such as RFLP (*restriction fragment length polymorphisms*), AFLP (*amplified fragment-length polymorphisms*) or RAPD (*randomly amplified polymorphic DNAs*) produce a specific DNA fragment banding pattern for an individual or a taxon. Such banding patterns may be phylogenetically evaluated using distance, parsimony or probabilistic analysis. Basic principles are described in Felsenstein (2004: Chapter 15). However, caution must be exercised with some standard methods that are used in sequence analysis, e.g., bootstrapping (see section 7), because the considered characters are not independent.

10. PHYLOGENETIC ANALYSIS BASED ON GENOME OR PROTEOME DATA

The most powerful molecular phylogenetic analyses that can be implemented today use genome data. The number of published genomes is steadily increasing; in October 2007 there were 676 whole genomes available (48 archaeal, 552 bacterial, 76 eukaryal), with a reported number of ongoing genome projects of no less than 2318 (including 878 eukaryotic genomes; www.genomesonline.org). Since the first sequenced eukaryotic genome was that of *Saccharomyces cerevisiae* (Goffeau et al. 1996), an early focus in eukaryotic genome sequencing has been on the Saccharomycetales, and subsequently this fungal group has become a key group for comparative (including phylogenetic) analysis of eukaryotic genomes. Since a separate chapter of this book has been dedicated to yeast phylogenomics (Chapter 11) we will only give some brief notes on available methods for phylogenetic reconstruction from genome data here; for a broader introduction, see the review of Snel et al. (2005). Many of these methods have first been applied to prokaryotic genomes, and to mitochondrial genomes in order to estimate phylogenetic relationships in eukaryotic organisms. Most of these methods can also be applied to derive phylogenetic hypotheses from proteome data.

10.1. Cladistic Analysis Using Genome-Related Characters

A straightforward method of cladistic analysis using genomes is to use character matrices, in which each character is defined by the presence or absence of a certain homologous gene in a genome. These data can then be analyzed using the maximum parsimony criterion (see section 5), preferentially under the constraint that a gene can be lost independently along several branches in a phylogenetic tree, but can be gained only once (*Dollo parsimony*; Farris 1977, Le Quesne 1974).

Genomes, however, also offer characters that can more or less directly be used as apomorphies to define monophyletic groups. Examples are the order in which certain genes appear in a genome (*gene arrangement*; e.g., Boore et al. 1998, Korbel et al. 2002) or the occurrence of specific indels at a genomic locus (e.g., Qiu et al. 1998). Retroposed elements are repetitive DNA sequences that frequently occur in eukaryotic genomes and can be copied and pasted into new sites in the genome by processes that rely on RNA intermediates (Shedlock and Okada 2000). They are considered as nearly homoplasy-free genomic characters, and have recently been used to resolve phylogenetic relationships that had been highly controversial in the past (e.g., Kriegs et al. 2006). Additional examples of genome-level characters that have successfully been used in cladistic phylogenetic analysis are reviewed in Boore (2006). Not all of these methods require fully sequenced genomes. If the locations of tentatively useful genomic elements are known from the analysis of exemplar genomes, other taxa can be screened for the occurrence of these elements using PCR-based techniques (e.g., Kriegs et al. 2006).

10.2. Distances Derived From Genomes

A number of ways have been described for deriving distances between genomes. Such genomic distances can be used to construct phylogenetic trees or networks according to one of the distance methods described in section 4. Here are some examples for distance measures between two genomes G_1, G_2.

A straightforward distance based on the proportion of genes shared between G_1 and G_2 is (Snel et al. 1999)

$$d_{\text{genecont}}(G_1, G_2) = 1 - \frac{|G_1 \cap G_2|}{\min\ (|G_1|, |G_2|)},$$

where $|G_i|$ denotes the number of genes contained in G_i, and $|G_1 \cap G_2|$ the number of genes shared between G_1 and G_2. Distances can also be derived from the minimal number of operations (such as inversions and transpositions) that are needed to transform an ordered set of genes in G_1 to the order in which the same genes are arranged in G_2 (e.g., Blanchette et al. 1999).

Naturally, methods for deriving distances from unaligned sequence data (see section 4.2) can also be applied to whole genomes. Some of these methods, e.g., distances based on shared information (Li et al. 2001), the average lengths of maximum common substrings (Ulitsky et al. 2006) or the frequency of amino acid *K*-strings in complete proteomes (Qi et al. 2004) were in fact

designed for the estimation of phylogenetic trees from complete genomes or proteomes. These methods have been shown to yield highly-resolved phylogenetic hypotheses that are close to accepted state-of-the art phylogenies for the examplary datasets tested.

A recently proposed genomic distance that involves pairwise alignments of genomic fragments (Auch et al. 2006, Henz et al. 2005) is based on the *Basic Local Alignment Search Tool* (BLAST; Altschul et al. 1997), an algorithm that detects significantly similar local regions between DNA or amino acid sequences. BLAST can be used to compare two full genome sequences G and H with each other. The result is a set of sequence pairs (matches) of significant similarity. To deal with repeats in the genomes, which may confuse the BLAST result, a maximum subset of matches is then selected such that any nucleotide position in either genome is contained in at most one selected match. Then a possible BLAST distance is given by

$$d_{\text{match}}(G,H) = -\log\frac{|G_{\text{match}}| + |H_{\text{match}}|}{|G| + |H|}.$$

Here, $|G|$ and $|H|$ denote the length of genomes G and H, respectively (in base pairs), and $|G_{\text{match}}|$ and $|H_{\text{match}}|$ the number of base pairs in G and H that are contained in one of the matches.

10.3. Concatenated Alignments and Supertrees

A number of highly-resolved phylogenetic trees have been published recently which are based on the analysis of concatenated alignments of single genes or single proteins for which homologues exist in each of the sampled genomes (e.g., Ciccarelli et al. 2006, Fitzpatrick et al. 2006, Kuramae et al. 2006, Rokas et al. 2003). Distance-, parsimony- or likelihood-based methods, as described in this chapter, have been used. However, the more genomes that are included in such phylogenetic analyses, the smaller becomes the number of homologous gene or protein sequences common to all genomes. A workaround to deal with this problem is to use supertrees (see section 2.2.2). Here, in a first step phylogenetic trees are computed from single-gene or multigene alignments that do not necessarily include all of the taxa for which a big tree is to be constructed. In a second step these trees are then combined into a supertree that covers the whole taxon sampling (e.g., Dutilh et al. 2007, Fitzpatrick et al. 2006).

11. CONCLUSION

The past decades have seen a dramatic acceleration in the evolution of methods for molecular phylogenetic reconstruction. This was clearly caused by the even more dramatic increase in production of sequence data. Today whole genomes are being published at ever-shortening intervals. Phylogenetic analyses of these data have completely changed our classification concepts, particularly in organisms such as yeast-forming fungi, where only a limited number of morphological or physiological characteristics are available.

However, as the amount of sequence data increases and can be analyzed with more sophisticated methods, there is also increasing evidence that a "tree of life" may not be a suitable model for evolution. Phylogenomic studies (e.g., Holland et al. 2004a, Rokas et al. 2003) have highlighted the long known divergence of gene trees vs species trees, a problem that cannot even be unequivocally solved by the concatenation of a large number of single-gene or single-protein alignments (Kuramae et al. 2006b). Among the possible reasons for this problem are mechanisms such as hybridization events (Hegarty and Hiscock 2005), genome duplication with subsequent gene losses (Wolfe 2006), or horizontal (lateral) gene transfer (Choi and Kim 2007).

It is therefore crucial to keep in mind that the tree-building phylogenetic methods outlined in this chapter, which still represent the majority of methods used in molecular phylogenetic reconstruction, can only give limited approximations of the complex reality of evolution. In the future, we will certainly see a greater diversity of methods, allowing a better reflection of this complex evolutionary reality. This will only increase the power and fascination of the dynamic field of molecular phylogenetic reconstruction.

Note:
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Key to Species

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INTRODUCTION

Species given in this key are those yeasts that readily grow in the standard media used for fermentation and growth tests. Consequently, species of *Coccidiascus*, *Endomyces*, Endomycete-like species, *Malassezia* and those assigned to several other genera are excluded. Some species occur more than once in the key, depending on variability of fermentation and growth reactions.

When sexual states are known for anamorphic species, the taxon is given in the key under the teleomorphic name. For example, *Phaffia rhodozyma* is given as *Xanthophyllomyces dendrorhous*. Known anamorph–teleomorph connections can be made by consulting the indexes.

Species separations in this key are often made from the reaction on a single test. Consequently, species descriptions need to be consulted to verify the identification.

To simplify keying, reactions used in the key, as well as in the table "Summary of Species Characteristics", have been reduced to four choices: +, positive; −, negative; v, variable; n, absence of data. The following symbols are grouped under positive reactions: +, +/l, l, d, +/w, w, ws, lw. Variable reactions include: v, +/−, w/− and −/l. These symbols, which are also used in various chapters, are defined in the chapter "Use of this Book".

No.	Test	Positive	Negative
1	DBB	2	592
2	Nitrate growth	3	220
3	*myo*-Inositol growth	4	75
4	Starch formation	5	50
5	Growth at 25°C	6	40
6	D-Glucosamine growth	7	15
7	Melibiose growth	8	12
8	Vitamin-free growth	*Cryptococcus aerius* *Cryptococcus phenolicus*	9
9	Glycerol growth	10	11
10	Erythritol growth	*Bullera taiwanensis*	*Cryptococcus silvicola*
11	Ethanol growth	*Cryptococcus cylindricus*	*Bullera cylindrica*
12	Vitamin-free growth	*Cryptococcus terreus*	13
13	Saccharate growth	14	*Cryptococcus chernovii*
14	Growth at 30°C	*Cryptococcus magnus* *Filobasidium floriforme*	*Cryptococcus magnus* *Cryptococcus oeirensis*
15	Growth at 30°C	16	32
16	Methyl-α-D-glucoside growth	17	28
17	Galactitol growth	18	23
18	DL-Lactate growth	19	21
19	Growth at 35°C	20	*Cryptococcus albidus* var. *albidus* *Cryptococcus liquefaciens* *Cryptococcus wieringae*

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No.	Test	Positive	Negative
20	Soluble starch growth	*Cryptococcus albidus* var. *albidus*	*Cryptococcus albidus* var. *ovalis*
21	Melibiose growth	*Cryptococcus aerius*	22
22	Ethylamine growth	*Cryptococcus magnus*	*Cryptococcus wieringae*
23	Saccharate growth	24	*Cryptococcus diffluens*
24	Ethylamine growth	25	27
25	Ribitol growth	*Cryptococcus albidosimilis*	26
26	L-Sorbose growth	*Cryptococcus uzbekistanensis*	*Cryptococcus saitoi*
27	Soluble starch growth	*Cryptococcus albidus* var. *albidus* *Cryptococcus uzbekistanensis*	*Cryptococcus albidus* var. *ovalis* *Cryptococcus uzbekistanensis*
28	DL-Lactate growth	29	31
29	Soluble starch growth	*Cryptococcus albidus* var. *albidus*	30
30	Growth at 35°C	*Cryptococcus albidus* var. *ovalis*	*Cryptococcus albidus* var. *kuetzingii*
31	Glycerol growth	*Cystofilobasidium ferigula*	*Cryptococcus adeliensis*
32	Methyl-α-D-glucoside growth	33	35
33	Melibiose growth	34	22
34	Galactitol growth	*Cryptococcus aerius*	*Guehomyces pullulans*
35	Erythritol growth	36	37
36	L-Rhamnose growth	*Cystofilobasidium lacus-mascardii*	*Cystofilobasidium macerans*
37	L-Sorbose growth	38	39
38	Melibiose growth	*Cystofilobasidium bisporidii*	*Cystofilobasidium infirmominiatum*
39	Ethanol growth	*Cryptococcus albidus* var. *kuetzingii*	*Cryptococcus fuscescens*
40	Galactitol growth	41	44
41	Methanol growth	42	43
42	Melibiose growth	*Udeniomyces pyricola*	*Udeniomyces puniceus*
43	Methyl-α-D-glucoside growth	*Cryptococcus nyarrowii*	*Cystofilobasidium capitatum*
44	Erythritol growth	45	46
45	Methyl-α-D-glucoside growth	*Guehomyces pullulans*	*Tausonia pamirica*
46	Ribitol growth	47	49
47	Soluble starch growth	48	*Mrakia frigida*
48	Glycerol growth	*Mrakiella cryoconiti*	*Mrakia gelida*
49	Ethanol growth	*Cryptococcus antarcticus* var. *circumpolaris*	*Cryptococcus antarcticus* var. *antarcticus*
50	Vitamin-free growth	51	66
51	L-Rhamnose growth	52	57
52	Galactitol growth	53	55
53	Ribitol growth	54	*Cryptococcus terricola*
54	Melibiose growth	*Cryptococcus aerius*	*Ustilago maydis*
55	Methanol growth	*Pseudozyma rugulosa*	56
56	Melibiose growth	*Tilletiopsis albescens*	*Pseudozyma prolifica*
57	DL-Lactate growth	58	62
58	Ribitol growth	59	61
59	Methanol growth	*Pseudozyma flocculosa*	60
60	Soluble starch growth	*Tilletiopsis albescens* *Tilletiopsis pallescens*	*Pseudozyma fusiformata*
61	L-Sorbose growth	*Pseudozyma tsukubaensis*	*Rhodotorula phylloplana*
62	Glycerol growth	63	65
63	Melibiose growth	64	*Rhodotorula bacarum*
64	Soluble starch growth	*Tilletiopsis pallescens*	*Sympodiomycopsis paphiopedili*
65	L-Sorbose growth	*Tilletiopsis pallescens*	*Acaromyces ingoldii*
66	Growth at 30°C	67	71

No.	Test	Positive	Negative
67	Ethanol growth	68	*Pseudozyma aphidis*
68	Ribitol growth	69	*Bullera ninhbinhensis*
69	Melibiose growth	70	*Pseudozyma antarctica*
70	L-Rhamnose growth	*Pseudozyma parantarctica*	*Pseudozyma thailandica*
71	Methyl-α-D-glucoside growth	72	74
72	Ethanol growth	73	*Cryptococcus watticus*
73	Erythritol growth	*Rhodotorula bacarum*	*Rhodotorula yarrowii*
74	D-Glucosamine growth	*Itersonilia perplexans*	*Sporobolomyces inositophilus*
75	Soluble starch growth	76	140
76	Erythritol growth	77	94
77	Melibiose growth	78	87
78	Inulin growth	79	82
79	Galactitol growth	*Meira argovae*	80
80	Vitamin-free growth	*Tilletiopsis pallescens*	81
81	Lactose growth	*Tilletiopsis fulvescens* *Tilletiopsis minor*	*Tilletiopsis derxii*
82	Lactose growth	83	85
83	Vitamin-free growth	*Tilletiopsis pallescens*	84
84	Methyl-α-D-glucoside growth	*Sporobolomyces lophatheri*	*Bensingtonia ingoldii*
85	L-Sorbose growth	*Tilletiopsis pallescens*	86
86	Ethanol growth	*Tilletiopsis cremea* *Tilletiopsis washingtonensis*	*Tilletiopsis lilacina* *Tilletiopsis washingtonensis*
87	DL-Lactate growth	88	91
88	Raffinose growth	89	90
89	Galactitol growth	*Meira argovae*	*Tilletiopsis washingtonensis*
90	Growth at 30°C	*Sporobolomyces lactophilus*	*Rhodotorula hordea*
91	Glucose fermentation	92	93
92	Growth at 37°C	*Moniliella madida* *Moniliella megachiliensis*	*Moniliella suaveolens*
93	Ethanol growth	*Rhodotorula bacarum*	*Tilletiopsis penniseti*
94	Raffinose growth	95	129
95	DL-Lactate growth	96	108
96	Melibiose growth	97	101
97	Lactose growth	98	99
98	Inulin growth	*Tilletiopsis minor*	*Rhodotorula lactosa*
99	L-Sorbose growth	100	*Bensingtonia naganoensis*
100	Inulin growth	*Tilletiopsis flava*	*Sporobolomyces magnisporus*
101	Vitamin-free growth	102	105
102	Lactose growth	103	104
103	Galactose growth	*Rhodotorula ingeniosa*	*Rhodotorula vanillica*
104	D-Mannitol growth	*Sporidiobolus metaroseus*	*Sporobolomyces roseus*
105	Salicin growth	106	107
106	Galactose growth	*Kondoa aeria*	*Kondoa malvinella*
107	Ribitol growth	*Bensingtonia changbaiensis*	*Tilletiopsis oryzicola*
108	Starch formation	109	114
109	Galactose growth	110	112
110	Ribitol growth	111	*Cryptococcus bhutanensis*
111	Lactose growth	*Mrakiella aquatica*	*Mrakia gelida*
112	D-Mannitol growth	113	*Cryptococcus vishniacii*
113	Melibiose growth	*Udeniomyces pannonicus*	*Udeniomyces megalosporus*

No.	Test	Positive	Negative
114	L-Sorbose growth	115	123
115	Ethanol growth	116	121
116	D-Arabinose growth	117	119
117	Ribitol growth	118	*Sporobolomyces salmoneus*
118	Galactitol growth	*Rhodotorula javanica*	*Sporobolomyces nylandii*
119	Methanol growth	*Ascoidea africana*	120
120	Inulin growth	*Sporobolomyces bannaensis*	*Sporobolomyces jilinensis*
121	Glycerol growth	122	*Sporobolomyces blumeae*
122	Ribitol growth	*Cyrenella elegans*	*Sporobolomyces patagonicus*
123	Methyl-α-D-glucoside growth	124	125
124	Ethanol growth	*Sporobolomyces phaffii*	*Sporobolomyces xanthus*
125	Melezitose growth	126	128
126	D-Glucosamine growth	*Itersonilia perplexans*	127
127	Ethylamine growth	*Bensingtonia naganoensis*	*Bensingtonia thailandica*
128	Glycerol growth	*Bensingtonia changbaiensis*	*Sporobolomyces taupoensis*
129	Starch formation	130	132
130	Ribitol growth	131	*Cryptococcus friedmannii*
131	Saccharate growth	*Cryptococcus huempii*	*Mrakia curviuscula*
132	D-Arabinose growth	133	138
133	Galactose growth	134	136
134	Galactitol growth	*Sporobolomyces poonsookiae*	135
135	L-Sorbose growth	*Sporobolomyces yunnanensis*	*Sporobolomyces griseoflavus*
136	Lactose growth	*Sporobolomyces lactophilus*	137
137	Methyl-α-D-glucoside growth	*Sporidiobolus johnsonii*	*Rhodotorula buffonii*
138	Methanol growth	*Ascoidea africana*	139
139	Melezitose growth	*Bensingtonia phyllada*	*Leucosporidium antarcticum*
140	Melezitose growth	141	180
141	Raffinose growth	142	167
142	Erythritol growth	143	148
143	Vitamin-free growth	144	146
144	Galactitol growth	*Rhodotorula diffluens*	145
145	DL-Lactate growth	*Moniliella spathulata*	*Moniliella suaveolens*
146	Ethanol growth	147	*Rhodotorula acheniorum*
147	Galactose growth	*Kurtzmanomyces* sp. (*Mycogloea nipponica*)	*Kurtzmanomyces insolitus*
148	L-Sorbose growth	149	163
149	D-Glucosamine growth	150	156
150	L-Rhamnose growth	151	154
151	Galactitol growth	152	153
152	Growth at 35°C	*Rhodotorula pacifica*	*Leucosporidium scottii*
153	Galactose growth	*Leucosporidiella yakutica*	*Leucosporidiella creatinivora*
154	DL-Lactate growth	155	*Leucosporidiella muscorum*
155	Saccharate growth	*Leucosporidium golubevii*	*Leucosporidiella fragaria*
156	Galactitol growth	157	159
157	L-Rhamnose growth	*Rhodotorula pacifica*	158
158	Vitamin-free growth	*Rhodosporidium fluviale*	*Rhodosporidium sphaerocarpum*
159	L-Rhamnose growth	160	161
160	DL-Lactate growth	*Rhodosporidium babjevae*	*Rhodosporidium diobovatum*
161	Inulin growth	*Rhodosporidium diobovatum*	162
162	Xylitol growth	*Rhodotorula glutinis*	*Rhodosporidium kratochvilovae*

No.	Test	Positive	Negative
163	Ethanol growth	164	166
164	Ribitol growth	165	*Sporobolomyces ruberrimus*
165	Galactitol growth	*Rhodotorula dairenensis*	*Rhodosporidium toruloides*
166	Glycerol growth	*Bensingtonia pseudonaganoensis*	*Cryptococcus vishniacii*
167	Vitamin-free growth	168	171
168	L-Sorbose growth	169	170
169	Galactitol growth	*Kriegeria eriophori*	*Rhodotorula pilati*
170	Erythritol growth	*Moniliella suaveolens*	*Rhodotorula cresolica*
171	Lactose growth	172	175
172	Galactose growth	173	174
173	Glycerol growth	*Rhodotorula ferulica*	*Mrakia curviuscula*
174	Ethylamine growth	*Sporobolomyces tsugae*	*Bensingtonia phyllada*
175	D-Ribose growth	176	178
176	DL-Lactate growth	*Erythrobasidium hasegawianum*	177
177	Growth at 35°C	*Rhodotorula crocea*	*Sporobolomyces foliicola*
178	Xylitol growth	179	*Bensingtonia phyllada*
179	D-Arabinose growth	*Rhodotorula aurantiaca*	*Rhodotorula colostri*
180	Vitamin-free growth	181	195
181	Erythritol growth	182	186
182	Sucrose fermentation	183	185
183	Growth at 37°C	184	*Moniliella suaveolens*
184	Lactose growth	*Moniliella acetoabutens*	*Moniliella madida* *Moniliella megachiliensis*
185	D-Mannitol growth	*Moniliella nigrescens*	*Moniliella fonsecae*
186	Galactitol growth	187	189
187	Maltose growth	*Rhodosporidium paludigenum* *Sporidiobolus ruineniae*	188
188	Raffinose growth	*Sporidiobolus microsporus*	*Rhodosporidium lusitaniae*
189	Ethanol growth	190	194
190	L-Rhamnose growth	*Rhodotorula graminis*	191
191	D-Glucosamine growth	*Rhodotorula foliorum*	192
192	Xylitol growth	193	*Rhodotorula araucariae* *Sporobolomyces odoratus*
193	Growth at 35°C	*Sporidiobolus salmonicolor*	*Sporobolomyces odoratus*
194	Glycerol growth	*Leucosporidium fellii*	*Cryptococcus vishniacii*
195	D-Arabinose growth	196	202
196	Raffinose growth	197	200
197	Ethanol growth	198	199
198	Galactitol growth	*Rhodosporidium azoricum*	*Mrakia frigida*
199	Galactitol growth	*Sporobolomyces salicinus*	*Sporobolomyces subbrunneus*
200	Erythritol growth	*Sterigmatomyces halophilus*	201
201	Galactitol growth	*Sporobolomyces kluyveri-nielii*	*Rhodotorula pustula*
202	Maltose growth	203	207
203	Galactose growth	204	206
204	Erythritol growth	205	*Rhodotorula colostri*
205	Sucrose fermentation	*Moniliella oedocephalis*	*Moniliella mellis*
206	Erythritol growth	*Moniliella madida* *Moniliella megachiliensis*	*Leucosporidium antarcticum*
207	Ethanol growth	208	212
208	Ribitol growth	209	210

No.	Test	Positive	Negative
209	Glycerol growth	*Bensingtonia ciliata*	*Kurtzmanomyces nectairei*
210	Galactose growth	*Sporobolomyces falcatus*	211
211	Growth at 25°C	*Kurtzmanomyces tardus*	*Leucosporidium antarcticum*
212	Growth at 25°C	213	219
213	DL-Lactate growth	214	217
214	D-Gluconate growth	215	216
215	Ribitol growth	*Rhodotorula sonckii*	*Sporobolomyces coprosmicola*
216	Cellobiose growth	*Bensingtonia miscanthi*	*Sporobolomyces linderae*
217	Glycerol growth	218	*Sporobolomyces dimennae*
218	Cellobiose growth	*Bensingtonia miscanthi*	*Sporobolomyces novazealandicus*
219	Ribitol growth	*Bensingtonia yuccicola*	*Leucosporidium antarcticum*
220	Melibiose growth	221	397
221	Ethanol growth	222	301
222	Erythritol growth	223	278
223	Starch formation	224	262
224	Lactose growth	225	258
225	DL-Lactate growth	226	252
226	Creatinine growth	227	237
227	Glycerol growth	228	234
228	*myo*-Inositol growth	229	*Tremella fuciformis*
229	Vitamin-free growth	*Bullera coprosmaensis*	230
230	Inulin growth	231	232
231	Hexadecane growth	*Bulleromyces albus* *Cryptococcus musci*	*Bulleromyces albus* *Cryptococcus fragicola*
232	Hexadecane growth	*Cryptococcus allantoinivorans* *Cryptococcus longus* *Cryptococcus musci*	233
233	Growth at 35°C	*Cryptococcus allantoinivorans* *Cryptococcus laurentii*	*Cryptococcus allantoinivorans* *Cryptococcus fragicola*
234	Ribitol growth	235	*Cryptococcus podzolicus*
235	D-Glucosamine growth	236	*Bullera miyagiana*
236	Hexadecane growth	*Cryptococcus musci*	*Cryptococcus laurentii*
237	Galactitol growth	238	249
238	Soluble starch growth	239	246
239	Ribitol growth	240	245
240	*myo*-Inositol growth	241	*Tremella fuciformis*
241	Inulin growth	*Bulleromyces albus*	242
242	Growth at 30°C	243	*Bullera coprosmaensis*
243	Nitrite growth	*Cryptococcus flavescens* *Trichosporon dermatis* *Trichosporon mucoides*	244
244	Vitamin-free growth	*Cryptococcus flavescens*	*Cryptococcus daszewskae*
245	D-Arabinose growth	*Bulleromyces albus*	*Trichosporon jirovecii*
246	Melezitose growth	247	*Cryptococcus pseudolongus*
247	Vitamin-free growth	*Cryptococcus flavescens*	248
248	Inulin growth	*Bulleromyces albus* *Cryptococcus humicola*	*Cryptococcus humicola* *Cryptococcus ramirezgomezianus*
249	Glycerol growth	250	*Bullera miyagiana*
250	D-Gluconate growth	251	*Trichosporon lignicola*
251	Inulin growth	*Bulleromyces albus*	*Trichosporon moniliiforme*

No.	Test	Positive	Negative
252	Glycerol growth	253	256
253	Galactitol growth	254	*Trichosporon lignicola*
254	Methyl-α-D-glucoside growth	255	*Fellomyces fuzhouensis*
255	Vitamin-free growth	*Cryptococcus flavescens*	*Bullera taiwanensis* *Cryptococcus nemorosus*
256	Ribitol growth	257	*Cryptococcus podzolicus*
257	Galactose growth	*Cryptococcus flavescens*	*Cuniculitrema polymorpha*
258	Growth at 30°C	259	260
259	Galactitol growth	*Bullera kunmingensis* *Bullera sinensis* var. *sinensis* *Bullera sinensis* var. *lactis* *Cryptococcus fragicola* *Cryptococcus surugaensis*	*Cryptococcus amylolentus*
260	Soluble starch growth	261	*Cryptococcus luteolus*
261	L-Sorbose growth	*Bullera kunmingensis*	*Bullera coprosmaensis*
262	Ribitol growth	263	274
263	DL-Lactate growth	264	271
264	Galactitol growth	265	269
265	*myo*-Inositol growth	266	*Meira geulakonigii*
266	Soluble starch growth	267	*Cryptococcus humicola*
267	Nitrite growth	*Trichosporon porosum*	268
268	50% Glucose growth	*Trichosporon terricola*	*Cryptococcus daszewskae*
269	Melezitose growth	270	*Trichosporon debeurmannianum*
270	Salicin growth	*Trichosporon cutaneum*	*Trichosporon smithiae*
271	D-Mannitol growth	272	273
272	Methyl-α-D-glucoside growth	*Kockovaella barringtoniae*	*Fellomyces fuzhouensis*
273	L-Sorbose growth	*Rhodotorula benthica*	*Rhodotorula calyptogenae*
274	D-Arabinose growth	275	276
275	Glycerol growth	*Trichosporon mycotoxinivorans*	*Cryptococcus podzolicus*
276	D-Glucosamine growth	277	*Trichosporon jirovecii*
277	Nitrite growth	*Trichosporon wieringae*	*Trichosporon dehoogii*
278	Methyl-α-D-glucoside growth	279	296
279	Starch formation	280	287
280	Glycerol growth	281	284
281	Inulin growth	*Bulleromyces albus*	282
282	Galactitol growth	283	*Trichosporon loubieri*
283	Nitrite growth	*Trichosporon laibachii*	*Tremella encephala* *Tremella indecorata*
284	Ribitol growth	285	*Cryptococcus podzolicus*
285	Galactose growth	286	*Cuniculitrema polymorpha*
286	L-Sorbose growth	*Tremella indecorata*	*Papiliotrema bandonii*
287	Soluble starch growth	288	294
288	*myo*-Inositol growth	289	293
289	Galactitol growth	290	292
290	Glycerol growth	291	*Cryptococcus podzolicus*
291	Ribitol growth	*Bullera pseudoalba*	*Trichosporon sporotrichoides*
292	Raffinose growth	*Trichosporon loubieri*	*Trichosporon gamsii*
293	Methanol growth	*Ascoidea africana*	*Bannoa hahajimensis*
294	Ribitol growth	295	*Trichosporon guehoae*
295	Galactitol growth	*Cryptococcus arrabidensis*	*Trichosporon vadense*

No.	Test	Positive	Negative
296	Methanol growth	297	298
297	*myo*-Inositol growth	*Chionosphaera cuniculicola*	*Ascoidea africana*
298	Galactitol growth	299	300
299	Glycerol growth	*Curvibasidium pallidicorallinum*	*Tremella neofoliacea*
300	D-Glucosamine growth	*Itersonilia perplexans*	*Bensingtonia subrosea*
301	Starch formation	302	362
302	*myo*-Inositol growth	303	349
303	Lactose growth	304	339
304	Growth at 30°C	305	320
305	Erythritol growth	306	316
306	L-Sorbose growth	307	314
307	Vitamin-free growth	308	309
308	Methyl-α-D-glucoside growth	*Fellomyces borneensis*	*Fellomyces thailandicus*
309	DL-Lactate growth	310	312
310	Inulin growth	*Bulleromyces albus*	311
311	Growth at 37°C	*Fellomyces penicillatus*	*Bullera japonica* *Cryptococcus peneaus* *Cryptococcus taeanensis*
312	Glycerol growth	313	*Bullera siamensis*
313	Growth at 37°C	*Fellomyces penicillatus*	*Bullera penniseticola*
314	Inulin growth	*Bulleromyces albus*	315
315	Nitrite growth	*Bullera mrakii* *Bullera oryzae*	*Auriculibuller fuscus* *Bullera mrakii*
316	Inulin growth	317	318
317	DL-Lactate growth	*Bulleromyces albus*	*Cryptococcus aureus*
318	Methyl-α-D-glucoside growth	319	*Fellomyces chinensis*
319	L-Sorbose growth	*Bullera melastomae*	*Bulleribasidium oberjochense*
320	Ribitol growth	321	335
321	DL-Lactate growth	322	330
322	Methyl-α-D-glucoside growth	323	*Fellomyces chinensis* *Fellomyces lichenicola*
323	L-Sorbose growth	324	326
324	Inulin growth	*Bulleromyces albus*	325
325	D-Glucitol growth	*Cryptococcus carnescens* *Cryptococcus tephrensis* *Trimorphomyces papilionaceus*	*Cryptococcus perniciosus*
326	D-Glucitol growth	327	*Cryptococcus paraflavus*
327	Inulin growth	*Bulleromyces albus*	328
328	Erythritol growth	329	*Bulleribasidium oberjochense*
329	Glycerol growth	*Cryptococcus carnescens*	*Bullera mrakii*
330	L-Sorbose growth	331	332
331	Erythritol growth	*Bullera penniseticola* *Cryptococcus heimaeyensis* *Cryptococcus tephrensis* *Cryptococcus victoriae* *Trimorphomyces papilionaceus*	*Cryptococcus armeniacus* *Trimorphomyces papilionaceus*
332	Soluble starch growth	333	*Cryptococcus cistialbidi*
333	Erythritol growth	334	*Bulleribasidium oberjochense* *Cryptococcus amylolyticus*
334	Glycerol growth	*Cryptococcus victoriae*	*Bullera unica*

No.	Test	Positive	Negative
335	Glycerol growth	336	337
336	Methyl-α-D-glucoside growth	*Bulleromyces albus*	*Fellomyces lichenicola*
337	D-Glucitol growth	338	*Dioszegia catarinonii* *Dioszegia takashimae*
338	Erythritol growth	*Bullera sakaeratica*	*Bullera pseudovariabilis*
339	DL-Lactate growth	340	346
340	Erythritol growth	341	344
341	Citrate growth	342	*Bullera nakasei* *Bullera panici*
342	Soluble starch growth	343	*Cryptococcus luteolus*
343	L-Sorbose growth	*Bullera pseudohuiaensis* *Bullera pseudoschimicola* *Bullera waltii*	*Bullera mrakii*
344	Citrate growth	345	*Bullera cylindrica*
345	L-Sorbose growth	*Bullera pseudohuiaensis* *Bullera variabilis*	*Bullera variabilis* *Bulleribasidium oberjochense*
346	Ribitol growth	347	*Bullera komagatae*
347	Raffinose growth	348	*Tremella neofoliacea*
348	Citrate growth	*Bullera formosana* *Bulleribasidium oberjochense*	*Bullera huiaensis*
349	D-Glucitol growth	350	360
350	Lactose growth	351	355
351	Methyl-α-D-glucoside growth	352	354
352	Cellobiose growth	353	*Bullera anomala*
353	L-Sorbose growth	*Trimorphomyces papilionaceus*	*Bullera hannae*
354	Erythritol growth	*Tremella nivalis*	*Fellomyces mexicanus*
355	Glycerol growth	356	357
356	Saccharate growth	*Dioszegia crocea*	*Dioszegia aurantiaca*
357	Ribitol growth	358	359
358	Methyl-α-D-glucoside growth	*Dioszegia fristingensis*	*Dioszegia statzelliae*
359	Methyl-α-D-glucoside growth	*Bullera begoniae*	*Dioszegia changbaiensis*
360	L-Arabinitol growth	361	*Dioszegia catarinonii* *Dioszegia takashimae*
361	D-Mannitol growth	*Dioszegia zsoltii* var. *zsoltii*	*Dioszegia zsoltii* var. *yunnanensis*
362	Methyl-α-D-glucoside growth	363	374
363	Lactose growth	364	370
364	L-Sorbose growth	365	368
365	D-Glucosamine growth	366	*Bullera siamensis*
366	D-Gluconate growth	367	*Kockovaella thailandica*
367	Growth at 30°C	*Fellomyces polyborus*	*Trimorphomyces papilionaceus*
368	DL-Lactate growth	*Bullera boninensis* *Cryptococcus flavus*	369
369	Erythritol growth	*Bullera arundinariae*	*Kockovaella sacchari*
370	Glycerol growth	371	372
371	Galactose growth	*Bannoa hahajimensis* *Sporobolomyces syzygii*	*Sporobolomyces ruber*
372	Erythritol growth	*Bullera schimicola*	373
373	*myo*-Inositol growth	*Bullera hubeiensis*	*Bullera setariae*
374	Erythritol growth	375	382
375	*myo*-Inositol growth	376	379

No.	Test	Positive	Negative
376	DL-Lactate growth	377	378
377	L-Sorbose growth	*Kockovaella litseae*	*Fellomyces sichuanensis*
378	Ribitol growth	*Fellomyces thailandicus*	*Kockovaella vietnamensis*
379	Glycerol growth	380	381
380	Galactitol growth	*Fellomyces distylii*	*Tilletiopsis derxii*
381	L-Sorbose growth	*Kockovaella cucphuongensis*	*Kockovaella machilophila*
382	Galactitol growth	383	390
383	D-Ribose growth	384	387
384	Glycerol growth	385	386
385	*myo*-Inositol growth	*Fellomyces chinensis* *Fellomyces lichenicola*	*Fellomyces ogasawarensis*
386	*myo*-Inositol growth	*Kockovaella imperatae*	*Kockovaella calophylli*
387	Galactose growth	388	389
388	L-Sorbose growth	*Sporobolomyces ogasawarensis*	*Sporobolomyces pyrrosiae*
389	Lactose growth	*Sporobolomyces diospyroris*	*Sporobolomyces dracophylli*
390	L-Sorbose growth	391	394
391	D-Ribose growth	392	393
392	D-Mannitol growth	*Kockovaella thailandica*	*Fellomyces horovitziae*
393	Growth at 30°C	*Sporobolomyces bischofiae*	*Sporobolomyces ogasawarensis*
394	D-Glucosamine growth	*Itersonilia perplexans*	395
395	Glycerol growth	396	*Sporobolomyces clavatus*
396	Maltose growth	*Bensingtonia subrosea*	*Tilletiaria anomala*
397	Maltose growth	398	540
398	*myo*-Inositol growth	399	471
399	Methyl-α-D-glucoside growth	400	455
400	Starch formation	401	435
401	DL-Lactate growth	402	421
402	Erythritol growth	403	411
403	Raffinose growth	404	408
404	Inulin growth	*Bulleromyces albus*	405
405	Glycerol growth	406	407
406	Nitrite growth	*Cryptococcus curvatus* *Fibulobasidium inconspicuum*	*Cryptococcus curvatus* *Sirobasidium intermedium*
407	D-Glucosamine growth	*Fibulobasidium inconspicuum*	*Cryptococcus heveanensis*
408	Galactitol growth	*Sirobasidium magnum*	409
409	Nitrite growth	410	*Trichosporon asahii* *Trichosporon faecale*
410	Cycloheximide 0.1% growth	*Trichosporon asahii*	*Trichosporon coremiiforme*
411	D-Glucosamine growth	412	417
412	Inulin growth	*Bulleromyces albus*	413
413	Ethanol growth	414	*Tremella moriformis*
414	Galactitol growth	415	416
415	Growth at 30°C	*Tremella encephala* *Tremella indecorata*	*Tremella aurantia* *Tremella indecorata*
416	Raffinose growth	*Tremella aurantia*	*Trichosporon asahii*
417	Cellobiose growth	418	*Filobasidium uniguttulatum*
418	Inulin growth	*Bulleromyces albus*	419
419	Galactitol growth	420	*Trichosporon asahii*
420	L-Sorbose growth	*Holtermannia corniformis*	*Cryptococcus festucosus*
421	Lactose growth	422	430

No.	Test	Positive	Negative
422	Galactitol growth	423	427
423	D-Glucitol growth	424	*Bullera hoabinhensis*
424	Ribitol growth	425	*Cryptococcus magnus* *Cryptococcus mycelialis*
425	D-Glucosamine growth	*Cryptococcus magnus* *Tremella encephala*	426
426	Cadaverine growth	*Cryptococcus magnus*	*Kwoniella mangroviensis*
427	Raffinose growth	428	429
428	Glycerol growth	*Cryptococcus mycelialis*	*Bullera formosensis*
429	D-Arabinose growth	*Trichosporon asahii*	*Cryptococcus gastricus*
430	Glycerol growth	431	433
431	Glucose fermentation	*Filobasidium capsuligenum*	432
432	Galactitol growth	*Cryptococcus nyarrowii*	*Filobasidium uniguttulatum*
433	Galactitol growth	434	*Cryptococcus gastricus*
434	Growth at 40°C	*Filobasidiella neoformans*	*Filobasidiella bacillispora*
435	Raffinose growth	436	445
436	Growth at 30°C	437	443
437	Erythritol growth	438	441
438	Ribitol growth	439	*Trichosporon ovoides*
439	Xylitol growth	440	*Trichosporon caseorum*
440	Hexadecane growth	*Cryptococcus haglerorum*	*Cryptococcus curvatus*
441	Ribitol growth	442	*Trichosporon ovoides*
442	Lactose growth	*Trichosporon veenhuisii*	*Filobasidium uniguttulatum*
443	Ethanol growth	*Rhodotorula bacarum*	444
444	Saccharate growth	*Bullera koratensis*	*Bullera lagerstroemiae*
445	Soluble starch growth	446	454
446	L-Rhamnose growth	447	451
447	D-Mannitol growth	448	450
448	L-Arabinitol growth	*Trichosporon coremiiforme*	449
449	Ribitol growth	*Trichosporon siamense*	*Trichosporon ovoides*
450	Nitrite growth	*Trichosporon coremiiforme*	*Trichosporon asteroides*
451	D-Mannitol growth	452	*Trichosporon asteroides*
452	D-Gluconate growth	453	*Trichosporon domesticum*
453	D-Glucitol growth	*Trichosporon montevideense*	*Trichosporon inkin*
454	Ribitol growth	*Trichosporon caseorum*	*Trichosporon lactis*
455	Raffinose growth	456	463
456	Ethanol growth	457	460
457	DL-Lactate growth	458	459
458	Erythritol growth	*Cryptococcus curvatus*	*Trichosporon dulcitum*
459	D-Glucosamine growth	*Itersonilia perplexans*	*Rhodotorula pinicola*
460	Melezitose growth	461	*Bullera globispora*
461	L-Sorbose growth	*Sporobolomyces ogasawarensis*	462
462	Galactitol growth	*Dioszegia hungarica*	*Itersonilia perplexans*
463	D-Arabinose growth	464	467
464	Methanol growth	*Tremella foliacea*	465
465	Ethanol growth	466	*Cryptotrichosporon anacardii*
466	Lactose growth	*Bullera dendrophila*	*Holtermannia corniformis*
467	Glycerol growth	468	470
468	Xylitol growth	*Trichosporon dulcitum*	469
469	Lactose growth	*Cryptococcus gilvescens*	*Trichosporon brassicae*

No.	Test	Positive	Negative
470	Ethanol growth	*Cryptococcus gastricus*	*Filobasidium globisporum*
471	Galactose growth	472	519
472	Growth at 30°C	473	496
473	Lactose growth	474	488
474	Growth at 37°C	475	479
475	Galactitol growth	476	477
476	Xylitol growth	*Cryptococcus curvatus*	*Trichosporon caseorum*
477	Raffinose growth	*Cryptococcus curvatus*	478
478	Starch formation	*Trichosporon asahii*	*Trichosporon asteroides* *Trichosporon japonicum*
479	Raffinose growth	480	482
480	Ethanol growth	481	*Rhodotorula marina*
481	D-Glucitol growth	*Cryptococcus curvatus*	*Rhodotorula lysiniphila*
482	Soluble starch growth	483	485
483	Ethanol growth	484	*Tremella flava*
484	Glycerol growth	*Trichosporon scarabaeorum*	*Trichosporon aquatile*
485	Melezitose growth	486	487
486	Erythritol growth	*Tremella cinnabarina*	*Occultifur externus*
487	D-Mannitol growth	*Trichosporon lactis*	*Prototheca stagnora*
488	Raffinose growth	489	493
489	Soluble starch growth	490	492
490	D-Arabinose growth	491	*Sporobolomyces japonicus*
491	L-Arabinose growth	*Sporidiobolus pararoseus*	*Sporobolomyces salmoneus*
492	Ethanol growth	*Rhodotorula mucilaginosa*	*Sporobolomyces oryzicola*
493	L-Arabinose growth	*Rhodotorula lamellibrachii*	494
494	Trehalose growth	495	*Prototheca stagnora*
495	D-Glucitol growth	*Sakaguchia dacryoidea*	*Colacogloea papilionacea*
496	D-Glucosamine growth	497	507
497	Raffinose growth	498	503
498	L-Sorbose growth	499	501
499	Methanol growth	*Ascoidea africana*	500
500	D-Ribose growth	*Dioszegia buhagiarii*	*Sporobolomyces ogasawarensis*
501	Galactitol growth	502	*Itersonilia perplexans* *Kockovaella phaffii*
502	Soluble starch growth	*Kockovaella schimae*	*Fellomyces mexicanus*
503	Melezitose growth	504	506
504	Methanol growth	*Ascoidea africana*	505
505	Erythritol growth	*Tremella globispora*	*Rhodotorula bogoriensis*
506	D-Mannitol growth	*Tremella brasiliensis*	*Prototheca stagnora*
507	L-Arabinose growth	508	512
508	Ethanol growth	509	510
509	Galactitol growth	*Sporobolomyces phyllomatis*	*Rhodotorula aurantiaca*
510	Melezitose growth	511	*Bensingtonia sorbi*
511	Methyl-α-D-glucoside growth	*Sporobolomyces coprosmae*	*Sporobolomyces ogasawarensis*
512	D-Arabinose growth	513	515
513	D-Mannitol growth	514	*Prototheca stagnora*
514	Inulin growth	*Sporobolomyces carnicolor*	*Sporidiobolus longiusculus* *Sporobolomyces salmoneus*
515	Sucrose growth	516	518
516	Cellobiose growth	517	*Bensingtonia yamatoana*

No.	Test	Positive	Negative
517	DL-Lactate growth	*Mastigobasidium intermedium*	*Bensingtonia subrosea*
518	D-Mannitol growth	*Sporobolomyces fushanensis*	*Prototheca stagnora*
519	Trehalose growth	520	537
520	Glycerol growth	521	531
521	Cellobiose growth	522	530
522	Soluble starch growth	523	529
523	L-Arabinose growth	524	526
524	Methanol growth	*Ascoidea africana*	525
525	Erythritol growth	*Rhodotorula bacarum*	*Xanthophyllomyces dendrorhous*
526	D-Arabinose growth	527	528
527	Methyl-α-D-glucoside growth	*Sporobolomyces salmoneus*	*Sporobolomyces beijingensis*
528	Methanol growth	*Ascoidea africana*	*Bensingtonia subrosea*
529	Ethanol growth	*Rhodotorula aurantiaca*	*Sporobolomyces elongatus*
530	Xylitol growth	*Rhodotorula terpenoidalis*	*Bensingtonia yamatoana* *Rhodotorula auriculariae*
531	Ethanol growth	532	534
532	Ribitol growth	533	*Sporobolomyces beijingensis*
533	Sucrose growth	*Leucosporidium fasciculatum*	*Chionosphaera apobasidialis*
534	Raffinose growth	535	536
535	Ribitol growth	*Sporobolomyces sasicola*	*Cryptococcus vishniacii*
536	Sucrose growth	*Filobasidium elegans*	*Bensingtonia sakaguchii*
537	D-Mannitol growth	538	539
538	Erythritol growth	*Moniliella megachiliensis*	*Rhodotorula aurantiaca*
539	Growth at 37°C	*Prototheca zopfii* var. *zopfii* *Prototheca zopfii* var. 1 *Prototheca zopfii* var. 3 *Prototheca zopfii* var. *portoricensis*	*Prototheca zopfii* var. *zopfii* *Prototheca zopfii* var. 2 *Prototheca zopfii* var. 3 *Prototheca zopfii* var. *portoricensis*
540	Starch formation	541	555
541	*myo*-Inositol growth	542	547
542	Sucrose growth	543	544
543	Ethanol growth	*Cryptococcus dimennae*	*Fibulobasidium murrhardtense*
544	Erythritol growth	*Sirobasidium magnum*	545
545	Ribitol growth	546	*Trichosporon gracile*
546	Salicin growth	*Cryptococcus skinneri*	*Tremella neofoliacea*
547	D-Mannitol growth	548	552
548	Ethanol growth	549	550
549	Erythritol growth	*Tremella mesenterica*	*Tremella taiwanensis*
550	Erythritol growth	*Tremella resupinata*	551
551	Melezitose growth	*Tremella coalescens*	*Tremella tropica*
552	Galactose growth	553	554
553	Ethanol growth	*Prototheca wickerhamii*	*Tremella giraffa*
554	Sucrose growth	*Cryptococcus vishniacii*	*Prototheca ulmea*
555	Melezitose growth	556	566
556	D-Arabinose growth	557	562
557	Raffinose growth	558	560
558	Erythritol growth	*Agaricostilbum hyphaenes*	559
559	Galactitol growth	*Curvibasidium pallidicorallinum*	*Itersonilia perplexans*
560	Lactose growth	*Rhodotorula minuta* *Rhodotorula slooffiae*	561
561	Ethanol growth	*Rhodotorula laryngis*	*Sporobolomyces vermiculatus*

No.	Test	Positive	Negative
562	D-Glucosamine growth	563	564
563	Methanol growth	*Ascoidea africana*	*Itersonilia perplexans*
564	Ribitol growth	565	*Sakaguchia dacryoidea*
565	D-Mannitol growth	*Rhodotorula oryzae*	*Sporobolomyces symmetricus*
566	Growth at 30°C	567	581
567	Vitamin-free growth	568	573
568	D-Gluconate growth	569	571
569	Galactitol growth	*Rhodotorula nothofagi*	570
570	Growth at 35°C	*Rhodotorula retinophila*	*Rhodotorula philyla*
571	Ribitol growth	*Rhodotorula cycloclastica*	572
572	D-Glucitol growth	*Colacogloea peniophorae*	*Reniforma strues*
573	Trehalose growth	574	579
574	Salicin growth	575	577
575	Erythritol growth	576	*Cystobasidium fimetarium*
576	Galactitol growth	*Sterigmatomyces elviae*	*Bensingtonia musae*
577	Galactose growth	578	*Rhodotorula pallida*
578	D-Gluconate growth	*Sakaguchia dacryoidea*	*Prototheca wickerhamii*
579	D-Mannitol growth	*Naohidea sebacea*	580
580	*myo*-Inositol growth	*Sporopachydermia quercuum*	*Prototheca ulmea*
581	Galactose growth	582	586
582	DL-Lactate growth	583	585
583	Ethanol growth	584	*Rhodotorula armeniaca*
584	Ribitol growth	*Curvibasidium pallidicorallinum*	*Mastigobasidium intermedium*
585	Erythritol growth	*Sterigmatomyces halophilus*	*Curvibasidium cygneicollum*
586	Trehalose growth	587	591
587	Erythritol growth	588	589
588	*myo*-Inositol growth	*Cryptococcus marinus*	*Sterigmatomyces halophilus*
589	Ethanol growth	590	*Sporobolomyces gracilis*
590	Ribitol growth	*Sporobolomyces singularis*	*Rhodotorula lignophila*
591	D-Mannitol growth	*Rhodotorula hylophila*	*Prototheca ulmea*
592	Sucrose growth	593	1446
593	Erythritol growth	594	794
594	Melibiose growth	595	657
595	*myo*-Inositol growth	596	618
596	Glucose fermentation	597	608
597	Sucrose fermentation	598	601
598	Galactitol growth	599	600
599	Nitrate growth	*Blastobotrys raffinosifermentans*	*Blastobotrys proliferans* *Candida tartarivorans*
600	Nitrate growth	*Blastobotrys adeninivorans*	*Candida hyderabadensis*
601	Soluble starch growth	602	605
602	Maltose fermentation	603	604
603	Ethanol growth	*Blastobotrys nivea*	*Blastobotrys aristata*
604	Nitrate growth	*Blastobotrys peoriensis*	*Trichomonascus apis*
605	Galactitol growth	606	607
606	Nitrate growth	*Zygoascus ofunaensis*	*Candida transvaalensis*
607	Methanol growth	*Ogataea ganodermae*	*Candida santjacobensis*
608	Inulin growth	609	613
609	Citrate growth	610	611
610	Nitrate growth	*Aureobasidium pullulans*	*Lipomyces starkeyi* *Lipomyces tetrasporus*

No.	Test	Positive	Negative
611	Lactose growth	612	*Candida allociferrii*
612	L-Sorbose growth	*Candida digboiensis*	*Ascoidea rubescens*
613	Galactitol growth	614	616
614	Nitrate growth	*Sugiyamaella smithiae*	615
615	D-Glucosamine growth	*Blastobotrys serpentis*	*Trichomonascus ciferrii*
616	Glycerol growth	617	*Candida marilandica*
617	Nitrate growth	*Sugiyamaella chiloensis*	*Myxozyma monticola*
618	Inulin growth	619	638
619	Vitamin-free growth	620	630
620	Glucose fermentation	621	623
621	Raffinose fermentation	622	*Schwanniomyces vanrijiae* var. *vanrijiae*
622	L-Rhamnose growth	*Schwanniomyces polymorphus* var. *africanus*	*Schwanniomyces polymorphus* var. *polymorphus*
623	D-Gluconate growth	624	628
624	Cycloheximide 0.1% growth	625	627
625	D-Arabinose growth	626	*Lipomyces starkeyi* *Schwanniomyces vanrijiae* var. *vanrijiae*
626	Butane 2,3 diol growth	*Lipomyces starkeyi* *Lipomyces tetrasporus*	*Lipomyces orientalis*
627	Growth at 35°C	*Schwanniomyces vanrijiae* var. *vanrijiae*	*Lipomyces lipofer*
628	Lactose growth	*Lipomyces doorenjongii* *Lipomyces starkeyi*	629
629	Citrate growth	*Lipomyces starkeyi*	*Lipomyces kockii*
630	Galactitol growth	631	635
631	Glucose fermentation	632	634
632	Ethanol growth	633	*Blastobotrys aristata*
633	50% Glucose growth	*Candida membranifaciens*	*Debaryomyces hansenii*
634	Glycerol growth	*Debaryomyces hansenii* *Lipomyces starkeyi*	*Lipomyces doorenjongii* *Lipomyces starkeyi*
635	Growth at 30°C	636	*Debaryomyces maramus*
636	DL-Lactate growth	637	*Debaryomyces hansenii* *Lipomyces starkeyi*
637	Growth at 37°C	*Debaryomyces subglobosus*	*Debaryomyces hansenii*
638	Soluble starch growth	639	649
639	Growth at 37°C	640	643
640	L-Sorbose growth	641	642
641	Hexadecane growth	*Schwanniomyces vanrijiae* var. *vanrijiae*	*Debaryomyces nepalensis*
642	L-Rhamnose growth	*Candida silvanorum*	*Candida silvicultrix*
643	Growth at 30°C	644	648
644	Ethanol growth	645	*Blastobotrys aristata*
645	L-Rhamnose growth	646	647
646	Nitrate growth	*Wickerhamomyces sydowiorum*	*Debaryomyces hansenii* *Schwanniomyces pseudopolymorphus*
647	50% Glucose growth	*Candida fennica*	*Debaryomyces fabryi* *Debaryomyces hansenii* *Debaryomyces nepalensis*
648	L-Rhamnose growth	*Debaryomyces udenii*	*Debaryomyces maramus*

No.	Test	Positive	Negative
649	L-Sorbose growth	650	653
650	Trehalose growth	651	*Candida hyderabadensis*
651	D-Gluconate growth	652	*Candida entomophila*
652	50% Glucose growth	*Candida friedrichii*	*Candida insectorum* *Debaryomyces hansenii*
653	Nitrate growth	*Wickerhamomyces sydowiorum*	654
654	L-Rhamnose growth	655	656
655	Growth at 37°C	*Yamadazyma mexicana* *Yamadazyma scolyti*	*Debaryomyces hansenii* *Yamadazyma scolyti*
656	50% Glucose growth	*Candida elateridarum*	*Debaryomyces hansenii*
657	Soluble starch growth	658	708
658	Vitamin-free growth	659	671
659	Galactitol growth	660	666
660	Melezitose growth	661	665
661	Raffinose fermentation	622	662
662	Growth at 37°C	663	664
663	*myo*-Inositol growth	*Candida blankii*	*Candida gotoi*
664	D-Arabinose growth	*Lipomyces tetrasporus*	*Schwanniomyces vanrijiae* var. *yarrowii*
665	Trehalose growth	*Blastobotrys mokoenaii*	*Blastobotrys illinoisensis*
666	L-Rhamnose growth	667	670
667	*myo*-Inositol growth	668	669
668	D-Gluconate growth	*Candida blankii*	*Blastobotrys malaysiensis*
669	Nitrate growth	*Wickerhamomyces ciferrii*	*Candida homilentoma*
670	Nitrate growth	*Wickerhamomyces anomalus*	*Candida fennica* *Hyphopichia burtonii*
671	L-Rhamnose growth	672	688
672	Nitrate growth	673	676
673	*myo*-Inositol growth	*Blastobotrys terrestris*	674
674	L-Arabinose growth	675	*Ambrosiozyma platypodis*
675	Maltose fermentation	*Candida ishiwadae*	*Candida pomicola* *Nakazawaea holstii*
676	*myo*-Inositol growth	677	680
677	Glucose fermentation	678	679
678	Ethanol growth	*Blastobotrys capitulata*	*Blastobotrys aristata*
679	Melezitose growth	*Blastobotrys chiropterorum*	*Trichomonascus ciferrii*
680	Maltose fermentation	681	684
681	Ethanol growth	682	*Blastobotrys aristata*
682	Raffinose growth	*Debaryomyces hansenii*	683
683	D-Arabinose growth	*Candida tenuis* *Scheffersomyces stipitis* *Yamadazyma nakazawae*	*Candida homilentoma*
684	50% Glucose growth	685	686
685	Galactitol growth	*Candida dendronema*	*Candida naeodendra*
686	Raffinose growth	*Debaryomyces hansenii*	687
687	Growth at 37°C	*Candida peltata*	*Candida tenuis*
688	Sucrose fermentation	689	696
689	2-Keto-D-gluconate growth	690	694
690	D-Gluconate growth	691	*Candida litsaeae*
691	Raffinose growth	692	693
692	50% Glucose growth	*Candida fennica*	*Debaryomyces hansenii*

No.	Test	Positive	Negative
693	D-Arabinose growth	*Yamadazyma akitaensis*	*Candida fennica*
694	*myo*-Inositol growth	*Saccharomycopsis fibuligera*	695
695	Nitrate growth	*Wickerhamomyces subpelliculosus*	*Candida ontarioensis*
696	Growth at 37°C	697	699
697	Methanol growth	*Ogataea siamensis*	698
698	Glucose fermentation	*Spathaspora passalidarum*	*Debaryomyces prosopidis*
699	Galactose growth	700	707
700	Galactitol growth	701	703
701	Ethanol growth	702	*Blastobotrys aristata*
702	D-Gluconate growth	*Debaryomyces hansenii*	*Candida lignosa*
703	Trehalose growth	704	*Priceomyces melissophilus*
704	Growth at 30°C	705	*Debaryomyces maramus*
705	Raffinose growth	*Candida shehatae* *Debaryomyces hansenii*	706
706	DL-Lactate growth	*Candida jeffriesii*	*Candida shehatae*
707	Xylitol growth	*Candida fukazawae*	*Ambrosiozyma ambrosiae*
708	2-Keto-D-gluconate growth	709	760
709	Raffinose growth	710	721
710	Vitamin-free growth	711	716
711	Galactitol growth	712	713
712	L-Sorbose growth	*Schwanniomyces vanrijiae* var. *yarrowii*	*Hyphopichia heimii*
713	Citrate growth	714	715
714	Trehalose growth	*Debaryomyces robertsiae*	*Candida hyderabadensis*
715	Gelatin liquefaction	*Candida pseudorhagii*	*Candida rhagii*
716	Trehalose growth	717	*Candida hyderabadensis*
717	*myo*-Inositol growth	*Trichomonascus ciferrii*	718
718	Citrate growth	719	*Candida rhagii* *Debaryomyces hansenii*
719	L-Sorbose growth	*Candida insectorum* *Debaryomyces hansenii*	720
720	Growth at 37°C	*Yamadazyma mexicana*	*Debaryomyces hansenii*
721	L-Rhamnose growth	722	738
722	D-Glucosamine growth	723	736
723	Melezitose growth	724	734
724	DL-Lactate growth	725	728
725	50% Glucose growth	726	727
726	Ethanol growth	*Candida temnochilae*	*Candida blattariae*
727	Lactose growth	*Candida gorgasii* *Candida tenuis*	*Candida tammaniensis* *Candida tenuis*
728	D-Ribose growth	729	733
729	Sucrose fermentation	730	731
730	Lactose fermentation	*Candida taylori*	*Candida tenuis*
731	50% Glucose growth	732	*Candida diospyri* *Candida tenuis*
732	L-Sorbose growth	*Candida bribrorum* *Candida diospyri*	*Candida bribrorum* *Candida temnochilae*
733	Cycloheximide 0.01% growth	*Candida bribrorum*	*Candida taliae*
734	Ethanol growth	735	*Blastobotrys parvus*
735	Methyl-α-D-glucoside growth	*Candida tenuis*	*Candida takamatsizuyensis*

No.	Test	Positive	Negative
736	Galactitol growth	..... *Candida sinolaborantium*	 737
737	Trehalose growth	..... *Candida tenuis* *Candida trypodendroni*	..... *Candida hyderabadensis*
738	Cycloheximide 0.01% growth	 739	 748
739	DL-Lactate growth	 740	 744
740	Cellobiose growth	 741	 743
741	Lactose growth	..... *Candida tumicola*	 742
742	Maltose growth	..... *Candida athensensis*	..... *Candida grinbergsii*
743	Methanol growth	..... *Candida boidinii*	..... *Candida hyderabadensis*
744	Trehalose fermentation	 745	 746
745	Salicin growth	..... *Candida anneliseae* *Candida bribrorum*	..... *Yamadazyma philogaea*
746	Ribitol growth	 747	..... *Candida incommunis*
747	Glucose fermentation	..... *Candida tumicola*	..... *Priceomyces melissophilus*
748	L-Arabinose growth	 749	 751
749	Melezitose growth	 750	..... *Candida germanica*
750	Galactose fermentation	..... *Candida diddensiae* *Yamadazyma philogaea*	..... *Candida ambrosiae*
751	Galactose fermentation	 752	 756
752	Galactose growth	 753	..... *Candida bromeliacearum*
753	Cellobiose growth	 754	..... *Candida sophiae-reginae*
754	D-Arabinose growth	..... *Candida diddensiae* *Candida taliae*	 755
755	Growth at 37°C	..... *Candida diddensiae*	..... *Candida canberraensis*
756	Succinate growth	 757	 759
757	Trehalose fermentation	 758	..... *Candida mesenterica*
758	D-Xylose growth	..... *Candida anneliseae*	..... *Candida maxii*
759	Glucose fermentation	..... *Candida bromeliacearum*	..... *Priceomyces melissophilus*
760	Nitrate growth	 761	 769
761	Methanol growth	 762	 765
762	DL-Lactate growth	 763	 764
763	Glucose fermentation	..... *Candida boidinii*	..... *Ogataea methylivora*
764	Growth at 45°C	..... *Ogataea polymorpha*	..... *Ogataea thermomethanolica*
765	Raffinose growth	 766	 767
766	Inulin growth	..... *Wickerhamomyces lynferdii*	..... *Wickerhamomyces subpelliculosus*
767	Galactose fermentation	..... *Wickerhamomyces silvicola*	 768
768	Xylitol growth	..... *Candida chilensis*	..... *Ambrosiozyma platypodis*
769	L-Arabinose growth	 770	 787
770	L-Rhamnose growth	 771	 781
771	L-Sorbose growth	 772	 777
772	DL-Lactate growth	 773	 775
773	Methanol growth	..... *Candida endomychidarum*	 774
774	Sucrose fermentation	..... *Candida amphixiae*	..... *Candida cerambycidarum*
775	Raffinose growth	..... *Candida insectorum*	 776
776	Succinate growth	..... *Candida diospyri*	..... *Candida spencermartinsiae*
777	DL-Lactate growth	 778	 779
778	Methanol growth	..... *Ogataea naganishii*	..... *Candida michaelii*
779	Ethanol growth	 780	..... *Blastobotrys parvus*
780	Galactitol growth	..... *Yamadazyma triangularis*	..... *Candida atlantica*
781	Ethanol growth	 782	 786

No.	Test	Positive	Negative
782	Galactose growth	783	*Ambrosiozyma cicatricosa* *Ambrosiozyma monospora*
783	Melezitose growth	784	785
784	Trehalose fermentation	*Candida diddensiae*	*Candida aaseri*
785	Methanol growth	*Ogataea methanolica*	*Candida atmosphaerica*
786	D-Mannitol growth	*Candida lessepsii*	*Kazachstania hellenica*
787	Galactose growth	788	793
788	Glucose fermentation	789	792
789	Cycloheximide 0.01% growth	790	791
790	Lactose growth	*Candida coipomoensis*	*Candida hyderabadensis*
791	L-Rhamnose growth	*Candida ubatubensis*	*Candida diddensiae*
792	Glycerol growth	*Priceomyces melissophilus*	*Candida ghanaensis*
793	D-Glucosamine growth	*Ambrosiozyma philentoma*	*Ambrosiozyma ambrosiae* *Ogataea falcaomoraisii*
794	Glucose fermentation	795	1326
795	Cellobiose growth	796	1133
796	Galactose growth	797	1052
797	Raffinose growth	798	872
798	Hexadecane growth	799	845
799	D-Xylose growth	800	841
800	Melibiose growth	801	809
801	Inulin growth	802	806
802	D-Arabinose growth	803	804
803	Growth at 37°C	*Candida carpophila* *Meyerozyma caribbica* *Meyerozyma guilliermondii*	*Candida carpophila* *Debaryomyces hansenii*
804	L-Rhamnose growth	*Debaryomyces hansenii* *Schwanniomyces capriottii*	805
805	10% NaCl/5% glucose growth	*Candida carpophila* *Debaryomyces hansenii*	*Candida carpophila* *Schwanniomyces occidentalis* var. *occidentalis*
806	L-Arabinose growth	807	808
807	*myo*-Inositol growth	*Candida valdiviana*	*Candida carpophila* *Debaryomyces hansenii*
808	Ethanol growth	*Candida melibiosica*	*Candida pseudoglaebosa*
809	Galactitol growth	810	819
810	*myo*-Inositol growth	811	812
811	L-Rhamnose growth	*Zygoascus hellenicus* *Zygoascus meyerae*	*Candida bituminiphila*
812	DL-Lactate growth	813	816
813	Glycerol growth	814	*Candida pseudointermedia*
814	D-Gluconate growth	815	*Candida lignosa*
815	Vitamin-free growth	*Schwanniomyces vanrijiae* var. *yarrowii*	*Debaryomyces hansenii*
816	Lactose growth	*Candida intermedia* *Debaryomyces hansenii*	817
817	D-Gluconate growth	818	*Candida carpophila* *Meyerozyma caribbica*
818	Vitamin-free growth	*Schwanniomyces vanrijiae* var. *yarrowii*	*Candida carpophila* *Debaryomyces hansenii*

No.	Test	Positive	Negative
819	L-Rhamnose growth	820	825
820	Growth at 37°C	821	822
821	*myo*-Inositol growth	*Zygoascus hellenicus*	*Candida odintsovae*
822	Glycerol growth	823	824
823	Lactose growth	*Candida intermedia* *Debaryomyces hansenii*	*Candida rhagii* *Debaryomyces hansenii*
824	Lactose growth	*Candida intermedia*	*Candida akabanensis*
825	Sucrose fermentation	826	834
826	Lactose growth	827	828
827	10% NaCl/5% glucose growth	*Candida intermedia* *Debaryomyces hansenii*	*Candida intermedia* *Schwanniomyces occidentalis* var. *occidentalis*
828	L-Arabinose growth	829	831
829	Citrate growth	805	830
830	Cycloheximide 0.01% growth	*Candida carpophila* *Debaryomyces hansenii*	*Candida rhagii* *Debaryomyces hansenii*
831	Citrate growth	832	*Candida rhagii*
832	Soluble starch growth	*Schwanniomyces occidentalis* var. *occidentalis*	833
833	Xylitol growth	*Candida leandrae*	*Kodamaea ohmeri*
834	L-Arabinose growth	835	837
835	Growth at 30°C	836	*Metschnikowia corniflorae*
836	Maltose fermentation	*Candida shehatae* *Debaryomyces hansenii*	*Candida carpophila* *Debaryomyces hansenii*
837	Melezitose growth	838	840
838	Galactose fermentation	839	*Candida restingae*
839	Gelatin liquefaction	*Candida insectosa*	*Candida shehatae*
840	Ribitol growth	*Candida leandrae*	*Candida gropengiesseri*
841	50% Glucose growth	842	844
842	Trehalose growth	*Kodamaea kakaduensis* *Kodamaea ohmeri*	843
843	Nitrate growth	*Candida vaccinii*	*Candida gropengiesseri*
844	Ribitol growth	*Kodamaea nitidulidarum*	*Dekkera anomala* *Dekkera bruxellensis*
845	D-Glucosamine growth	846	855
846	*myo*-Inositol growth	847	850
847	L-Rhamnose growth	848	849
848	Nitrate growth	*Zygoascus ofunaensis*	*Zygoascus hellenicus* *Zygoascus meyerae*
849	Glycerol growth	*Candida polysorbophila*	*Candida paludigena*
850	D-Gluconate growth	851	854
851	50% Glucose growth	*Candida salmanticensis*	852
852	Growth at 30°C	853	*Metschnikowia corniflorae*
853	10% NaCl/5% glucose growth	*Debaryomyces hansenii*	*Schwanniomyces occidentalis* var. *occidentalis*
854	Ribitol growth	*Meyerozyma caribbica*	*Dekkera anomala*
855	Melezitose growth	856	865
856	L-Arabinose growth	857	860
857	D-Gluconate growth	858	859
858	2-Keto-D-gluconate growth	*Debaryomyces hansenii*	*Wickerhamomyces strasburgensis*

No.	Test	Positive	Negative
859	Ethanol growth	*Meyerozyma caribbica*	*Kazachstania hellenica*
860	Lactose growth	861	862
861	Lactose fermentation	*Kluyveromyces lactis* var. *lactis*	*Kluyveromyces lactis* var. *drosophilarum*
862	Citrate growth	863	864
863	Ribitol growth	*Meyerozyma caribbica*	*Kluyveromyces dobzhanskii*
864	Galactose fermentation	*Lachancea fermentati*	*Kazachstania piceae*
865	Growth at 37°C	866	871
866	Methyl-α-D-glucoside growth	867	869
867	Melibiose growth	*Lachancea kluyveri*	868
868	DL-Lactate growth	*Lachancea fermentati*	*Kodamaea anthophila*
869	Nitrate growth	*Candida sorbosivorans*	870
870	Ethanol growth	*Kluyveromyces marxianus*	*Kazachstania bulderi*
871	Ribitol growth	*Debaryomyces hansenii*	*Kluyveromyces aestuarii*
872	Citrate growth	873	1004
873	Cycloheximide 0.1% growth	874	909
874	L-Rhamnose growth	875	881
875	*myo*-Inositol growth	*Zygoascus hellenicus* *Zygoascus meyerae*	876
876	Nitrate growth	877	878
877	D-Arabinose growth	*Nakazawaea holstii*	*Wickerhamomyces silvicola*
878	Growth at 37°C	879	880
879	L-Arabinose growth	*Candida peltata*	*Clavispora lusitaniae*
880	Galactitol growth	*Schwanniomyces yamadae*	*Candida tenuis*
881	Growth at 37°C	882	890
882	Soluble starch growth	883	886
883	Lactose growth	*Candida fluviatilis*	884
884	Maltose fermentation	*Candida tropicalis* *Candida viswanathii*	885
885	L-Arabinose growth	*Candida carpophila*	*Candida sojae*
886	L-Arabinose growth	887	889
887	Galactose fermentation	888	*Candida carpophila* *Schwanniomyces etchellsii*
888	DL-Lactate growth	*Candida athensensis*	*Candida carpophila*
889	*myo*-Inositol growth	*Candida bentonensis*	*Candida maltosa*
890	DL-Lactate growth	891	898
891	Galactose fermentation	892	897
892	L-Sorbose growth	893	895
893	Galactitol growth	*Candida lignosa*	894
894	L-Arabinose growth	*Candida labiduridarum*	*Candida oleophila* *Candida railenensis*
895	Xylitol growth	896	*Candida labiduridarum*
896	Melezitose growth	*Candida smithsonii*	*Candida athensensis*
897	Nitrate growth	*Barnettozyma pratensis*	*Candida qinlingensis*
898	L-Arabinose growth	899	902
899	Glycerol growth	900	*Candida paludigena*
900	Maltose fermentation	*Candida shehatae*	901
901	Vitamin-free growth	*Candida tibetensis*	*Candida carpophila* *Candida kruisii*
902	L-Sorbose growth	903	905

No.	Test	Positive	Negative
903	Melezitose growth	904	*Scheffersomyces segobiensis*
904	Maltose fermentation	*Candida oleophila* *Candida shehatae*	*Candida asparagi* *Candida cretensis* *Candida oleophila*
905	D-Ribose growth	906	907
906	Maltose fermentation	839	*Candida atbi*
907	Ethanol growth	908	*Candida aglyptinia*
908	Xylitol growth	*Candida barrocoloradensis*	*Candida stri*
909	Galactose fermentation	910	958
910	D-Arabinose growth	911	921
911	L-Rhamnose growth	912	914
912	Nitrate growth	*Nakazawaea holstii*	913
913	Growth at 37°C	*Clavispora lusitaniae*	*Candida tenuis*
914	Melezitose growth	915	919
915	Soluble starch growth	*Candida shehatae*	916
916	L-Sorbose growth	917	*Candida kunorum*
917	Hexadecane growth	918	*Candida buinensis*
918	Methyl-α-D-glucoside growth	*Candida asparagi* *Metschnikowia reukaufii*	*Candida hawaiiana* *Metschnikowia reukaufii*
919	Ethanol growth	920	*Candida lycoperdinae*
920	Trehalose fermentation	*Scheffersomyces segobiensis*	*Candida ergatensis*
921	Trehalose fermentation	922	945
922	Xylitol growth	923	934
923	Melibiose growth	924	925
924	Galactitol growth	*Zygoascus ofunaensis*	*Candida melibiosica*
925	Methyl-α-D-glucoside growth	926	933
926	L-Rhamnose growth	927	928
927	Cycloheximide 0.01% growth	*Clavispora lusitaniae*	*Candida chickasaworum*
928	D-Ribose growth	929	930
929	Soluble starch growth	*Candida shehatae* *Candida tritomae*	*Candida pallodes* *Candida tritomae*
930	L-Sorbose growth	931	932
931	DL-Lactate growth	*Clavispora opuntiae*	*Candida chickasaworum* *Candida kipukae*
932	Maltose fermentation	*Candida pallodes*	*Candida chickasaworum*
933	L-Rhamnose growth	*Clavispora lusitaniae*	*Candida hawaiiana*
934	50% Glucose growth	935	943
935	Ethanol growth	936	942
936	Melezitose growth	937	*Candida chickasaworum* *Candida panamensis*
937	D-Gluconate growth	938	*Candida chickasaworum* *Candida wounanorum*
938	Sucrose fermentation	939	940
939	Propane 1,2 diol growth	*Candida terraborum*	*Candida guaymorum*
940	L-Sorbose growth	941	*Candida chickasaworum* *Candida guaymorum*
941	Growth at 35°C	*Candida emberorum*	*Candida chickasaworum*
942	Melezitose growth	*Candida panamericana*	*Candida yuchorum*
943	Soluble starch growth	*Candida shehatae*	944
944	Growth at 37°C	*Clavispora opuntiae*	*Candida sake*

No.	Test	Positive	Negative
945	L-Rhamnose growth	946	948
946	Galactitol growth	*Schwanniomyces yamadae*	947
947	Nitrate growth	*Wickerhamomyces silvicola*	*Clavispora lusitaniae*
948	Xylitol growth	949	956
949	DL-Lactate growth	950	952
950	Methyl-α-D-glucoside growth	951	*Candida natalensis*
951	Maltose fermentation	*Candida lyxosophila*	*Metschnikowia fructicola* *Metschnikowia pulcherrima*
952	Melibiose growth	*Candida melibiosica*	953
953	L-Arabinose growth	*Candida bohiensis*	954
954	Methyl-α-D-glucoside growth	955	*Candida hawaiiana* *Metschnikowia reukaufii*
955	Gelatin liquefaction	*Candida kipukae* *Metschnikowia reukaufii*	*Metschnikowia pulcherrima* *Metschnikowia reukaufii*
956	Soluble starch growth	*Candida lyxosophila*	957
957	Growth at 37°C	*Candida alai*	*Candida sake*
958	Methyl-α-D-glucoside growth	959	986
959	L-Arabinose growth	960	964
960	D-Arabinose growth	961	963
961	Nitrate growth	*Nakazawaea holstii*	962
962	L-Rhamnose growth	*Candida tenuis*	*Candida tibetensis*
963	Ribitol growth	*Schwanniomyces etchellsii*	*Candida qinlingensis*
964	Xylitol growth	965	979
965	DL-Lactate growth	966	969
966	L-Rhamnose growth	913	967
967	Ethanol growth	968	*Metschnikowia noctiluminum*
968	Nitrate growth	*Barnettozyma pratensis*	*Metschnikowia kunwiensis* *Metschnikowia pulcherrima*
969	Trehalose fermentation	970	974
970	L-Rhamnose growth	913	971
971	D-Glucosamine growth	972	*Metschnikowia borealis* *Metschnikowia continentalis* *Metschnikowia lochheadii*
972	50% Glucose growth	*Candida kipukae* *Metschnikowia santaceciliae*	973
973	Melezitose growth	*Metschnikowia kamakouana*	*Candida gatunensis*
974	L-Rhamnose growth	913	975
975	D-Gluconate growth	976	*Candida ipomoeae*
976	Growth at 30°C	977	*Metschnikowia kamakouana* *Metschnikowia pulcherrima*
977	Growth at 37°C	*Metschnikowia lunata* *Metschnikowia reukaufii*	978
978	Gelatin liquefaction	*Candida kipukae* *Metschnikowia reukaufii* *Metschnikowia viticola*	*Candida kofuensis* *Metschnikowia pulcherrima* *Metschnikowia reukaufii* *Metschnikowia viticola*
979	D-Arabinose growth	980	982
980	D-Ribose growth	*Candida tenuis*	981
981	DL-Lactate growth	*Candida atakaporum*	*Candida bokatorum*
982	Nitrate growth	*Barnettozyma pratensis*	983

No.	Test	Positive	Negative
983	Cycloheximide 0.01% growth	*Candida tanzawaensis*	984
984	Trehalose fermentation	*Candida sake*	985
		Metschnikowia lochheadii	
985	50% Glucose growth	*Candida ipomoeae*	*Candida sake*
986	Growth at 37°C	987	989
987	Glycerol growth	988	*Metschnikowia agaves*
988	L-Rhamnose growth	*Clavispora lusitaniae*	*Metschnikowia lunata*
			Metschnikowia reukaufii
989	D-Gluconate growth	990	1001
990	Hexadecane growth	991	998
991	50% Glucose growth	992	996
992	Growth at 30°C	993	*Metschnikowia hamakuensis*
			Metschnikowia mauinuiana
993	Trehalose fermentation	994	*Candida hawaiiana*
			Metschnikowia reukaufii
994	Ethanol growth	995	*Candida hawaiiana*
			Metschnikowia hibisci
995	D-Glucosamine growth	*Candida hawaiiana*	*Metschnikowia hawaiiensis*
996	Xylitol growth	997	*Candida sake*
997	Melezitose growth	*Metschnikowia reukaufii*	*Candida neerlandica*
998	50% Glucose growth	999	1000
999	Ethanol growth	*Metschnikowia orientalis*	*Metschnikowia colocasiae*
1000	Xylitol growth	*Candida fragi*	*Candida sake*
1001	Xylitol growth	1002	*Candida sake*
			Metschnikowia lochheadii
1002	D-Glucosamine growth	*Metschnikowia dekortorum*	1003
1003	Trehalose fermentation	*Metschnikowia lochheadii*	*Metschnikowia cerradonensis*
1004	Cycloheximide 0.01% growth	1005	1027
1005	Lactose growth	1006	1009
1006	D-Mannitol growth	1007	1008
1007	Methanol growth	*Candida hungarica*	861
1008	D-Glucitol growth	*Kluyveromyces wickerhamii*	*Dekkera anomala*
1009	Growth at 37°C	1010	1018
1010	L-Rhamnose growth	1011	1012
1011	Galactitol growth	*Zygoascus meyerae*	947
1012	D-Mannitol growth	1013	1016
1013	L-Arabinose growth	*Candida carpophila*	1014
1014	Hexadecane growth	1015	*Lachancea fermentati*
1015	Soluble starch growth	*Candida tropicalis*	*Candida maltosa*
1016	Ribitol growth	*Candida carpophila*	1017
1017	D-Glucitol growth	*Candida gelsemii*	*Dekkera anomala*
			Dekkera bruxellensis
1018	Ribitol growth	1019	1025
1019	L-Arabinose growth	1020	1022
1020	Nitrate growth	*Wickerhamomyces silvicola*	1021
1021	Trehalose growth	*Candida carpophila*	*Candida heliconiae*
1022	Trehalose growth	1023	*Candida heliconiae*
1023	Galactose fermentation	1024	*Metschnikowia zizyphicola*
1024	D-Ribose growth	*Metschnikowia zobellii*	*Metschnikowia shanxiensis*
			Metschnikowia sinensis

No.	Test	Positive	Negative
1025	D-Mannitol growth	1026	*Candida gelsemii*
1026	D-Gluconate growth	*Metschnikowia bicuspidata* var. *californica*	*Metschnikowia bicuspidata* var. *chathamia*
1027	Methyl-α-D-glucoside growth	1028	1042
1028	D-Glucosamine growth	1029	1035
1029	D-Gluconate growth	1030	1033
1030	Xylitol growth	1031	*Candida sake*
1031	DL-Lactate growth	*Metschnikowia kunwiensis*	1032
1032	Ethylamine growth	*Metschnikowia koreensis* *Metschnikowia reukaufii*	*Metschnikowia andauensis*
1033	Xylitol growth	1034	*Candida sake*
1034	Glycerol growth	*Candida ergatensis*	*Metschnikowia similis*
1035	Raffinose fermentation	1036	1037
1036	Melibiose growth	*Lachancea kluyveri*	*Kluyveromyces aestuarii*
1037	Hexadecane growth	1038	1039
1038	Xylitol growth	*Candida rancensis* *Metschnikowia reukaufii*	*Candida sake*
1039	Nitrate growth	*Wickerhamomyces silvicola*	1040
1040	50% Glucose growth	1041	*Candida sake*
1041	Galactose fermentation	*Metschnikowia shanxiensis* *Metschnikowia sinensis*	*Metschnikowia zizyphicola*
1042	Xylitol growth	1043	1048
1043	Ribitol growth	1044	1046
1044	D-Mannitol growth	1045	*Metschnikowia lachancei*
1045	Hexadecane growth	*Metschnikowia reukaufii*	*Metschnikowia aberdeeniae* *Metschnikowia orientalis*
1046	Hexadecane growth	*Metschnikowia reukaufii*	1047
1047	Trehalose growth	*Metschnikowia bicuspidata* var. *bicuspidata*	*Metschnikowia gruessii*
1048	*N*-Acetyl-D-glucosamine growth	1049	1051
1049	50% Glucose growth	*Metschnikowia gruessii*	1050
1050	Gelatin liquefaction	*Candida gelsemii*	*Candida sake*
1051	Glycerol growth	*Kluyveromyces aestuarii*	*Metschnikowia arizonensis*
1052	Nitrate growth	1053	1068
1053	Raffinose growth	1054	1061
1054	Vitamin-free growth	1055	1056
1055	Maltose growth	*Lindnera jadinii* *Lindnera saturnus*	*Lindnera saturnus* *Lindnera suaveolens*
1056	L-Sorbose growth	1057	1058
1057	Ethanol growth	*Candida peoriensis*	*Candida vaccinii*
1058	Raffinose fermentation	1059	1060
1059	Maltose fermentation	*Lindnera fabianii*	*Lindnera petersonii* *Lindnera subsufficiens*
1060	D-Mannitol growth	*Candida nakhonratchasimensis*	*Dekkera bruxellensis*
1061	Growth at 37°C	1062	1065
1062	L-Rhamnose growth	1063	1064
1063	Ribitol growth	*Candida ulmi*	*Lindnera bimundalis*
1064	D-Mannitol growth	*Lindnera euphorbiiphila*	*Dekkera bruxellensis*
1065	Melezitose growth	1066	*Barnettozyma californica*
1066	L-Rhamnose growth	1067	*Candida vartiovaarae*

No.	Test	Positive	Negative
1067	D-Arabinose growth	*Candida populi*	*Lindnera americana* *Wickerhamomyces bisporus*
1068	L-Rhamnose growth	1069	1085
1069	Growth at 37°C	1070	1079
1070	Raffinose growth	1071	1073
1071	L-Arabinose growth	1072	*Candida mycetangii*
1072	Trehalose fermentation	*Wickerhamomyces rabaulensis*	*Candida odintsovae*
1073	2-Keto-D-gluconate growth	1074	1075
1074	L-Sorbose growth	*Clavispora lusitaniae*	*Barnettozyma wickerhamii*
1075	L-Arabinose growth	1076	1077
1076	Sucrose fermentation	*Lindnera euphorbiae* *Wickerhamomyces bovis*	*Lindnera mississippiensis* *Wickerhamomyces bovis*
1077	Melezitose growth	1078	*Lindnera meyerae*
1078	Gelatin liquefaction	*Lindnera japonica*	*Candida freyschussii* *Lindnera rhodanensis*
1079	*N*-Acetyl-D-glucosamine growth	1080	1081
1080	Glycerol growth	*Peterozyma toletana* *Peterozyma xylosa*	*Candida oregonensis*
1081	Raffinose growth	1082	1083
1082	Trehalose growth	*Candida maritima* *Lindnera veronae*	*Lindnera lachancei*
1083	Ribitol growth	*Wickerhamomyces hampshirensis*	1084
1084	Soluble starch growth	*Candida maritima* *Candida pattaniensis*	*Candida maritima* *Lindnera euphorbiae*
1085	Methyl-α-D-glucoside growth	1086	1114
1086	2-Keto-D-gluconate growth	1087	1099
1087	DL-Lactate growth	1088	1091
1088	Citrate growth	1089	1090
1089	D-Xylose growth	*Kodamaea laetipori*	*Scheffersomyces spartinae*
1090	Galactose fermentation	*Lachancea fermentati*	*Candida solani*
1091	D-Glucosamine growth	1092	1096
1092	L-Sorbose growth	1093	1095
1093	Raffinose growth	*Kodamaea kakaduensis*	1094
1094	Succinate growth	*Metschnikowia koreensis* *Metschnikowia reukaufii*	*Candida bromeliacearum*
1095	Melezitose growth	*Candida sagamina*	*Candida derodonti*
1096	Hexadecane growth	1097	1098
1097	Sucrose fermentation	*Scheffersomyces spartinae*	*Candida rancensis* *Metschnikowia reukaufii*
1098	Ribitol growth	*Candida suecica*	*Wickerhamomyces mucosus*
1099	Growth at 37°C	1100	1109
1100	L-Arabinose growth	1101	1106
1101	Raffinose growth	1102	1103
1102	Ribitol growth	*Wickerhamomyces rabaulensis*	*Wickerhamomyces onychis*
1103	Ethanol growth	1104	*Candida yuanshanicus*
1104	Soluble starch growth	1105	*Lindnera mississippiensis* *Wickerhamomyces bovis*
1105	Salicin growth	*Wickerhamomyces bovis*	*Lindnera amylophila*
1106	*myo*-Inositol growth	*Saccharomycopsis fibuligera*	1107
1107	D-Mannitol growth	1108	*Dekkera bruxellensis*

No.	Test	Positive	Negative
1108	Galactose fermentation	*Lachancea fermentati*	*Wickerhamomyces onychis*
1109	Ribitol growth	1110	1112
1110	Ethanol growth	1111	*Candida dajiaensis*
1111	Glycerol growth	*Aciculoconidium aculeatum*	*Ambrosiozyma angophorae*
1112	Raffinose growth	*Lindnera maclurae*	1113
1113	Trehalose growth	*Peterozyma toletana*	*Candida quercuum*
1114	D-Glucitol growth	1115	1122
1115	Glycerol growth	1116	1121
1116	L-Sorbose growth	1117	1120
1117	Raffinose growth	*Candida gropengiesseri*	1118
1118	Ribitol growth	*Candida chrysomelidarum* *Metschnikowia reukaufii*	1119
1119	Hexadecane growth	*Metschnikowia reukaufii*	*Metschnikowia gruessii*
1120	D-Mannitol growth	*Peterozyma toletana*	*Candida gelsemii*
1121	Ribitol growth	*Candida ortonii*	*Metschnikowia arizonensis*
1122	Melezitose growth	1123	1128
1123	*N*-Acetyl-D-glucosamine growth	1124	1126
1124	Ribitol growth	*Metschnikowia lachancei*	1125
1125	L-Sorbose growth	*Metschnikowia gruessii*	*Dekkera bruxellensis*
1126	Xylitol growth	1127	*Metschnikowia arizonensis*
1127	Salicin growth	*Candida flosculorum*	*Metschnikowia vanudenii*
1128	Sucrose fermentation	1129	1132
1129	Raffinose fermentation	*Saccharomycodes ludwigii*	1130
1130	Cycloheximide 0.01% growth	*Dekkera bruxellensis*	1131
1131	Trehalose growth	*Hanseniaspora occidentalis* var. *citrica*	*Hanseniaspora occidentalis* var. *occidentalis*
1132	Cycloheximide 0.01% growth	*Dekkera bruxellensis*	*Hanseniaspora osmophila* *Hanseniaspora vineae*
1133	D-Xylose growth	1134	1187
1134	Cycloheximide 0.01% growth	1135	1161
1135	Succinate growth	1136	1155
1136	Cycloheximide 0.1% growth	1137	1147
1137	Maltose fermentation	1138	1140
1138	Soluble starch growth	*Candida albicans* *Candida dubliniensis* *Candida tropicalis*	1139
1139	Raffinose growth	*Lachancea cidri*	*Candida buenavistaensis* *Candida maltosa*
1140	Trehalose growth	1141	1145
1141	Methanol growth	*Candida pignaliae*	1142
1142	Vitamin-free growth	*Schwanniomyces vanrijiae* var. *yarrowii*	1143
1143	L-Arabinose growth	*Candida carpophila*	1144
1144	Sucrose fermentation	*Candida maltosa*	*Lodderomyces elongisporus*
1145	Galactitol growth	*Schwanniomyces vanrijiae* var. *yarrowii*	1146
1146	L-Sorbose growth	*Candida hyderabadensis*	*Kluyveromyces marxianus*
1147	Melezitose growth	1148	1153
1148	Growth at 37°C	1149	1151
1149	L-Arabinose growth	1150	*Lodderomyces elongisporus*

No.	Test	Positive	Negative
1150	50% Glucose growth	*Candida orthopsilosis* *Candida parapsilosis*	*Candida metapsilosis*
1151	Glycerol growth	1152	*Candida picinguabensis*
1152	Galactitol growth	*Schwanniomyces vanrijiae* var. *yarrowii*	*Candida quercitrusa*
1153	Galactitol growth	*Candida tolerans*	1154
1154	Galactose fermentation	*Kluyveromyces marxianus*	*Candida gropengiesseri*
1155	Raffinose growth	1156	1158
1156	Glycerol growth	1157	*Lachancea waltii*
1157	D-Glucitol growth	*Candida gropengiesseri*	*Kazachstania bulderi*
1158	Xylitol growth	1159	1160
1159	Glycerol growth	*Candida buenavistaensis*	*Candida frijolesensis*
1160	D-Glucosamine growth	*Candida labiduridarum*	*Candida tetrigidarum*
1161	Melezitose growth	1162	1176
1162	Growth at 37°C	1163	1166
1163	L-Arabinose growth	*Candida parapsilosis*	1164
1164	D-Ribose growth	*Kurtzmaniella cleridarum*	1165
1165	Citrate growth	*Lodderomyces elongisporus*	*Torulaspora delbrueckii*
1166	Methyl-α-D-glucoside growth	1167	1172
1167	Galactitol growth	*Schwanniomyces vanrijiae* var. *yarrowii*	1168
1168	Xylitol growth	1169	1171
1169	Citrate growth	1170	*Torulaspora delbrueckii*
1170	Glycerol growth	*Candida gigantensis*	*Candida saopaulonensis*
1171	*N*-Acetyl-D-glucosamine growth	*Candida sake*	*Torulaspora delbrueckii*
1172	Trehalose growth	1173	*Metschnikowia vanudenii*
1173	Gelatin liquefaction	*Candida multigemmis*	1174
1174	*N*-Acetyl-D-glucosamine growth	1175	*Torulaspora delbrueckii*
1175	Xylitol growth	*Candida musae*	*Candida sake*
1176	Trehalose growth	1177	1183
1177	*N*-Acetyl-D-glucosamine growth	1178	1181
1178	Xylitol growth	1179	1180
1179	Methyl-α-D-glucoside growth	*Candida leandrae*	*Candida mogii*
1180	Galactose growth	*Candida sake*	*Candida suecica*
1181	Melibiose growth	*Lachancea kluyveri*	1182
1182	Growth at 30°C	*Torulaspora delbrueckii*	*Candida suecica*
1183	Citrate growth	1184	1186
1184	Ribitol growth	*Candida spandovensis*	1185
1185	Hexadecane growth	*Candida gropengiesseri*	*Candida apicola*
1186	Galactose fermentation	*Lachancea kluyveri*	*Candida floricola*
1187	Raffinose growth	1188	1274
1188	Trehalose growth	1189	1233
1189	Vitamin-free growth	1190	1201
1190	Melezitose growth	1191	1195
1191	L-Rhamnose growth	*Candida haemulonii*	1192
1192	Ethanol growth	1193	1194
1193	10% NaCl/5% glucose growth	*Torulaspora delbrueckii* *Torulaspora maleeae*	*Zygotorulaspora florentina*
1194	Maltose fermentation	*Torulaspora maleeae*	*Saccharomyces arboricolus*
1195	Nitrate growth	1196	1197

No.	Test	Positive	Negative
1196	L-Sorbose growth	*Citeromyces matritensis*	*Citeromyces siamensis*
1197	Methyl-α-D-glucoside growth	1198	1199
1198	Melibiose growth	*Lachancea kluyveri*	*Torulaspora delbrueckii* *Torulaspora franciscae*
1199	2-Keto-D-gluconate growth	1200	*Saccharomyces bayanus* var. *bayanus* *Saccharomyces bayanus* var. *uvarum*
1200	Cycloheximide 0.01% growth	*Torulaspora globosa*	*Torulaspora delbrueckii*
1201	D-Mannitol growth	1202	1215
1202	Melibiose growth	1203	1208
1203	Inulin growth	1204	1206
1204	Galactose growth	1205	*Schwanniomyces occidentalis* var. *persoonii*
1205	Maltose growth	*Zygotorulaspora florentina*	*Torulaspora microellipsoides*
1206	Galactitol growth	*Saccharomyces mikatae*	1207
1207	Maltose fermentation	*Lachancea cidri*	*Lachancea kluyveri*
1208	Soluble starch growth	1209	1210
1209	Galactose fermentation	*Schwanniomyces occidentalis* var. *persoonii*	*Candida tsuchiyae*
1210	Cadaverine growth	1211	1213
1211	Melezitose growth	*Lachancea meyersii* *Lachancea thermotolerans*	1212
1212	Ethanol growth	*Saccharomycopsis vini*	*Candida bombi*
1213	2-Keto-D-gluconate growth	1214	*Saccharomyces paradoxus*
1214	Galactose growth	*Torulaspora delbrueckii* *Torulaspora pretoriensis*	*Saccharomycopsis vini* *Torulaspora delbrueckii*
1215	Maltose growth	1216	1223
1216	L-Sorbose growth	1217	1219
1217	Melibiose growth	*Lachancea kluyveri*	1218
1218	Melezitose growth	*Lachancea thermotolerans*	*Saccharomycopsis vini*
1219	Melibiose growth	*Lachancea kluyveri*	1220
1220	*N*-Acetyl-D-glucosamine growth	*Dekkera bruxellensis*	1221
1221	Ethanol growth	1222	*Eremothecium ashbyi*
1222	Trehalose fermentation	*Eremothecium coryli*	*Saccharomyces cerevisiae* *Saccharomyces pastorianus*
1223	Galactose fermentation	1224	1230
1224	D-Gluconate growth	1225	1228
1225	DL-Lactate growth	1226	1227
1226	Ethanol growth	*Kazachstania lodderae*	*Kazachstania barnettii*
1227	2-Keto-D-gluconate growth	*Kazachstania naganishii*	*Vanderwaltozyma polyspora*
1228	*N*-Acetyl-D-glucosamine growth	*Dekkera bruxellensis*	1229
1229	Cadaverine growth	*Kazachstania lodderae*	*Candida milleri* *Kazachstania exigua*
1230	D-Glucitol growth	1212	1231
1231	Succinate growth	*Cyniclomyces guttulatus*	1232
1232	Raffinose fermentation	*Kazachstania zonata*	*Dekkera bruxellensis*
1233	Galactose fermentation	1234	1247
1234	Citrate growth	1235	1239
1235	L-Sorbose growth	1236	1237
1236	Galactitol growth	*Candida spandovensis*	*Candida hyderabadensis*
1237	DL-Lactate growth	1238	*Vanderwaltozyma polyspora*

No.	Test	Positive	Negative
1238	D-Gluconate growth	*Wickerhamia fluorescens*	*Kluyveromyces marxianus*
1239	Maltose growth	1240	1243
1240	Raffinose fermentation	1241	*Dekkera bruxellensis*
1241	Maltose fermentation	1242	*Lachancea kluyveri*
1242	2-Keto-D-gluconate growth	*Torulaspora maleeae*	*Saccharomyces pastorianus*
1243	Succinate growth	1244	1246
1244	Melibiose growth	*Zygotorulaspora mrakii*	1245
1245	Ethanol growth	*Kluyveromyces marxianus*	*Magnusiomyces magnusii*
1246	D-Mannitol growth	*Saccharomyces cariocanus*	*Dekkera bruxellensis*
1247	D-Glucitol growth	1248	1259
1248	Nitrate growth	1249	1251
1249	Maltose growth	*Starmerella meliponinorum*	1250
1250	Cycloheximide 0.01% growth	*Candida sorbosivorans*	*Candida magnoliae*
1251	Sucrose fermentation	1252	1257
1252	Maltose fermentation	1253	1254
1253	Melezitose growth	*Torulaspora maleeae*	*Candida floricola*
1254	Ethanol growth	1255	*Candida bombi*
1255	Growth at 30°C	1256	*Zygosaccharomyces lentus*
1256	2-Keto-D-gluconate growth	*Saccharomycopsis vini*	*Starmerella bombicola*
1257	Citrate growth	1185	1258
1258	Galactitol growth	*Candida sergipensis*	*Saccharomycopsis vini*
1259	Ethanol growth	1260	1266
1260	Vitamin-free growth	1261	1262
1261	Maltose growth	*Torulaspora maleeae*	*Torulaspora globosa*
1262	Inulin growth	*Saccharomyces kudriavzevii*	1263
1263	Growth at 30°C	1264	*Zygosaccharomyces lentus*
1264	D-Mannitol growth	*Starmerella bombicola*	1265
1265	Raffinose fermentation	*Saccharomyces pastorianus*	*Dekkera bruxellensis*
1266	Nitrate growth	1267	1268
1267	Raffinose fermentation	*Candida lactis-condensi*	*Dekkera bruxellensis*
1268	Cycloheximide 0.01% growth	*Dekkera bruxellensis*	1269
1269	L-Lysine growth	1270	1272
1270	Maltose growth	*Torulaspora maleeae*	1271
1271	Sucrose fermentation	*Candida stellata* *Candida zemplinina*	*Candida davenportii*
1272	Melezitose growth	*Torulaspora maleeae*	1273
1273	Growth at 37°C	*Schizosaccharomyces japonicus*	*Schizosaccharomyces pombe*
1274	D-Glucosamine growth	1275	1286
1275	2-Keto-D-gluconate growth	1276	1280
1276	Galactose growth	1277	1279
1277	Xylitol growth	*Candida quercitrusa*	1278
1278	Trehalose growth	*Candida sake*	*Candida caryicola*
1279	L-Sorbose growth	*Saccharomycopsis vini*	*Candida arcana*
1280	Ribitol growth	1281	1283
1281	Xylitol growth	1282	*Candida sake*
1282	50% Glucose growth	*Candida picachoensis*	*Candida pimensis*
1283	Methanol growth	*Candida floccosa*	1284
1284	D-Glucitol growth	1050	1285
1285	Succinate growth	*Candida sake*	*Dekkera bruxellensis*
1286	Ribitol growth	1287	1296

No.	Test	Positive	Negative
1287	Trehalose growth	1288	1292
1288	*N*-Acetyl-D-glucosamine growth	1289	1291
1289	Succinate growth	*Candida sake*	1290
1290	Maltose growth	*Metschnikowia chrysoperlae*	*Zygosaccharomyces bailii*
1291	L-Sorbose growth	*Saccharomycopsis vini* *Torulaspora delbrueckii*	*Torulaspora delbrueckii* *Zygosaccharomyces bailii*
1292	Galactose fermentation	1293	1294
1293	Xylitol growth	*Candida hyderabadensis*	*Nadsonia fulvescens* var. *fulvescens*
1294	Galactitol growth	*Candida sergipensis*	1295
1295	Growth at 30°C	*Saccharomycopsis vini*	*Zygosaccharomyces lentus*
1296	Growth at 30°C	1297	1323
1297	*N*-Acetyl-D-glucosamine growth	1298	1303
1298	Inulin growth	*Kazachstania gamospora*	1299
1299	50% Glucose growth	*Zygosaccharomyces rouxii*	1300
1300	D-Glucitol growth	1050	1301
1301	Succinate growth	*Candida sake*	1302
1302	Hexadecane growth	*Dekkera bruxellensis*	*Kazachstania turicensis*
1303	Galactose fermentation	1304	1308
1304	Cadaverine growth	1305	1306
1305	Melibiose growth	*Lachancea kluyveri*	*Metschnikowia vanudenii*
1306	D-Mannitol growth	*Torulaspora delbrueckii*	1307
1307	Cycloheximide 0.1% growth	*Kazachstania servazzii*	*Naumovozyma castellii*
1308	Ethanol growth	1309	1316
1309	Nitrate growth	*Candida magnoliae*	1310
1310	Melezitose growth	1311	1312
1311	Trehalose growth	*Torulaspora delbrueckii*	*Metschnikowia vanudenii*
1312	D-Mannitol growth	1313	1315
1313	Maltose fermentation	*Torulaspora delbrueckii* *Zygosaccharomyces rouxii*	1314
1314	2-Keto-D-gluconate growth	*Saccharomycopsis vini* *Torulaspora delbrueckii*	*Starmerella bombicola*
1315	D-Glucitol growth	*Saccharomycopsis vini*	*Kazachstania gamospora*
1316	Raffinose fermentation	1317	1319
1317	Nitrate growth	*Candida lactis-condensi*	1318
1318	Xylitol growth	*Metschnikowia vanudenii*	*Candida zemplinina*
1319	Melezitose growth	*Metschnikowia vanudenii*	1320
1320	D-Mannitol growth	*Zygosaccharomyces rouxii*	1321
1321	D-Glucitol growth	*Eremothecium sinecaudum*	1322
1322	D-Gluconate growth	*Nakaseomyces bacillisporus*	*Schizosaccharomyces octosporus*
1323	50% Glucose growth	*Zygosaccharomyces kombuchaensis* *Zygosaccharomyces lentus*	1324
1324	D-Mannitol growth	1325	1050
1325	Trehalose growth	*Candida sake*	*Nadsonia fulvescens* var. *fulvescens*
1326	Nitrate growth	1327	1367
1327	Maltose growth	1328	1348
1328	Inulin growth	1329	1338
1329	Ethanol growth	1330	1335
1330	Methyl-α-D-glucoside growth	1331	1333
1331	Galactitol growth	*Protomyces lactucaedebilis*	1332
1332	*myo*-Inositol growth	*Taphrina virginica*	*Saitoella complicata*

No.	Test	Positive	Negative
1333	Ribitol growth	*Taphrina carpini*	1334
1334	D-Glucitol growth	*Taphrina sacchari*	*Taphrina betulina*
1335	Salicin growth	1336	1337
1336	Ribitol growth	*Protomyces inouyei*	*Protomyces gravidus*
1337	D-Glucitol growth	*Protomyces inundatus* *Protomyces pachydermus*	*Protomyces macrosporus*
1338	Starch formation	1339	1343
1339	Raffinose growth	1340	1341
1340	Nitrite growth	*Lalaria inositophila* *Lalaria veronaerambellii*	*Taphrina betulina*
1341	D-Glucitol growth	1342	*Taphrina robinsoniana*
1342	Melezitose growth	*Lalaria carpini*	*Taphrina tosquinetii*
1343	L-Sorbose growth	1344	1347
1344	Methanol growth	1345	1346
1345	Lactose growth	*Candida hungarica*	*Ascoidea africana*
1346	Ribitol growth	*Candida boreocaroliniensis*	*Candida floridensis*
1347	Growth at 37°C	*Wickerhamomyces canadensis*	*Wickerhamomyces alni* *Wickerhamomyces bisporus*
1348	Melezitose growth	1349	1354
1349	Inulin growth	1350	1351
1350	D-Mannitol growth	*Taphrina sadebeckii*	*Taphrina epiphylla*
1351	L-Lysine growth	1352	1353
1352	Methanol growth	*Ascoidea africana*	*Lalaria arrabidae*
1353	Glycerol growth	*Taphrina alni*	*Taphrina ulmi*
1354	Citrate growth	1355	1360
1355	Trehalose growth	1356	1358
1356	Ethanol growth	1357	*Candida vanderwaltii*
1357	Ribitol growth	*Taphrina wiesneri*	*Taphrina tormentillae*
1358	Ethanol growth	1359	*Taphrina confusa*
1359	D-Mannitol growth	*Wickerhamiella domercqiae*	*Taphrina americana*
1360	Raffinose growth	1361	1364
1361	Galactose growth	1362	1363
1362	Glycerol growth	*Taphrina letifera*	*Taphrina vestergrenii*
1363	Ethanol growth	*Taphrina pruni-subcordatae*	*Taphrina dearnessii*
1364	Ribitol growth	*Taphrina flavorubra*	1365
1365	D-Arabinose growth	*Taphrina padi*	1366
1366	Inulin growth	*Taphrina pruni*	*Taphrina deformans*
1367	Melibiose growth	1368	1395
1368	L-Sorbose growth	1369	1389
1369	Vitamin-free growth	1370	1379
1370	Inulin growth	1371	1378
1371	Growth at 40°C	*Lipomyces spencer-martinsiae*	1372
1372	Succinate growth	1373	1376
1373	Citrate growth	1374	1375
1374	Butane 2,3 diol growth	*Lipomyces mesembrius* *Lipomyces starkeyi*	*Lipomyces kononenkoae* *Lipomyces mesembrius*
1375	D-Gluconate growth	*Lipomyces kononenkoae*	*Lipomyces kockii*
1376	D-Gluconate growth	1377	*Lipomyces kockii*
1377	Galactitol growth	*Lipomyces kononenkoae* *Lipomyces yarrowii*	*Lipomyces kononenkoae* *Lipomyces yamadae*

No.	Test	Positive	Negative
1378	Methanol growth	*Ascoidea africana*	*Lipomyces mesembrius*
1379	D-Glucosamine growth	1380	1382
1380	Methanol growth	*Ascoidea africana*	1381
1381	D-Mannitol growth	*Debaryomyces hansenii*	*Myxozyma neotropica*
1382	Succinate growth	1383	*Dipodascopsis uninucleata* var. *uninucleata*
1383	Maltose growth	1384	1388
1384	Citrate growth	1385	1387
1385	D-Gluconate growth	*Debaryomyces hansenii* *Lipomyces mesembrius* *Lipomyces starkeyi*	1386
1386	Inulin growth	*Lipomyces mesembrius* *Lipomyces starkeyi*	*Lipomyces mesembrius* *Priceomyces carsonii*
1387	Raffinose growth	*Debaryomyces hansenii*	*Candida azyma*
1388	L-Rhamnose growth	*Myxozyma kluyveri*	*Lipomyces mesembrius*
1389	Ribitol growth	1390	1393
1390	L-Arabinose growth	*Debaryomyces hansenii* *Lipomyces mesembrius*	1391
1391	DL-Lactate growth	1392	*Lipomyces mesembrius*
1392	Lactose growth	*Candida glaebosa*	*Candida palmioleophila*
1393	Growth at 35°C	1394	*Blastobotrys robertii* *Lipomyces mesembrius*
1394	D-Mannitol growth	*Blastobotrys muscicola*	*Eremothecium cymbalariae*
1395	D-Xylose growth	1396	1433
1396	*myo*-Inositol growth	1397	1403
1397	D-Glucosamine growth	1398	1399
1398	Glycerol growth	*Zygoascus hellenicus* *Zygoascus meyerae*	*Candida paludigena*
1399	L-Arabinose growth	1400	1402
1400	Galactitol growth	*Myxozyma geophila*	1401
1401	Raffinose growth	*Dipodascopsis tothii*	*Myxozyma udenii*
1402	Glycerol growth	*Babjeviella inositovora*	*Candida castrensis*
1403	Galactose growth	1404	1421
1404	D-Gluconate growth	1405	1410
1405	Raffinose growth	815	1406
1406	L-Rhamnose growth	1407	1408
1407	*N*-Acetyl-D-glucosamine growth	*Candida tenuis*	*Myxozyma mucilagina*
1408	L-Arabinose growth	*Myxozyma vanderwaltii*	1409
1409	Cycloheximide 0.01% growth	*Candida vadensis*	*Candida sake*
1410	Soluble starch growth	1411	1414
1411	D-Arabinose growth	1412	1413
1412	Ethanol growth	*Candida tenuis*	*Protomyces inouyei*
1413	Methanol growth	*Ascoidea africana*	*Priceomyces carsonii*
1414	Methyl-α-D-glucoside growth	1415	1418
1415	Trehalose growth	1416	*Candida subhashii*
1416	L-Rhamnose growth	*Candida tenuis*	1417
1417	50% Glucose growth	*Candida ipomoeae*	*Candida saitoana* *Candida sake*
1418	L-Arabinose growth	1419	1420
1419	Lactose growth	*Lipomyces japonicus*	*Candida azymoides*

No.	Test	Positive	Negative
1420	Cycloheximide 0.01% growth	*Candida tepae*	*Candida sake* *Metschnikowia australis*
1421	Melezitose growth	1422	1428
1422	Ethanol growth	1423	1426
1423	Soluble starch growth	1424	1425
1424	Methanol growth	*Ascoidea africana*	*Candida easanensis*
1425	*N*-Acetyl-D-glucosamine growth	*Peterozyma xylosa*	*Wickerhamomyces canadensis*
1426	Raffinose growth	1427	*Candida plutei*
1427	L-Arabinose growth	*Protomyces inouyei*	*Protomyces pachydermus*
1428	Growth at 30°C	1429	1431
1429	D-Mannitol growth	*Peterozyma xylosa*	1430
1430	Trehalose growth	*Saccharomycopsis schoenii*	*Lipomyces smithiae*
1431	Ribitol growth	1432	*Candida tepae*
1432	Succinate growth	*Candida petrohuensis*	*Candida suecica*
1433	*N*-Acetyl-D-glucosamine growth	1434	1438
1434	Soluble starch growth	1435	1436
1435	Ribitol growth	*Candida fungicola*	*Blastobotrys muscicola*
1436	Glycerol growth	*Candida sake* *Metschnikowia australis*	1437
1437	Succinate growth	*Candida sake*	*Kazachstania turicensis*
1438	D-Mannitol growth	1439	1442
1439	Galactose growth	1440	1441
1440	Ribitol growth	*Candida sergipensis*	*Candida apis*
1441	Ethanol growth	*Metschnikowia krissii*	*Protomyces pachydermus*
1442	Raffinose growth	1443	1445
1443	Citrate growth	*Eremothecium ashbyi* *Eremothecium gossypii*	1444
1444	Gelatin liquefaction	*Eremothecium ashbyi*	*Eremothecium cymbalariae*
1445	Ethanol growth	*Saccharomycopsis schoenii*	*Eremothecium sinecaudum*
1446	Cellobiose growth	1447	1619
1447	Glucose fermentation	1448	1552
1448	Erythritol growth	1449	1493
1449	Galactose growth	1450	1481
1450	*myo*-Inositol growth	1451	1456
1451	Melibiose growth	1452	1454
1452	Nitrate growth	*Zygoascus ofunaensis*	1453
1453	Galactose fermentation	*Blastobotrys nivea*	*Blastobotrys americana*
1454	Ethanol growth	1455	*Blastobotrys attinorum*
1455	L-Rhamnose growth	*Blastobotrys capitulata*	*Candida auringiensis*
1456	D-Glucosamine growth	1457	1471
1457	D-Arabinose growth	1458	1467
1458	Growth at 37°C	1459	1462
1459	Methanol growth	*Candida succiphila*	1460
1460	Galactose fermentation	1461	*Sugiyamaella americana*
1461	Hexadecane growth	*Candida lignohabitans*	*Sugiyamaella japonica*
1462	Citrate growth	1463	1465
1463	Ribitol growth	1464	*Candida pinicola*
1464	D-Gluconate growth	*Candida choctaworum* *Sugiyamaella japonica*	*Candida choctaworum* *Trichomonascus farinosus*
1465	DL-Lactate growth	*Candida neomexicana*	1466

No.	Test	Positive	Negative
1466	D-Gluconate growth	*Candida conglobata*	*Trichomonascus farinosus*
1467	Nitrate growth	*Candida novakii*	1468
1468	Growth at 40°C	*Candida sithepensis*	1469
1469	Ethanol growth	1470	*Blastobotrys arbuscula* *Trichomonascus farinosus*
1470	D-Gluconate growth	*Candida bolitotheri*	*Trichomonascus farinosus*
1471	Growth at 37°C	1472	1476
1472	Methanol growth	1473	1474
1473	Nitrate growth	*Ogataea polymorpha*	*Candida sithepensis*
1474	Nitrate growth	*Wickerhamomyces silvicola*	1475
1475	Maltose fermentation	*Millerozyma acaciae*	*Millerozyma farinosa*
1476	Galactose fermentation	1477	1480
1477	Growth at 30°C	1478	1479
1478	Nitrate growth	*Wickerhamomyces silvicola*	*Trichomonascus farinosus*
1479	Raffinose growth	*Candida linzhiensis*	*Candida sequanensis*
1480	Methanol growth	*Ogataea methanolica* *Trichomonascus farinosus*	*Candida boleticola* *Trichomonascus farinosus*
1481	Nitrate growth	1482	1483
1482	D-Glucosamine growth	*Kuraishia capsulata* *Kuraishia molischiana*	*Ogataea glucozyma* *Ogataea polymorpha*
1483	Growth at 37°C	1484	1490
1484	L-Rhamnose growth	1485	1487
1485	DL-Lactate growth	*Ogataea corticis*	1486
1486	2-Keto-D-gluconate growth	*Ogataea neopini* *Ogataea pini*	*Ogataea pini* *Ogataea zsoltii*
1487	Methanol growth	1488	*Saccharomycopsis malanga*
1488	Trehalose growth	1489	*Ogataea kodamae*
1489	L-Sorbose growth	*Ogataea dorogensis* *Ogataea pini*	*Candida arabinofermentans* *Ogataea pini*
1490	Methanol growth	1491	*Saccharomycopsis capsularis*
1491	DL-Lactate growth	*Candida ovalis*	1492
1492	Trehalose fermentation	*Ogataea nitratoaversa* *Ogataea pini*	*Ogataea pilisensis* *Ogataea pini*
1493	Nitrate growth	1494	1509
1494	L-Arabinose growth	1495	1499
1495	Galactose fermentation	1496	1498
1496	Methanol growth	*Candida methanosorbosa*	1497
1497	Galactitol growth	*Zygoascus ofunaensis*	*Wickerhamomyces silvicola*
1498	L-Rhamnose growth	*Candida wickerhamii*	*Pachysolen tannophilus*
1499	*N*-Acetyl-D-glucosamine growth	1500	1501
1500	D-Mannitol growth	*Candida wyomingensis*	*Dekkera bruxellensis*
1501	DL-Lactate growth	1502	1508
1502	D-Gluconate growth	1503	1505
1503	Raffinose growth	*Lindnera mrakii*	1504
1504	L-Sorbose growth	*Barnettozyma californica*	*Candida norvegica* *Lindnera misumaiensis*
1505	Ethanol growth	1506	*Candida sanyiensis*
1506	Vitamin-free growth	*Candida berthetii*	1507
1507	D-Mannitol growth	*Candida norvegica*	*Barnettozyma hawaiiensis*
1508	Methanol growth	*Ogataea minuta*	*Candida versatilis*

No.	Test	Positive	Negative
1509	D-Mannitol growth	1510	1541
1510	Growth at 37°C	1511	1526
1511	Soluble starch growth	1512	1515
1512	Galactose fermentation	1513	1514
1513	*myo*-Inositol growth	*Trichomonascus petasosporus*	*Candida tropicalis*
1514	Melezitose growth	*Candida insectamans*	*Saccharomycopsis malanga*
1515	Trehalose growth	1516	1520
1516	Cycloheximide 0.01% growth	1517	1519
1517	L-Rhamnose growth	*Clavispora lusitaniae*	1518
1518	Maltose growth	*Lachancea fermentati*	*Candida marionensis*
1519	Ribitol growth	*Metschnikowia drosophilae*	*Candida xylopsoci*
1520	Galactose growth	1521	1523
1521	Galactose fermentation	*Geotrichum fermentans*	1522
1522	Ribitol growth	*Candida geochares*	*Candida xylopsoci*
1523	Methanol growth	*Candida sonorensis*	1524
1524	L-Sorbose growth	*Wickerhamomyces pijperi*	1525
1525	L-Rhamnose growth	*Lindnera sargentensis*	*Starmera quercuum*
1526	L-Arabinose growth	1527	1531
1527	DL-Lactate growth	1528	1529
1528	Raffinose growth	*Cephaloascus albidus*	*Geotrichum fermentans*
1529	*myo*-Inositol growth	*Blastobotrys indianensis*	1530
1530	D-Gluconate growth	*Candida torresii*	*Candida piceae* *Trichomonascus farinosus*
1531	Glycerol growth	1532	1539
1532	Trehalose growth	1533	1538
1533	Methanol growth	1534	1535
1534	Galactose growth	*Trichomonascus farinosus*	*Ogataea minuta*
1535	D-Gluconate growth	*Candida sake* *Candida santamariae*	1536
1536	Xylitol growth	1537	*Candida sake* *Trichomonascus farinosus*
1537	Vitamin-free growth	*Candida savonica*	*Trichomonascus farinosus*
1538	Galactose fermentation	*Geotrichum fermentans*	*Wickerhamomyces pijperi*
1539	Succinate growth	1540	*Brettanomyces nanus*
1540	Cycloheximide 0.01% growth	*Brettanomyces naardenensis*	*Candida sake*
1541	Succinate growth	1542	1545
1542	Trehalose growth	1543	1544
1543	Raffinose growth	*Kazachstania sinensis*	1540
1544	Citrate growth	*Pichia norvegensis*	*Candida dendrica*
1545	2-Keto-D-gluconate growth	1546	1547
1546	Growth at 37°C	*Hanseniaspora guilliermondii* *Hanseniaspora opuntiae* *Hanseniaspora pseudoguilliermondii*	*Hanseniaspora clermontiae* *Hanseniaspora meyeri* *Hanseniaspora uvarum*
1547	Cycloheximide 0.01% growth	1548	1551
1548	D-Gluconate growth	1549	1550
1549	Ethanol growth	*Candida anatomiae*	*Hanseniaspora lachancei*
1550	Growth at 37°C	*Dekkera bruxellensis* *Kloeckera lindneri*	*Hanseniaspora valbyensis* *Kloeckera lindneri*
1551	Melezitose growth	*Metschnikowia arizonensis*	*Hanseniaspora osmophila* *Hanseniaspora vineae*

No.	Test	Positive	Negative
1552	Nitrate growth	1553	1572
1553	Growth at 30°C	1554	1563
1554	Erythritol growth	1555	1559
1555	L-Rhamnose growth	1556	1558
1556	Maltose growth	*Ogataea nakhonphanomensis*	1557
1557	L-Sorbose growth	*Ogataea trehaloabstinens*	*Ogataea henricii*
1558	Ribitol growth	*Ogataea allantospora*	*Ogataea chonburiensis*
1559	Ribitol growth	1560	1561
1560	Methanol growth	*Ogataea nonfermentans*	*Candida jianshihensis*
1561	D-Mannitol growth	1562	*Barnettozyma hawaiiensis*
1562	L-Rhamnose growth	*Barnettozyma populi*	*Starmera dryadoides*
1563	D-Xylose growth	1564	1570
1564	Citrate growth	1565	1568
1565	D-Glucosamine growth	1566	1567
1566	Methanol growth	*Ascoidea africana*	*Taphrina caerulescens*
1567	Galactose growth	*Dipodascus macrosporus*	*Lalaria kurtzmanii*
1568	Methanol growth	*Ascoidea africana*	1569
1569	Galactose growth	*Taphrina mirabilis*	*Taphrina communis* *Taphrina deformans*
1570	Trehalose growth	1571	*Taphrina populina*
1571	Xylitol growth	*Taphrina johansonii*	*Taphrina populi-salicis*
1572	Trehalose growth	1573	1591
1573	Erythritol growth	1574	1582
1574	Galactose growth	1575	1580
1575	Maltose growth	1576	1579
1576	Raffinose growth	*Priceomyces castillae*	1577
1577	Lactose growth	*Blastobotrys elegans*	1578
1578	L-Sorbose growth	*Priceomyces medius*	*Debaryomyces coudertii*
1579	Methanol growth	*Candida nemodendra*	*Myxozyma nipponensis*
1580	Methanol growth	1581	*Sporopachydermia cereana*
1581	L-Sorbose growth	*Ogataea paradorogensis* *Ogataea pini*	*Ogataea neopini* *Ogataea pini*
1582	Methanol growth	1583	1584
1583	*myo*-Inositol growth	*Ascoidea hylecoeti*	*Ascoidea africana*
1584	Cycloheximide 0.1% growth	1585	1588
1585	Melibiose growth	*Lipomyces mesembrius*	1586
1586	D-Mannitol growth	*Candida zeylanoides*	1587
1587	Ethanol growth	*Myxozyma lipomycoides*	*Lipomyces arxii*
1588	Lactose growth	1589	1590
1589	D-Mannitol growth	*Candida scorzettiae*	*Myxozyma lipomycoides*
1590	Growth at 37°C	*Candida insectalens*	*Candida sake*
1591	Galactose growth	1592	1606
1592	DL-Lactate growth	1593	1600
1593	D-Mannitol growth	1594	1596
1594	Erythritol growth	*Yarrowia lipolytica*	1595
1595	L-Sorbose growth	*Dipodascus macrosporus*	*Geotrichum cucujoidarum*
1596	D-Xylose growth	1597	1598
1597	L-Sorbose growth	*Magnusiomyces spicifer*	*Candida ponderosae*
1598	Maltose growth	*Prototheca stagnora*	1599
1599	L-Sorbose growth	*Saprochaete clavata*	*Wickerhamomyces chambardii*

No.	Test	Positive	Negative
1600	Melibiose growth	1601	1602
1601	*myo*-Inositol growth	*Myxozyma melibiosi*	*Lipomyces mesembrius*
1602	D-Mannitol growth	1603	1604
1603	Glycerol growth	*Lipomyces suomiensis*	*Kluyveromyces nonfermentans*
1604	D-Xylose growth	1605	*Prototheca stagnora*
1605	Ethanol growth	*Myxozyma neglecta*	*Dipodascopsis anomala*
1606	L-Rhamnose growth	1607	1611
1607	2-Keto-D-gluconate growth	1608	1609
1608	D-Glucitol growth	*Barnettozyma salicaria*	*Candida montana*
1609	Methanol growth	*Ogataea populialbae*	1610
1610	Citrate growth	*Phaffomyces opuntiae*	*Phaffomyces thermotolerans*
1611	D-Mannitol growth	1612	1616
1612	Erythritol growth	*Candida deformans* *Yarrowia lipolytica*	1613
1613	DL-Lactate growth	1614	1615
1614	Growth at 37°C	*Phaffomyces thermotolerans*	*Candida orba*
1615	Melibiose growth	*Lipomyces mesembrius*	*Candida zeylanoides*
1616	Melibiose growth	*Lipomyces mesembrius*	1617
1617	Lactose growth	*Dipodascopsis anomala*	1618
1618	Maltose growth	*Prototheca zopfii* var. 1	*Candida orba* *Prototheca ulmea*
1619	D-Mannitol growth	1620	1807
1620	Glucose fermentation	1621	1707
1621	D-Ribose growth	1622	1650
1622	Erythritol growth	1623	1635
1623	Methanol growth	1624	1629
1624	*N*-Acetyl-D-glucosamine growth	1625	1627
1625	Galactose fermentation	*Candida nanaspora*	1626
1626	Galactose growth	*Candida cidri*	*Candida boidinii*
1627	Glycerol growth	1628	*Candida pini*
1628	Nitrate growth	*Ogataea polymorpha*	*Ogataea trehalophila*
1629	2-Keto-D-gluconate growth	1630	1632
1630	Galactose fermentation	*Candida schatavii*	1631
1631	Trehalose fermentation	*Candida boleticola*	*Trigonopsis cantarellii*
1632	Galactose growth	1633	1634
1633	Ribitol growth	*Millerozyma farinosa*	*Debaryomyces singareniensis*
1634	L-Arabinose growth	*Ogataea salicorniae*	*Candida llanquihuensis*
1635	Nitrate growth	1636	1642
1636	Methanol growth	1637	1638
1637	D-Arabinose growth	*Ogataea ramenticola*	*Candida nitratophila*
1638	Ethanol growth	1639	1640
1639	Sucrose fermentation	*Candida magnoliae*	*Candida etchellsii*
1640	Growth at 37°C	1641	*Candida etchellsii*
1641	Galactose growth	*Candida cellae*	*Candida bombiphila*
1642	Galactose growth	1643	1649
1643	Cycloheximide 0.01% growth	1644	1647
1644	Ethanol growth	1645	*Kazachstania aerobica*
1645	DL-Lactate growth	*Candida albicans* *Candida tropicalis*	1646
1646	Trehalose fermentation	*Candida tropicalis*	*Candida catenulata*

No.	Test	Positive	Negative
1647	Trehalose growth	*Candida sake*	1648
1648	Ethanol growth	*Candida pyralidae*	*Candida powellii*
1649	DL-Lactate growth	*Saccharomycopsis crataegensis*	*Candida fructus*
1650	Trehalose growth	1651	1671
1651	L-Rhamnose growth	1652	1656
1652	D-Glucosamine growth	1653	1655
1653	Methanol growth	1654	*Zygoascus tannicolus*
1654	Ribitol growth	*Candida methanosorbosa*	*Candida floccosa*
1655	Vitamin-free growth	*Komagataella pseudopastoris*	*Komagataella pastoris* *Komagataella phaffii*
1656	Succinate growth	1657	1667
1657	Galactose growth	1658	1664
1658	Cycloheximide 0.01% growth	1659	1661
1659	Ethanol growth	1660	*Kazachstania aerobia*
1660	Cycloheximide 0.1% growth	1645	*Candida aurita*
1661	*N*-Acetyl-D-glucosamine growth	1662	1663
1662	50% Glucose growth	*Candida anglica*	*Candida sake*
1663	Ethanol growth	*Torulaspora delbrueckii*	*Kazachstania spencerorum*
1664	2-Keto-D-gluconate growth	*Saccharomycopsis vini* *Torulaspora delbrueckii*	1665
1665	Gelatin liquefaction	1666	*Saturnispora dispora* *Saturnispora zaruensis*
1666	Glycerol growth	*Saturnispora hagleri*	*Saturnispora saitoi*
1667	L-Sorbose growth	1668	1669
1668	Citrate growth	*Candida prunicola*	*Saccharomycopsis vini* *Torulaspora delbrueckii*
1669	Ribitol growth	*Torulaspora delbrueckii* *Zygosaccharomyces bailii*	1670
1670	Ethanol growth	*Torulaspora delbrueckii* *Zygosaccharomyces rouxii*	*Zygosaccharomyces mellis* *Zygosaccharomyces rouxii*
1671	DL-Lactate growth	1672	1688
1672	D-Xylose growth	1673	1682
1673	Galactose growth	1674	1680
1674	Maltose growth	1675	1676
1675	Maltose fermentation	*Candida albicans*	*Dipodascus geniculatus*
1676	Vitamin-free growth	1677	1678
1677	Growth at 35°C	*Galactomyces candidus*	*Geotrichum klebahnii*
1678	Glycerol growth	1679	*Candida sorbophila*
1679	Ribitol growth	*Galactomyces citri-aurantii* *Geotrichum histeridarum*	*Galactomyces geotrichum* *Geotrichum histeridarum*
1680	D-Glucitol growth	1681	*Starmera caribaea*
1681	L-Sorbose growth	*Geotrichum carabidarum*	*Candida stellimalicola*
1682	L-Sorbose growth	1683	1685
1683	Nitrate growth	*Candida etchellsii*	1684
1684	D-Gluconate growth	*Candida cylindracea*	*Saprochaete gigas* *Saprochaete suaveolens*
1685	Gelatin liquefaction	*Saturnispora ahearnii* *Saturnispora besseyi*	1686
1686	Nitrate growth	*Candida etchellsii*	1687
1687	D-Glucitol growth	*Candida silvae*	*Starmera caribaea*

No.	Test	Positive	Negative
		Saturnispora mendoncae	
1688	Ethanol growth	1689	1701
1689	Sucrose fermentation	1690	1692
1690	Maltose fermentation	1691	1256
1691	Raffinose growth	*Saccharomyces kudriavzevii*	*Zygosaccharomyces rouxii*
1692	L-Sorbose growth	1693	1695
1693	Nitrate growth	*Candida etchellsii*	1694
1694	D-Xylose growth	*Galactomyces geotrichum*	*Saccharomycopsis vini*
			Zygosaccharomyces bisporus
1695	Succinate growth	1696	1699
1696	*N*-Acetyl-D-glucosamine growth	1697	1698
1697	Glycerol growth	*Candida catenulata*	*Kregervanrija delftensis*
1698	Nitrate growth	*Candida etchellsii*	*Candida diversa*
			Candida silvae
1699	Nitrate growth	*Candida etchellsii*	1700
1700	Maltose fermentation	*Zygosaccharomyces rouxii*	*Zygosaccharomyces bisporus*
1701	Growth at 37°C	1702	1705
1702	D-Gluconate growth	1703	1704
1703	Maltose fermentation	*Candida floris*	*Candida batistae*
		Zygosaccharomyces rouxii	*Candida floris*
1704	L-Sorbose growth	*Candida riodocensis*	*Zygosaccharomyces rouxii*
1705	Ribitol growth	*Candida tilneyi*	1706
1706	Nitrate growth	*Candida etchellsii*	*Zygosaccharomyces mellis*
			Zygosaccharomyces rouxii
1707	Erythritol growth	1708	1723
1708	*myo*-Inositol growth	1709	1712
1709	Maltose growth	1710	1711
1710	Gelatin liquefaction	*Saccharomycopsis microspora*	*Saccharomycopsis synnaedendra*
1711	Galactose growth	*Myxozyma sirexii*	*Candida lassenensis*
1712	Citrate growth	1713	1718
1713	DL-Lactate growth	1714	1716
1714	D-Glucitol growth	1715	*Candida hollandica*
1715	*N*-Acetyl-D-glucosamine growth	*Yarrowia lipolytica*	*Candida galli*
1716	Methanol growth	1717	*Candida fermenticarens*
1717	Methyl-α-D-glucoside growth	*Candida krabiensis*	*Ogataea philodendri*
1718	Methanol growth	1719	1721
1719	Galactitol growth	*Candida nemodendra*	1720
1720	Galactose growth	*Candida suzukii*	*Ogataea wickerhamii*
1721	Galactitol growth	*Priceomyces haplophilus*	1722
1722	Trehalose growth	*Candida psychrophila*	*Trigonopis californica*
1723	DL-Lactate growth	1724	1765
1724	Galactose growth	1725	1751
1725	Vitamin-free growth	1726	1729
1726	L-Arabinose growth	*Cephaloascus fragrans*	1727
1727	Trehalose growth	*Candida sake*	1728
1728	L-Sorbose growth	1677	*Dipodascus armillariae*
1729	Growth at 37°C	1730	1737
1730	Trehalose growth	1731	1732
1731	Glycerol growth	*Trigonopsis variabilis*	*Candida caseinolytica*
1732	Ribitol growth	1733	1734

No.	Test	Positive	Negative
1733	Xylitol growth	..... *Candida rugosa* *Saprochaete fungicola*	..... *Candida rugosa* *Dipodascus australiensis*
1734	D-Xylose growth	 1735	 1736
1735	*N*-Acetyl-D-glucosamine growth	..... *Candida rugosa* *Dipodascus australiensis*	.....*Candida pararugosa* *Dipodascus australiensis*
1736	*N*-Acetyl-D-glucosamine growth	..... *Candida rugosa* *Magnusiomyces capitatus*	.....*Candida pararugosa* *Magnusiomyces capitatus*
1737	Ribitol growth	 1738	 1740
1738	Trehalose growth	.....*Candida sake*	 1739
1739	Growth at 30°C	..... *Dipodascus aggregatus* *Galactomyces citri-aurantii*	.....*Saprochaete psychrophila*
1740	D-Xylose growth	 1741	 1746
1741	Trehalose growth	.....*Candida sake*	 1742
1742	Citrate growth	 1743	 1745
1743	Maltose growth	..... *Dipodascus geniculatus*	 1744
1744	D-Glucosamine growth	..... *Trigonopsis vinaria*	..... *Dipodascus aggregatus* *Galactomyces geotrichum*
1745	Growth at 30°C	.....*Candida pararugosa* *Galactomyces geotrichum*	..... *Dipodascus albidus*
1746	Nitrate growth	.....*Candida etchellsii*	 1747
1747	Citrate growth	 1748	 1750
1748	Trehalose growth	.....*Candida sake*	 1749
1749	D-Glucosamine growth	..... *Trigonopsis vinaria*	..... *Saprochaete japonica*
1750	Trehalose growth	.....*Candida sake* *Magnusiomyces ovetensis*	.....*Candida pararugosa* *Magnusiomyces ovetensis*
1751	L-Rhamnose growth	 1752	 1753
1752	Methanol growth	..... *Ogataea populialbae*	.....*Phaffomyces antillensis* *Phaffomyces opuntiae*
1753	D-Xylose growth	 1754	 1756
1754	*myo*-Inositol growth	..... *Sporopachydermia lactativora*	 1755
1755	D-Ribose growth	.....*Saccharomycopsis crataegensis*	..... *Candida rugosa*
1756	Trehalose growth	 1757	 1759
1757	2-Keto-D-gluconate growth	.....*Ascobotryozyma americana* *Botryozyma mucatilis* *Botryozyma nematodophila*	 1758
1758	Cadaverine growth	.....*Candida hispaniensis*	.....*Ascobotryozyma americana*
1759	Growth at 37°C	 1760	 1763
1760	D-Glucitol growth	 1761	 1762
1761	2-Keto-D-gluconate growth	.....*Ascobotryzyma cognata*	..... *Candida rugosa*
1762	*N*-Acetyl-D-glucosamine growth	..... *Candida rugosa*	.....*Starmera pachycereana*
1763	Nitrate growth	.....*Candida etchellsii*	 1764
1764	2-Keto-D-gluconate growth	.....*Ascobotryzyma cognata* *Botryozyma mucatilis*	..... *Kregervanrija fluxuum* *Saturnispora mendoncae*
1765	Nitrate growth	 1766	 1770
1766	Cycloheximide 0.01% growth	 1767	 1769
1767	Citrate growth	 1768	..... *Wickerhamiella australiensis* *Wickerhamiella occidentalis*
1768	Ethanol growth	..... *Wickerhamiella cacticola*	..... *Candida vanderwaltii*
1769	Trehalose growth	.....*Taphrina communis*	.....*Candida etchellsii* *Wickerhamiella domercqiae*

No.	Test	Positive	Negative
1770	Succinate growth	1771	1801
1771	Growth at 37°C	1772	1778
1772	Cycloheximide 0.1% growth	1773	1776
1773	Citrate growth	1774	1775
1774	Methanol growth	*Ogataea populialbae*	*Lipomyces mesembrius*
1775	Ethanol growth	*Candida catenulata*	*Candida infanticola*
1776	Methanol growth	*Candida maris*	1777
1777	Trehalose growth	*Candida silvatica*	*Candida rugosa*
1778	Galactose growth	1779	1793
1779	Vitamin-free growth	1780	1783
1780	Melibiose growth	*Lipomyces mesembrius*	1781
1781	L-Arabinose growth	*Cephaloascus fragrans*	1782
1782	Trehalose growth	*Candida sake*	*Dipodascus armillariae*
1783	Ethanol growth	1784	1792
1784	L-Sorbose growth	1785	1789
1785	Melibiose growth	*Lipomyces mesembrius*	1786
1786	Trehalose growth	*Candida sake*	1787
1787	Growth at 30°C	1788	*Geotrichum restrictum*
1788	Citrate growth	*Dipodascus aggregatus* *Galactomyces geotrichum*	*Candida drosophilae* *Galactomyces geotrichum*
1789	Cycloheximide 0.01% growth	1790	1791
1790	Melibiose growth	*Lipomyces mesembrius*	*Candida catenulata*
1791	Trehalose growth	*Candida sake*	*Candida galacta*
1792	Melibiose growth	*Lipomyces mesembrius*	*Candida sake* *Schizoblastosporion starkeyi-henricii*
1793	Citrate growth	1794	1796
1794	Melibiose growth	*Lipomyces mesembrius*	1795
1795	Xylitol growth	*Candida anutae*	*Candida zeylanoides*
1796	Ethanol growth	1797	1800
1797	L-Sorbose growth	1798	1799
1798	*N*-Acetyl-D-glucosamine growth	*Candida zeylanoides*	*Candida drosophilae*
1799	*N*-Acetyl-D-glucosamine growth	*Kregervanrija delftensis*	*Kregervanrija fluxuum*
1800	Salicin growth	*Candida zeylanoides*	*Schizoblastosporion starkeyi-henricii* *Wickerhamiella lipophila*
1801	Ethanol growth	1802	1806
1802	Glycerol growth	1803	1805
1803	*myo*-Inositol growth	*Dipodascopsis uninucleata* var. *wickerhamii*	1804
1804	Growth at 30°C	*Candida rugosa*	*Geotrichum restrictum*
1805	D-Glucitol growth	*Kregervanrija pseudodelftensis*	*Kluyveromyces nonfermentans*
1806	D-Gluconate growth	*Candida floris*	*Candida riodocensis*
1807	Galactose growth	1808	1894
1808	Glucose fermentation	1809	1857
1809	Trehalose growth	1810	1832
1810	Growth at 37°C	1811	1824
1811	Glycerol growth	1812	1820
1812	L-Lysine growth	1813	1817
1813	Succinate growth	1814	1815
1814	Cadaverine growth	*Kazachstania spencerorum*	*Kazachstania aerobia*
1815	Methanol growth	*Kazachstania solicola*	1816

No.	Test	Positive	Negative
1816	Ribitol growth	*Zygosaccharomyces bailii*	*Dekkera bruxellensis*
1817	Ribitol growth	*Zygosaccharomyces bailii*	1818
1818	*N*-Acetyl-D-glucosamine growth	*Dekkera bruxellensis*	1819
1819	Cycloheximide 0.1% growth	*Kazachstania servazzii*	*Kazachstania viticola* *Naumovozyma castellii*
1820	*N*-Acetyl-D-glucosamine growth	1302	1821
1821	Cycloheximide 0.1% growth	1822	1823
1822	Ethanol growth	*Kazachstania aquatica* *Kazachstania unispora*	*Kazachstania siamensis*
1823	Ethanol growth	*Kazachstania unispora* *Naumovozyma castellii* *Naumovozyma dairenensis*	*Kazachstania transvaalensis* *Naumovozyma castellii* *Naumovozyma dairenensis*
1824	*N*-Acetyl-D-glucosamine growth	1825	1827
1825	Succinate growth	*Candida sake*	1826
1826	Glycerol growth	*Zygosaccharomyces bailii*	*Kazachstania turicensis*
1827	Ribitol growth	*Zygosaccharomyces bailii*	1828
1828	Raffinose growth	*Saccharomyces pastorianus*	1829
1829	D-Gluconate growth	*Kazachstania martiniae* *Naumovozyma castellii* *Tetrapisispora namnaonensis*	1830
1830	DL-Lactate growth	*Candida humilis*	1831
1831	Cycloheximide 0.1% growth	*Kazachstania servazzii*	*Kazachstania kunashirensis* *Naumovozyma castellii*
1832	Galactose fermentation	1833	1850
1833	D-Gluconate growth	1834	1839
1834	Raffinose growth	*Saccharomyces pastorianus*	1835
1835	DL-Lactate growth	*Kazachstania africana*	1836
1836	Glycerol growth	1837	1838
1837	Ethanol growth	*Naumovozyma castellii* *Tetrapisispora phaffii*	*Naumovozyma castellii* *Tetrapisispora nanseiensis*
1838	Growth at 37°C	*Naumovozyma castellii* *Naumovozyma dairenensis*	*Naumovozyma castellii* *Tetrapisispora iriomotensis*
1839	Growth at 30°C	1840	1849
1840	Maltose fermentation	1841	1843
1841	Raffinose fermentation	*Saccharomyces pastorianus*	1842
1842	*N*-Acetyl-D-glucosamine growth	*Dekkera bruxellensis*	*Kazachstania jiainica*
1843	Growth at 37°C	1844	1845
1844	*N*-Acetyl-D-glucosamine growth	*Dekkera bruxellensis*	*Kazachstania unispora* *Naumovozyma castellii* *Naumovozyma dairenensis*
1845	Glycerol growth	1846	1847
1846	L-Sorbose growth	*Saprochaete suaveolens*	*Naumovozyma castellii* *Tetrapisispora blattae*
1847	Cadaverine growth	*Kazachstania humatica*	1848
1848	L-Lysine growth	*Kazachstania yakushimaenisis*	*Naumovozyma castellii* *Saccharomycodes sinensis* *Tetrapisispora arboricola*
1849	Glycerol growth	*Vanderwaltozyma yarrowii*	*Kazachstania rosinii*
1850	Growth at 37°C	1851	1853
1851	D-Glucitol growth	*Magnusiomyces tetrasperma*	1852

No.	Test	Positive	Negative
1852	D-Gluconate growth	*Tetrapisispora fleetii*	*Dekkera bruxellensis*
1853	Raffinose growth	1854	1855
1854	Inulin growth	*Saccharomyces kudriavzevii*	*Saccharomyces pastorianus*
1855	Ribitol growth	*Saccharomycopsis selenospora*	1856
1856	Nitrate growth	*Candida etchellsii*	*Saprochaete suaveolens*
1857	Vitamin-free growth	1858	1865
1858	Trehalose growth	1859	1860
1859	Melibiose growth	*Lipomyces mesembrius*	*Candida sake* *Saprochaete chiloensis*
1860	D-Glucitol growth	1861	1862
1861	Melibiose growth	*Lipomyces mesembrius*	*Galactomyces pseudocandidus* *Geotrichum europaeum*
1862	Growth at 35°C	1863	1864
1863	L-Sorbose growth	*Magnusiomyces ingens*	*Saprochaete ingens*
1864	Melibiose growth	*Lipomyces mesembrius*	*Saprochaete quercus*
1865	Trehalose growth	1866	1873
1866	L-Arabinose growth	1867	1869
1867	Erythritol growth	*Candida mucifera*	1868
1868	Melibiose growth	*Lipomyces mesembrius*	*Debaryomyces mycophilus*
1869	DL-Lactate growth	1870	1871
1870	*N*-Acetyl-D-glucosamine growth	*Candida sake* *Magnusiomyces ovetensis*	*Magnusiomyces ovetensis* *Prototheca wickerhamii*
1871	Melibiose growth	*Lipomyces mesembrius*	1872
1872	Succinate growth	*Candida sake* *Schizoblastosporion starkeyi-henricii*	*Kazachstania turicensis*
1873	DL-Lactate growth	1874	1884
1874	Nitrate growth	*Candida etchellsii*	1875
1875	D-Glucosamine growth	1876	1877
1876	Maltose growth	*Prototheca stagnora*	*Trigonopsis vinaria*
1877	Maltose growth	*Prototheca stagnora*	1878
1878	D-Gluconate growth	1879	1881
1879	Cycloheximide 0.01% growth	1880	*Candida rugosa*
1880	Ribitol growth	*Candida oslonensis*	*Candida alimentaria*
1881	Growth at 37°C	1882	1883
1882	*N*-Acetyl-D-glucosamine growth	*Candida rugosa*	*Candida pararugosa*
1883	D-Xylose growth	*Candida pararugosa* *Galactomyces reessii*	*Candida pararugosa* *Magnusiomyces ovetensis*
1884	Growth at 37°C	1885	1888
1885	Growth at 35°C	1886	1887
1886	*N*-Acetyl-D-glucosamine growth	*Candida rugosa*	*Magnusiomyces starmeri*
1887	Melibiose growth	*Lipomyces mesembrius*	*Lipomyces oligophaga*
1888	Nitrate growth	*Candida etchellsii*	1889
1889	Melibiose growth	*Lipomyces mesembrius*	1890
1890	Maltose growth	*Prototheca stagnora*	1891
1891	Ethanol growth	1892	1893
1892	Galactitol growth	*Lipomyces oligophaga*	*Candida drosophilae*
1893	Succinate growth	*Schizoblastosporion starkeyi-henricii*	*Mixia osmundae*
1894	Glucose fermentation	1895	1956
1895	Succinate growth	1896	1930
1896	Vitamin-free growth	1897	1908

No.	Test	Positive	Negative
1897	Growth at 37°C	1898	1902
1898	Citrate growth	1899	1900
1899	Ribitol growth	*Pichia cecembensis*	*Pichia kudriavzevii* *Pichia manshurica*
1900	D-Glucosamine growth	1901	*Candida ethanolica*
1901	*N*-Acetyl-D-glucosamine growth	*Pichia manshurica* *Pichia occidentalis*	*Candida rugopelliculosa*
1902	Glycerol growth	1903	1906
1903	D-Glucitol growth	*Nadsonia fulvescens* var. *elongata*	1904
1904	Citrate growth	*Candida californica* *Pichia membranifaciens*	1905
1905	*N*-Acetyl-D-glucosamine growth	*Pichia membranifaciens*	*Pichia scutulata*
1906	*N*-Acetyl-D-glucosamine growth	1907	*Candida pseudolambica*
1907	10% NaCl/5% glucose growth	*Pichia membranifaciens*	*Pichia exigua*
1908	D-Glucosamine growth	1909	1917
1909	*N*-Acetyl-D-glucosamine growth	1910	1914
1910	Citrate growth	1911	1913
1911	Growth at 37°C	1912	*Pichia cephalocereana* *Pichia eremophila* *Pichia kluyveri* *Pichia membranifaciens*
1912	D-Xylose growth	*Pichia cephalocereana* *Pichia eremophila* *Pichia fermentans* *Pichia kluyveri*	*Candida inconspicua* *Pichia cephalocereana* *Pichia eremophila* *Pichia kluyveri* *Pichia manshurica*
1913	Growth at 37°C	*Pichia barkeri* *Pichia kluyveri* *Pichia manshurica*	*Pichia kluyveri* *Pichia membranifaciens*
1914	L-Sorbose growth	1915	1916
1915	D-Glucitol growth	*Saccharomycopsis vini*	*Pichia sporocuriosa*
1916	D-Xylose growth	*Pichia cactophila*	*Candida inconspicua*
1917	D-Glucitol growth	1918	1921
1918	Nitrate growth	*Candida etchellsii*	1919
1919	D-Xylose growth	*Geotrichum carabidarum*	1920
1920	2-Keto-D-gluconate growth	*Saccharomycopsis vini*	*Nadsonia fulvescens* var. *elongata*
1921	Trehalose growth	1922	1923
1922	D-Ribose growth	*Brettanomyces custersianus*	*Saccharomycopsis fermentans*
1923	Glycerol growth	1924	1929
1924	D-Xylose growth	1925	1927
1925	D-Gluconate growth	*Candida amapae*	1926
1926	*N*-Acetyl-D-glucosamine growth	*Pichia membranifaciens*	*Candida sorboxylosa*
1927	Nitrate growth	*Candida etchellsii*	1928
1928	*N*-Acetyl-D-glucosamine growth	*Pichia membranifaciens*	*Pichia nakasei* *Pichia terricola*
1929	*N*-Acetyl-D-glucosamine growth	*Pichia membranifaciens*	*Kazachstania bovina* *Kazachstania telluris*
1930	Growth at 37°C	1931	1944
1931	D-Gluconate growth	1932	1937
1932	Trehalose growth	1933	1934

No.	Test	Positive	Negative
1933	Ribitol growth	*Zygosaccharomyces bailii*	*Candida bracarensis* *Candida glabrata*
1934	Nitrate growth	*Candida glucosophila*	1935
1935	L-Lysine growth	*Candida castellii*	1936
1936	Trehalose fermentation	*Candida glabrata* *Candida nivariensis*	*Candida glabrata* *Nakaseomyces bacillisporus*
1937	Trehalose growth	1938	1940
1938	50% Glucose growth	1939	1302
1939	Ribitol growth	*Zygosaccharomyces bailii*	*Nakaseomyces delphensis*
1940	D-Xylose growth	*Candida glucosophila*	1941
1941	Raffinose fermentation	*Candida zemplinina*	1942
1942	*N*-Acetyl-D-glucosamine growth	*Dekkera bruxellensis*	1943
1943	Ethanol growth	*Kazachstania bovina* *Kazachstania heterogenica* *Kazachstania pintolopesii*	*Kazachstania heterogenica* *Kazachstania pintolopesii* *Kazachstania slooffiae* *Schizosaccharomyces octosporus*
1944	Trehalose growth	1945	1950
1945	Glycerol growth	1946	1949
1946	Maltose fermentation	*Zygosaccharomyces mellis*	1947
1947	D-Glucitol growth	1948	*Saccharomycopsis fermentans*
1948	L-Sorbose growth	*Saccharomycopsis vini*	*Zygosaccharomyces bailii*
1949	L-Rhamnose growth	*Candida anatomiae*	*Kazachstania turicensis*
1950	Ethanol growth	1951	1954
1951	Nitrate growth	*Candida etchellsii*	1952
1952	D-Glucitol growth	*Saccharomycopsis vini*	1953
1953	*N*-Acetyl-D-glucosamine growth	*Pichia membranifaciens*	*Pichia sporocuriosa*
1954	Nitrate growth	*Candida etchellsii*	1955
1955	Sucrose fermentation	*Candida zemplinina*	*Schizosaccharomyces octosporus* *Zygosaccharomyces mellis*
1956	Growth at 37°C	1957	1975
1957	Maltose growth	1958	1959
1958	Melibiose growth	*Lipomyces mesembrius*	*Prototheca zopfii* var. *zopfii* *Prototheca zopfii* var. 1 *Prototheca zopfii* var. 3 *Prototheca zopfii* var. *portoricensis*
1959	D-Glucosamine growth	1960	1963
1960	D-Xylose growth	1961	1962
1961	10% NaCl/5% glucose growth	*Pichia eremophila*	*Candida thaimueangensis* *Pichia cactophila*
1962	*N*-Acetyl-D-glucosamine growth	*Candida inconspicua* *Pichia eremophila* *Pichia manshurica*	*Candida inconspicua* *Pichia pseudocactophila*
1963	D-Xylose growth	1964	1969
1964	*myo*-Inositol growth	*Sporopachydermia lactativora*	1965
1965	Melibiose growth	*Lipomyces mesembrius*	1966
1966	D-Gluconate growth	1967	1968
1967	*N*-Acetyl-D-glucosamine growth	*Candida rugosa*	*Starmera amethionina*
1968	*N*-Acetyl-D-glucosamine growth	*Candida rugosa* *Candida thaimueangensis*	*Candida thaimueangensis* *Pichia heedii*
1969	Citrate growth	1970	1972

No.	Test	Positive	Negative
1970	Melibiose growth	*Lipomyces mesembrius*	1971
1971	L-Rhamnose growth	*Phaffomyces antillensis*	*Candida rugosa*
1972	Trehalose growth	*Kazachstania turicensis*	1973
1973	Vitamin-free growth	*Candida ethanolica*	1974
1974	*N*-Acetyl-D-glucosamine growth	*Candida rugosa*	*Pichia deserticola*
1975	DL-Lactate growth	1976	1982
1976	Maltose growth	1977	1978
1977	Nitrate growth	*Candida etchellsii*	*Prototheca zopfii* var. *zopfii* *Prototheca zopfii* var. 2 *Prototheca zopfii* var. 3 *Prototheca zopfii* var. *portoricensis*
1978	Nitrate growth	*Candida etchellsii*	1979
1979	Trehalose growth	*Ascobotryozyma americana*	1980
1980	L-Rhamnose growth	*Phaffomyces antillensis*	1981
1981	*N*-Acetyl-D-glucosamine growth	*Pichia eremophila* *Pichia membranifaciens* *Prototheca ulmea*	*Candida galis* *Prototheca ulmea*
1982	Trehalose growth	1983	1987
1983	Melibiose growth	*Lipomyces mesembrius*	1984
1984	D-Glucitol growth	*Schizoblastosporion starkeyi-henricii*	1985
1985	Glycerol growth	1986	*Kazachstania turicensis*
1986	*N*-Acetyl-D-glucosamine growth	*Saccharomycopsis javanensis*	*Saccharomycopsis schoenii*
1987	Soluble starch growth	1988	1989
1988	Melibiose growth	*Lipomyces mesembrius*	*Mixia osmundae*
1989	Nitrate growth	*Candida etchellsii*	1990
1990	Melibiose growth	*Lipomyces mesembrius*	1991
1991	Growth at 25°C	1992	*Nadsonia commutata*
1992	D-Glucitol growth	1993	1995
1993	Ethanol growth	1994	*Prototheca ulmea* *Schizoblastosporion starkeyi-henricii*
1994	Hexadecane growth	*Candida drosophilae*	*Prototheca ulmea*
1995	D-Xylose growth	1953	*Pichia membranifaciens* *Prototheca ulmea* *Saprochaete saccharophila*

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Summary of Species Characteristics

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Ln. no.	Species	Fermentation							Growth reactions and other characteristics																											
		Glucose	Galactose	Sucrose	Maltose	Lactose	Raffinose	Trehalose	Glucose	Inulin	Sucrose	Raffinose	Melibiose	Galactose	Lactose	Trehalose	Maltose	Melezitose	Methyl-α-D-glucoside	Soluble Starch	Cellobiose	Salicin	L-Sorbose	L-Rhamnose	D-Xylose	L-Arabinose	D-Arabinose	D-Ribose	Methanol	Ethanol	Glycerol	Erythritol	Ribitol	Galactitol	D-Mannitol	D-Glucitol
1	***Acaromyces***																																			
2	*A. ingoldii*	−	−	−	−	−	−	−	+	v	+	+	v	+	+	+	+	+	−	v	+	+	−	−	+	+	+	+	−	+	−	+	v	−	+	+
3	***Aciculoconidium***																																			
4	*A. aculeatum*	+	−	v	−	−	−	+	+	−	+	−	−	−	−	+	+	+	+	+	+	v	−	−	−	−	−	−	−	+	+	−	+	−	+	+
5	***Agaricostilbum***																																			
6	*A. hyphaenes*	−	−	−	−	−	−	−	+	−	+	+	−	−	+	+	−	+	+	−	+	+	+	−	+	+	+	+	−	+	+	+	+	−	+	+
7	***Ambrosiozyma***																																			
8	*A. ambrosiae*	v	−	−	−	−	−	−	+	−	+	−	−	−	−	+	+	+	+	v	+	+	−	−	+	−	−	v	−	v	+	+	+	−	+	+
9	*A. angophorae*	+	−	+	+	−	−	−	+	−	+	−	−	−	−	+	+	+	+	−	+	+	−	−	+	+	−	−	−	+	−	−	+	−	+	+
10	*A. cicatricosa*	+	−	v	+	−	−	v	+	−	+	−	−	−	−	+	+	+	+	−	+	v	−	−	+	+	−	v	−	+	+	+	+	−	+	+
11	*A. monospora*	+	−	v	v	−	−	+	+	−	+	−	−	−	−	+	+	+	+	−	+	+	−	−	+	+	−	v	−	+	+	+	+	−	+	+
12	*A. philentoma*	+	−	v	−	−	−	+	+	−	+	−	−	−	−	+	+	+	+	−	+	+	−	+	+	−	−	+	−	+	+	+	+	−	+	+
13	*A. platypodis*	+	−	−	v	−	−	v	+	−	+	−	−	−	−	+	+	+	+	v	+	+	−	+	+	−	−	+	−	+	+	+	+	−	+	+
14	***Ascobotryozyma***																																			
15	*A. americana*	−	−	−	−	−	−	−	+	−	−	−	−	−	−	+	−	−	−	−	−	−	v	−	−	−	−	−	−	v	+	−	−	−	v	+
16	*A. cognata*	−	−	−	−	−	−	−	+	−	−	−	−	−	−	−	−	−	−	−	−	−	v	−	−	−	−	−	−	v	+	−	−	−	+	+
17	***Ascoidea***																																			
18	*A. africana*	−	−	−	−	−	−	−	+	−	v	v	v	v	−	+	v	+	v	+	+	+	+	v	+	v	−	−	+	+	+	−	v	n	v	+
19	*A. hylecoeti*	−	−	−	−	−	−	−	+	−	−	−	+	−	−	+	−	+	−	+	+	+	+	+	+	+	−	−	+	+	+	−	+	n	+	+
20	*A. rubescens*	−	−	−	−	−	−	−	+	+	+	+	+	+	+	+	+	+	+	+	+	−	−	+	+	−	+	+	−	+	+	+	+	n	+	+
21	***Aureobasidium***																																			
22	*A. pullulans*	−	−	−	−	−	−	−	+	+	+	+	+	+	v	+	+	+	v	+	+	v	+	+	+	+	+	+	n	+	+	+	+	v	+	+
23	***Auriculibuller***																																			
24	*A. fuscus*	−	−	−	−	−	−	−	+	−	+	+	+	+	+	+	+	+	+	+	+	+	−	+	+	+	+	+	−	−	v	+	+	v	+	+
25	***Babjeviella***																																			
26	*B. inositovora*	−	−	−	−	−	−	−	+	−	+	−	−	+	−	+	+	+	+	−	+	+	+	−	+	−	+	−	−	+	+	−	+	−	+	+
27	***Bannoa***																																			
28	*B. hahajimensis*	−	−	−	−	−	−	−	+	−	+	+	+	+	−	+	+	+	+	+	+	+	+	+	+	+	v	v	−	v	+	−	v	v	+	+
29	***Barnettozyma***																																			
30	*B. californica*	+	−	−	−	−	−	−	+	−	v	−	−	−	−	v	v	−	v	−	+	+	+	v	+	−	−	−	−	+	+	−	−	−	+	v
31	*B. hawaiiensis*	v	−	−	−	−	−	−	+	−	−	−	−	−	−	−	−	−	−	−	+	+	−	+	+	−	v	−	−	+	+	−	−	−	−	−
32	*B. populi*	−	−	−	−	−	−	−	+	−	−	−	−	−	−	−	−	−	−	−	+	+	−	+	+	−	−	−	−	+	+	−	−	−	+	+
33	*B. pratensis*	+	−	+	−	−	−	−	+	−	+	−	−	+	−	+	+	+	+	−	+	+	−	−	+	−	−	−	−	+	+	−	−	−	+	+
34	*B. salicaria*	−	−	−	−	−	−	−	+	−	−	−	−	−	−	−	−	−	−	−	+	+	−	+	+	−	−	−	−	+	+	−	−	−	+	+
35	*B. wickerhamii*	+	−	−	−	−	−	−	+	−	+	−	−	−	−	v	+	+	+	−	+	+	−	+	+	v	−	−	−	+	+	−	+	−	+	+
36	***Bensingtonia***																																			
37	*B. changbaiensis*	−	−	−	−	−	−	−	+	v	+	+	−	−	−	+	+	−	−	+	+	−	−	−	v	v	−	−	−	−	+	−	+	−	+	+
38	*B. ciliata*	−	−	−	−	−	−	−	+	−	−	−	−	−	−	+	−	−	−	−	−	−	v	−	−	−	−	−	−	+	+	−	+	−	+	+
39	*B. ingoldii*	−	−	−	−	−	−	−	+	−	+	v	+	v	+	+	−	+	−	+	+	v	v	−	+	+	v	+	−	+	+	+	+	−	+	+
40	*B. miscanthi*	−	−	−	−	−	−	−	+	−	+	v	−	v	v	+	−	−	−	−	+	−	v	−	v	−	−	−	−	−	+	−	v	−	+	+
41	*B. musae*	−	−	−	−	−	−	−	+	−	v	−	−	v	−	+	−	−	−	−	−	+	+	−	+	v	v	+	−	+	+	+	+	−	+	+
42	*B. naganoensis*	−	−	−	−	−	−	−	+	−	+	+	+	−	−	v	+	+	−	+	+	v	−	−	v	v	−	−	−	−	+	−	v	v	+	+
43	*B. phyllada*	−	−	−	−	−	−	−	+	−	+	−	−	−	v	+	+	+	v	v	+	v	v	v	−	v	−	−	−	+	+	−	v	−	+	+
44	*B. pseudonaganoensis*	−	−	−	−	−	−	−	+	−	+	+	+	+	−	+	+	+	−	−	+	−	−	−	+	−	+	−	−	−	+	−	+	−	+	+
45	*B. sakaguchii*	−	−	−	−	−	−	−	+	−	−	−	−	−	+	+	+	+	v	+	+	v	−	−	−	−	−	−	−	−	−	−	v	−	+	v
46	*B. sorbi*	−	−	−	−	−	−	−	+	−	+	+	−	+	v	+	+	−	−	v	v	−	+	−	+	+	v	−	−	−	+	−	+	v	+	+
47	*B. subrosea*	−	−	−	−	−	−	−	+	−	+	v	v	v	v	+	+	v	−	+	+	v	−	−	v	−	−	−	−	v	+	−	v	−	v	v
48	*B. thailandica*	−	−	−	−	−	−	−	+	−	+	+	+	v	−	+	+	+	−	+	+	v	−	−	−	−	−	−	−	−	+	−	v	v	v	v
49	*B. yamatoana*	−	−	−	−	−	−	−	+	−	+	−	−	v	−	+	+	+	−	v	−	−	−	−	v	−	−	−	−	v	+	−	v	−	+	v
50	*B. yuccicola*	−	−	−	−	−	−	−	+	−	−	−	−	v	v	+	−	−	−	−	+	−	+	−	v	−	−	−	−	−	+	−	+	−	+	+
51	***Blastobotrys***																																			
52	*B. adeninivorans*	+	+	+	+	−	+	+	+	−	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	−	+	+	+	+	−	+	+
53	*B. americana*	+	−	−	−	−	−	+	+	−	−	+	+	+	−	+	−	−	+	−	+	+	+	−	+	+	+	+	−	+	+	+	+	+	+	+
54	*B. arbuscula*	+	+	−	+	−	−	+	+	v	−	−	−	+	−	+	+	−	v	+	+	−	+	−	+	+	−	+	n	−	+	+	+	+	+	+
55	*B. aristata*	+	v	−	+	−	−	+	+	v	+	v	v	+	+	+	+	−	v	+	+	+	+	v	+	+	+	+	n	−	+	+	+	+	+	+

Symbols: +, positive or weak; −, negative; v, variable (+/−, w/−); n, no data.

	Growth reactions and other characteristics																																							
	myo-Inositol	DL-Lactate	Succinate	Citrate	D-Gluconate	D-Glucosamine	*N*-Acetyl-D-glucosamine	Hexadecane	Nitrate	Nitrite	Vitamin-free	2-Keto-D-gluconate	5-Keto-D-gluconate	Saccharate	Xylitol	L-Arabinitol	Arbutin	Propane 1,2 diol	Butane 2,3 diol	Cadaverine	Creatinine	L-Lysine	Ethylamine	50% Glucose	10% NaCl/5% glucose	Starch formation	Urease	Gelatin liquefaction	Cycloheximide 0.01%	Cycloheximide 0.1%	Growth at 19°C	Growth at 25°C	Growth at 30°C	Growth at 35°C	Growth at 37°C	Growth at 40°C	Growth at 45°C	CoQ (Main component)	Mol% G + C (Ave.)	DBB
Acaromyces																																								
2	+	−	+	v	+	−	n	n	+	+	+	−	n	n	n	n	n	n	n	n	n	n	n	−	n	−	+	n	n	n	+	+	+	−	−	−	−	n	n	+
Aciculoconidium																																								
4	−	−	+	+	−	v	n	n	−	n	−	−	n	−	−	n	n	n	n	n	n	n	n	−	n	−	n	n	+	+	+	+	+	−	−	−	−	9	55.0	−
Agaricostilbum																																								
6	−	−	+	+	+	−	n	n	−	−	−	+	n	n	n	n	n	n	n	n	n	n	n	+	n	−	+	n	n	n	+	+	−	−	−	−	−	n	n	+
Ambrosiozyma																																								
8	−	v	+	+	−	−	n	n	−	n	−	−	n	−	−	n	n	n	n	n	n	n	n	−	n	−	n	n	+	+	+	+	+	v	−	−	−	7	34.7	−
9	−	−	+	+	−	+	+	−	−	n	−	−	−	−	n	n	n	n	n	n	n	n	n	−	n	−	n	n	n	v	+	+	+	+	−	−	−	n	33.0	−
10	−	+	+	+	−	−	n	n	−	n	−	−	n	−	−	n	n	n	n	n	n	n	n	−	n	−	n	n	+	+	+	+	+	+	+	n	n	7	40.2	−
11	−	+	+	v	−	v	n	n	−	n	−	−	n	−	−	n	n	n	n	n	n	n	n	−	n	−	n	n	+	+	+	+	+	+	+	n	n	7	38.0	−
12	−	+	+	+	−	+	n	n	−	n	−	−	n	−	−	n	n	n	n	n	n	n	n	−	n	−	n	n	+	+	+	+	+	−	−	−	−	7	35.1	−
13	−	v	+	+	−	+	n	n	+	n	−	−	n	−	−	n	n	n	n	n	n	n	n	−	n	−	n	n	+	+	+	+	+	v	−	−	−	7	34.0	−
Ascobotryozyma																																								
15	−	+	+	−	−	−	n	n	−	−	−	v	n	−	−	−	−	−	−	−	−	+	+	−	n	−	n	n	+	+	+	+	+	+	−	−	−	9	29.4	−
16	−	+	+	−	−	−	n	n	−	−	n	+	n	−	−	−	−	−	−	−	−	+	+	n	n	n	n	n	+	+	+	+	+	v	v	−	−	n	28.0	−
Ascoidea																																								
18	−	−	v	v	−	+	n	n	v	v	n	n	n	n	n	v	+	n	n	+	v	+	+	n	v	−	v	n	−	−	+	+	−	−	−	−	−	n	n	v
19	+	−	+	−	−	+	n	n	−	−	n	n	n	n	n	+	+	n	n	+	−	+	+	n	−	−	−	n	−	−	+	+	+	n	−	−	−	n	n	−
20	+	−	−	−	−	−	n	n	−	−	n	n	n	n	n	+	+	n	n	+	−	+	+	n	−	−	−	n	−	−	+	+	+	n	−	−	−	n	n	−
Aureobasidium																																								
22	+	v	+	+	+	+	n	n	+	n	+	+	+	+	n	n	n	n	n	n	n	n	n	n	+	n	n	+	n	n	+	+	+	n	−	−	−	10 (H_2)	53.9	−
Auriculibuller																																								
24	+	v	+	+	+	+	n	n	−	−	−	n	n	+	+	n	n	n	n	+	+	+	+	n	n	+	n	n	+	−	+	+	+	−	−	−	−	n	n	+
Babjeviella																																								
26	+	−	+	+	−	−	+	−	−	n	−	−	−	−	n	n	n	n	n	n	n	n	n	n	−	−	n	−	n	n	+	+	+	n	−	−	−	9	49.9	−
Bannoa																																								
28	−	v	+	+	n	n	n	n	−	−	−	+	+	n	n	n	n	n	n	−	n	+	−	−	n	−	+	n	n	n	n	n	n	n	−	−	−	10	47.8	+
Barnettozyma																																								
30	−	+	+	v	+	−	−	−	+	n	−	v	v	−	n	n	n	n	n	n	n	n	n	n	−	−	n	v	n	n	+	+	+	n	−	−	−	7	43.5	−
31	−	+	+	−	−	−	−	−	+	n	−	−	−	−	n	n	n	n	n	n	n	n	n	n	−	−	n	−	n	n	+	+	+	n	−	−	−	n	n	−
32	−	+	+	−	+	−	−	−	+	n	−	−	−	−	n	n	n	n	n	n	n	n	n	n	−	−	n	−	n	n	+	+	+	n	−	−	−	7	44	−
33	−	+	+	+	+	−	−	−	+	n	−	+	−	−	n	n	n	n	n	n	n	n	n	n	−	−	n	−	n	n	+	+	+	n	−	−	−	n	39.9	−
34	−	+	+	+	+	−	−	−	−	n	−	+	+	−	n	n	n	n	n	n	n	n	n	n	−	−	n	−	n	n	+	+	+	+	+	n	n	7	37.8	−
35	−	+	+	+	+	−	−	−	−	n	−	+	+	−	n	n	n	n	n	n	n	n	n	n	+	−	n	v	n	n	+	+	+	+	+	n	n	7	45.6	−
Bensingtonia																																								
37	−	v	v	v	−	−	−	−	+	+	−	−	−	−	−	−	n	n	n	−	n	+	−	−	n	−	+	−	n	n	+	+	−	−	−	−	−	9	n	+
38	−	+	+	+	−	−	−	−	+	−	−	−	−	−	−	−	n	v	−	+	n	−	−	−	n	−	+	n	n	n	+	+	−	−	−	−	−	9	47.0	+
39	−	v	+	+	+	−	−	−	+	v	−	+	+	−	+	+	n	v	−	+	n	+	+	−	n	−	+	−	n	n	+	+	−	−	−	−	−	9	58.3	+
40	−	v	+	+	−	−	−	−	+	+	−	−	−	−	+	−	n	−	−	−	n	−	−	−	n	−	+	−	n	n	+	+	−	−	−	−	−	9	47.8	+
41	−	−	+	+	+	−	−	−	−	−	−	+	+	+	+	+	n	+	−	+	n	+	+	−	n	−	n	−	n	n	+	+	+	−	−	−	−	9	53.7	+
42	−	v	v	−	v	−	−	−	+	+	−	−	−	−	v	−	n	v	−	+	n	+	+	−	n	−	+	−	n	n	+	+	−	−	−	−	−	9	54.8	+
43	−	v	+	v	−	−	−	−	+	+	−	−	−	−	−	−	n	+	−	−	n	+	−	−	n	−	+	−	n	n	+	+	−	−	−	−	−	9	47.7	+
44	−	−	−	−	n	−	n	−	+	−	+	n	n	n	n	n	n	n	n	+	n	−	−	−	n	−	+	n	n	n	+	+	−	−	−	−	−	9	n	+
45	−	−	+	+	−	−	−	−	−	−	−	−	−	−	−	−	n	+	−	+	n	−	+	−	n	−	+	−	n	n	+	+	+	−	−	−	−	9	52.7	+
46	−	v	v	v	+	−	−	−	−	−	−	−	+	−	+	−	n	−	−	+	n	+	−	−	n	−	+	n	n	n	+	+	−	−	−	−	−	9	n	+
47	−	−	+	v	−	−	−	−	−	−	−	v	v	−	−	−	n	−	−	−	n	−	−	−	n	−	+	−	n	n	+	+	−	−	−	−	−	9	46.0	+
48	−	−	+	+	−	−	−	−	+	+	−	+	+	−	−	−	n	−	−	−	n	−	−	−	n	−	+	−	n	n	+	+	−	−	−	−	−	9	47.5	+
49	−	−	v	v	v	−	−	−	−	−	−	+	+	−	−	−	n	v	−	−	n	+	+	−	n	−	+	v	n	n	+	v	−	−	−	−	−	9	53.3	+
50	−	v	+	+	v	−	−	−	+	+	−	−	v	−	−	−	n	−	−	−	n	−	−	−	n	−	+	−	n	n	+	−	−	−	−	−	−	9	45.2	+
Blastobotrys																																								
52	+	−	+	+	+	+	n	n	+	n	−	+	n	−	n	n	n	n	n	n	n	n	n	+	n	−	n	n	+	+	+	+	+	+	+	+	n	9	n	−
53	+	+	+	−	+	+	+	+	−	n	−	−	+	−	n	n	n	n	n	n	n	n	n	n	+	−	n	−	+	n	+	+	+	n	−	−	−	n	n	−
54	−	v	+	−	n	+	n	n	−	n	−	n	n	n	n	n	n	n	n	n	n	n	n	n	n	n	n	n	n	n	+	+	+	n	−	−	−	n	n	−
55	v	−	+	v	n	+	n	n	−	n	−	n	n	n	n	n	n	n	n	n	n	n	n	n	n	n	n	n	n	n	+	+	+	n	−	−	−	n	n	−

Symbols: +, positive or weak; −, negative; v, variable (+/−, w/−); n, no data.

		Fermentation							Growth reactions and other characteristics																											
Ln. no.	Species	Glucose	Galactose	Sucrose	Maltose	Lactose	Raffinose	Trehalose	Glucose	Inulin	Sucrose	Raffinose	Melibiose	Galactose	Lactose	Trehalose	Maltose	Melezitose	Methyl-α-D-glucoside	Soluble Starch	Cellobiose	Salicin	L-Sorbose	L-Rhamnose	D-Xylose	L-Arabinose	D-Arabinose	D-Ribose	Methanol	Ethanol	Glycerol	Erythritol	Ribitol	Galactitol	D-Mannitol	D-Glucitol
	Blastobotrys *(cont'd)*																																			
56	*B. attinorum*	+	−	−	v	−	−	−	+	−	−	−	−	+	−	−	+	−	+	+	+	+	+	+	+	+	+	+	−	−	+	+	+	+	+	+
57	*B. capitulata*	+	+	−	v	−	−	v	+	v	v	v	−	+	v	+	v	−	−	+	+	+	+	+	+	+	v	+	n	+	+	+	+	+	+	+
58	*B. chiropterorum*	−	−	−	−	−	−	−	+	−	+	+	−	+	−	+	+	+	+	+	+	+	+	+	+	+	+	+	−	−	+	+	+	+	+	+
59	*B. elegans*	−	−	−	−	−	−	−	+	v	−	−	−	+	+	+	+	−	−	v	+	v	v	−	+	v	−	+	n	+	+	+	+	v	+	+
60	*B. illinoisensis*	+	+	+	+	−	−	+	+	−	+	−	−	+	−	−	+	−	+	+	+	+	+	+	+	+	+	−	−	+	+	+	+	+	+	+
61	*B. indianensis*	+	+	−	+	−	−	+	+	−	−	+	+	+	−	+	+	−	+	+	+	−	+	−	+	+	+	−	−	+	+	−	+	−	+	+
62	*B. malaysiensis*	+	+	+	+	−	−	+	+	−	+	−	−	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	−	+	+	+	+	−	+	+
63	*B. mokoenaii*	+	+	−	−	−	−	+	+	+	+	−	−	+	−	+	+	−	+	+	+	−	+	+	+	+	−	−	−	+	+	+	+	+	+	+
64	*B. muscicola*	−	−	−	−	−	−	−	+	−	+	v	v	+	+	v	+	+	v	+	+	v	−	−	−	−	−	−	−	−	+	−	−	−	+	−
65	*B. nivea*	+	+	−	+	−	−	+	+	v	v	−	+	+	+	+	+	−	v	+	+	+	+	−	+	+	+	+	n	+	+	+	+	+	+	+
66	*B. parvus*	−	−	−	−	−	−	−	+	−	+	−	−	+	−	+	+	−	−	−	+	−	−	+	+	+	v	v	−	−	+	+	+	−	+	+
67	*B. peoriensis*	+	+	−	−	−	−	+	+	−	+	+	+	+	+	−	+	+	+	+	+	+	+	−	+	+	+	+	−	+	+	+	+	+	+	+
68	*B. proliferans*	+	+	+	+	−	+	v	+	v	+	+	+	+	+	+	+	v	v	v	+	+	+	v	+	+	+	v	n	+	+	+	+	+	+	+
69	*B. raffinosifermentans*	+	+	+	+	−	+	+	+	+	+	+	+	+	−	−	+	+	+	+	+	+	+	−	+	+	+	+	−	+	+	+	+	+	+	+
70	*B. robertii*	−	−	−	−	−	−	−	+	−	+	+	+	+	+	+	+	−	v	+	+	+	−	−	−	−	−	−	−	−	−	−	−	−	+	−
71	*B. serpentis*	−	−	−	−	−	−	−	+	−	+	+	+	+	−	+	+	−	n	−	+	+	+	+	+	+	+	+	−	−	+	+	+	+	n	+
72	*B. terrestris*	−	−	−	−	−	−	−	+	−	+	+	−	+	−	+	+	−	+	+	+	+	+	+	+	+	+	+	−	+	+	+	+	+	+	+
73	***Botryozyma***																																			
74	*B. mucatilis*	−	−	−	−	−	−	−	+	−	−	−	−	−	−	v	−	−	−	−	−	−	+	−	−	−	−	−	−	+	+	−	−	−	+	+
75	*B. nematodophila*	−	−	−	−	−	−	−	+	−	−	−	−	−	−	+	−	−	−	−	−	−	+	−	−	−	−	−	−	+	+	−	−	−	+	+
76	***Brettanomyces***																																			
77	*B. custersianus*	+	−	−	−	−	−	v	+	−	−	−	−	−	−	+	−	−	−	−	−	−	−	−	−	−	−	+	−	+	+	−	−	−	−	−
78	*B. naardenensis*	+	v	−	−	−	−	v	+	−	−	−	−	v	−	+	v	−	−	v	+	v	−	v	+	−	v	−	−	+	−	−	v	−	v	+
79	*B. nanus*	+	+	−	−	−	−	−	+	−	−	−	−	+	v	v	−	−	−	−	+	+	−	+	v	−	−	−	−	+	−	−	+	−	+	+
80	***Bullera***																																			
81	*B. anomala*	−	−	−	−	−	−	−	+	−	+	+	+	+	+	+	+	+	+	+	−	−	−	+	+	+	+	+	−	−	−	−	−	+	+	+
82	*B. arundinariae*	−	−	−	−	−	−	−	+	−	+	+	+	+	+	+	+	+	+	+	+	+	−	+	+	+	+	+	−	−	−	+	+	+	+	+
83	*B. begoniae*	−	−	−	−	−	−	−	+	−	+	+	+	+	−	+	+	+	+	+	+	+	+	+	+	+	+	+	−	−	−	−	−	+	v	+
84	*B. boninensis*	−	−	−	−	−	−	−	+	v	+	+	+	+	+	+	+	+	+	+	+	+	−	+	+	+	+	+	−	−	v	v	+	+	+	+
85	*B. coprosmaensis*	−	−	−	−	−	−	−	+	−	+	+	+	+	v	+	+	+	+	+	+	+	−	+	+	+	+	+	−	+	+	+	+	+	+	+
86	*B. cylindrica*	−	−	−	−	−	−	−	+	−	+	+	+	+	−	+	+	+	+	+	+	+	+	+	+	+	+	+	−	−	−	−	+	+	+	+
87	*B. dendrophila*	−	−	−	−	−	−	−	+	−	+	−	−	+	+	+	+	+	−	+	+	+	−	+	+	+	+	+	−	+	+	−	+	+	+	+
88	*B. formosana*	−	−	−	−	−	−	−	+	−	+	+	+	+	−	+	+	+	+	+	+	+	−	+	+	+	+	+	−	−	−	−	+	+	+	+
89	*B. formosensis*	−	−	−	−	−	−	−	+	−	+	+	−	+	+	+	+	+	+	+	+	+	−	+	+	+	+	+	−	−	−	−	+	−	+	+
90	*B. globispora*	−	−	−	−	−	−	−	+	−	+	+	−	+	−	+	+	−	−	v	+	v	−	+	+	+	+	+	−	−	+	−	+	+	+	+
91	*B. hannae*	−	−	−	−	−	−	−	+	−	+	+	+	+	+	+	+	+	+	+	+	−	−	−	+	+	+	−	−	−	−	−	v	+	+	+
92	*B. hoabinhensis*	−	−	−	−	−	−	−	+	−	+	+	−	+	+	+	+	+	+	+	+	+	−	+	+	+	+	+	n	+	+	−	+	+	+	−
93	*B. hubeiensis*	−	−	−	−	−	−	−	+	−	+	+	+	+	−	+	+	+	+	+	+	v	+	+	+	+	+	+	−	−	−	−	+	+	+	+
94	*B. huiaensis*	−	−	−	−	−	−	−	+	−	+	+	+	+	−	+	+	+	+	+	+	+	−	+	+	+	+	+	−	−	−	v	+	+	+	+
95	*B. japonica*	−	−	−	−	−	−	−	+	−	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	−	−	+	+	+	+	+	+
96	*B. komagatae*	−	−	−	−	−	−	−	+	−	+	+	+	+	−	+	+	+	+	+	+	+	−	+	+	+	+	+	−	−	−	−	−	+	+	+
97	*B. koratensis*	−	−	−	−	−	−	−	+	−	+	+	−	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	−	−	+	+	+	v	+	+
98	*B. kunmingensis*	−	−	−	−	−	−	−	+	−	+	+	+	+	−	+	+	+	+	+	+	+	+	+	+	+	+	+	−	+	+	+	+	+	+	+
99	*B. lagerstroemiae*	−	−	−	−	−	−	−	+	−	+	+	−	+	+	+	+	+	+	+	+	+	+	+	+	+	+	v	−	−	+	v	+	+	+	+
100	*B. melastomae*	−	−	−	−	−	−	−	+	−	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	−	−	−	−	+	+	+	+
101	*B. miyagiana*	−	−	−	−	−	−	−	+	−	+	+	+	+	+	+	+	+	+	+	+	+	−	+	+	+	+	+	−	+	−	+	+	−	+	+
102	*B. mrakii*	−	−	−	−	−	−	−	+	−	+	+	+	+	v	+	+	+	+	+	+	+	−	+	+	+	+	+	−	−	−	+	+	+	+	+
103	*B. nakasei*	−	−	−	−	−	−	−	+	−	+	+	+	+	−	+	+	+	+	+	+	+	+	+	+	+	+	+	−	−	−	+	v	+	+	+
104	*B. ninhbinhensis*	−	−	−	−	−	−	−	+	−	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	n	+	+	+	−	+	+	+
105	*B. oryzae*	−	−	−	−	−	−	−	+	−	+	+	+	+	+	+	+	+	+	+	+	+	−	+	+	+	+	+	−	−	−	+	+	+	+	+
106	*B. panici*	−	−	−	−	−	−	−	+	−	+	+	+	+	−	+	+	+	+	+	+	+	+	+	+	+	+	+	−	−	−	+	+	+	+	+
107	*B. penniseticola*	−	−	−	−	−	−	−	+	−	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	−	−	+	+	+	+	+	+
108	*B. pseudoalba*	−	−	−	−	−	−	−	+	v	+	+	+	+	+	+	+	+	+	+	+	+	−	+	+	+	+	+	−	+	+	−	+	+	+	+
109	*B. pseudohuiaensis*	−	−	−	−	−	−	−	+	−	+	+	+	+	−	+	+	+	+	+	+	+	+	+	+	+	+	+	−	−	−	v	+	+	+	+

Symbols: +, positive or weak; −, negative; v, variable (+/−, w/−); n, no data.

	Growth reactions and other characteristics																																							
	myo-Inositol	DL-Lactate	Succinate	Citrate	D-Gluconate	D-Glucosamine	*N*-Acetyl-D-glucosamine	Hexadecane	Nitrate	Nitrite	Vitamin-free	2-Keto-D-gluconate	5-Keto-D-gluconate	Saccharate	Xylitol	L-Arabinitol	Arbutin	Propane 1,2 diol	Butane 2,3 diol	Cadaverine	Creatinine	L-Lysine	Ethylamine	50% Glucose	10% NaCl/5% glucose	Starch formation	Urease	Gelatin liquefaction	Cycloheximide 0.01%	Cycloheximide 0.1%	Growth at 19°C	Growth at 25°C	Growth at 30°C	Growth at 35°C	Growth at 37°C	Growth at 40°C	Growth at 45°C	CoQ (Main component)	Mol% G + C (Ave.)	DBB
Blastobotrys (*cont'd*)																																								
56	+	+	−	−	+	n	+	−	−	n	−	−	n	n	n	n	n	n	n	n	n	n	n	+	n	−	n	n	+	+	+	+	+	+	+	n	n	n	n	−
57	+	−	+	v	n	+	n	n	−	n	−	n	n	n	n	n	n	n	n	n	n	n	n	n	n	n	n	n	n	n	+	+	+	+	+	n	n	n	n	−
58	+	+	−	+	+	+	+	−	−	n	−	+	+	−	−	−	+	−	−	+	n	+	+	+	+	n	n	n	+	+	+	+	+	+	+	−	−	9	48	−
59	−	−	+	v	n	v	n	n	−	n	−	n	n	n	n	n	n	n	n	n	n	n	n	n	n	n	n	n	n	n	+	+	+	n	−	−	−	n	n	−
60	+	−	+	+	+	+	+	+	−	n	+	+	+	−	n	n	n	n	n	n	n	n	n	n	+	−	n	+	+	n	+	+	+	+	+	n	n	n	n	−
61	+	−	+	+	−	+	+	+	−	n	−	+	+	−	n	n	n	n	n	n	n	n	n	n	+	−	n	−	+	n	+	+	+	n	−	−	−	n	n	−
62	+	+	+	+	−	+	+	−	−	n	+	+	+	−	n	n	n	n	n	n	n	n	n	n	+	−	n	+	+	n	+	+	+	+	+	n	n	n	n	−
63	+	−	+	+	+	+	n	n	−	n	+	+	n	n	+	+	−	−	n	+	n	+	+	−	+	n	n	n	+	+	+	+	+	+	+	+	+	n	47.8	−
64	−	−	+	+	−	v	+	−	−	n	v	−	−	−	n	n	n	n	n	n	n	n	n	n	−	−	n	+	+	n	+	+	+	+	+	n	n	n	n	−
65	+	−	+	+	n	+	n	n	−	n	−	n	n	n	n	n	n	n	n	n	n	n	n	n	n	n	n	n	n	n	+	+	+	+	+	n	n	n	n	−
66	+	−	−	−	−	+	+	−	−	n	−	n	n	−	n	n	n	n	n	n	n	n	n	−	−	−	−	−	n	n	+	+	−	−	−	−	−	9	46.3	−
67	+	−	+	−	+	+	+	+	+	n	−	+	+	−	n	n	n	n	n	n	n	n	n	n	+	−	n	−	+	n	+	+	+	n	−	−	−	n	n	−
68	+	v	+	+	n	+	n	n	−	n	−	n	n	n	n	n	n	n	n	n	n	n	n	n	n	n	n	n	n	n	+	+	+	+	+	n	n	n	n	−
69	+	+	+	+	+	+	+	+	+	n	−	+	+	−	n	n	n	n	n	n	n	n	n	n	+	−	n	−	+	n	+	+	+	+	+	n	n	n	n	−
70	−	−	+	+	v	−	+	+	−	n	−	n	n	n	n	n	n	n	n	n	n	n	n	n	n	n	n	n	n	n	+	+	+	−	−	−	−	n	n	−
71	+	+	+	+	+	+	n	n	−	n	−	−	n	−	n	n	n	n	n	n	n	n	n	n	n	−	n	n	+	+	+	+	+	−	−	−	−	9	50.2	−
72	+	+	+	+	+	−	n	n	+	n	−	−	n	−	+	n	n	n	n	n	n	n	n	+	n	−	n	n	+	+	+	+	+	+	+	+	n	9	n	−
Botryozyma																																								
74	−	+	+	−	−	−	n	n	−	−	−	+	n	−	−	−	−	−	−	−	−	+	+	−	n	−	n	n	+	+	+	+	+	+	−	−	−	n	n	−
75	−	+	+	−	−	−	n	n	−	−	−	+	n	−	−	−	−	−	−	n	n	n	n	n	n	n	n	n	n	n	+	+	n	n	n	n	n	9	29.6	−
Brettanomyces																																								
77	−	+	+	−	−	−	n	n	−	n	−	−	n	−	−	n	n	n	n	n	n	n	n	−	n	−	n	n	+	+	+	+	+	+	+	−	−	9	39.1	−
78	−	v	+	−	−	v	n	n	−	n	−	v	n	−	v	n	n	n	n	n	n	n	n	−	n	−	n	n	+	+	+	+	v	−	−	−	−	9	42.7	−
79	−	−	−	−	−	−	n	n	−	n	−	−	n	−	−	n	n	n	n	n	n	n	n	−	n	−	n	n	+	−	+	+	+	−	−	−	−	9	40.8	−
Bullera																																								
81	−	+	+	−	+	−	n	n	−	n	−	+	n	n	n	n	n	n	n	n	n	n	n	−	−	+	+	n	n	n	+	+	−	−	−	−	−	10	53.3	+
82	+	−	+	+	−	+	n	n	−	n	−	+	n	n	n	n	n	n	n	n	n	n	n	−	−	−	+	n	n	n	+	+	+	n	−	−	−	10	58.7	+
83	−	v	+	+	+	+	+	n	−	+	−	+	+	+	+	−	n	−	−	+	n	+	−	−	n	+	+	−	n	−	+	+	−	−	−	−	−	10	55.0	+
84	+	+	+	v	+	+	n	n	−	n	−	v	n	n	n	n	n	n	n	n	n	n	n	−	−	−	+	n	n	n	+	+	v	n	−	−	−	10	42.7	+
85	+	+	+	+	+	v	n	n	−	n	+	+	n	n	n	n	n	n	n	n	n	n	n	−	−	+	+	n	n	n	+	+	−	−	−	−	−	10	48.4	+
86	+	+	+	−	+	+	n	n	v	n	−	+	n	n	n	n	n	n	n	n	n	n	n	−	−	+	+	n	n	n	+	+	−	−	−	−	−	10	n	+
87	+	+	+	+	+	−	n	n	−	n	−	+	n	n	n	n	n	n	n	n	n	n	n	−	n	+	+	n	n	n	+	+	v	n	−	−	−	10	39.6	+
88	+	−	+	+	+	+	n	n	−	n	−	+	n	n	n	n	n	n	n	n	n	n	n	−	−	+	+	n	n	n	+	+	−	−	−	−	−	10	49.7	+
89	+	−	+	+	+	+	n	n	−	n	−	+	n	n	n	n	n	n	n	n	n	n	n	−	−	+	+	n	n	n	+	+	−	−	−	−	−	10	57.8	+
90	+	+	+	+	+	−	n	n	−	n	−	+	n	n	+	+	v	−	−	−	−	n	n	n	n	n	n	n	−	−	+	+	v	n	−	−	−	10	51.2	+
91	−	−	+	+	+	+	n	n	−	n	−	−	n	n	n	n	n	n	n	n	n	n	n	−	−	+	v	n	n	n	+	+	−	−	−	−	−	10	43.6	+
92	+	−	+	+	n	n	n	n	−	+	−	+	+	n	n	n	n	n	n	+	n	+	+	+	n	+	+	+	n	n	+	+	+	−	−	−	−	10	54.0	+
93	+	+	−	−	+	−	n	n	−	n	−	−	n	n	n	n	n	n	n	n	n	n	n	−	−	−	+	n	n	n	+	+	+	n	−	−	−	10	n	+
94	+	−	+	−	n	n	n	n	−	n	−	+	n	n	n	n	n	n	n	n	n	n	n	−	−	+	+	n	n	n	+	+	−	−	−	−	−	10	42.9	+
95	+	+	+	+	+	+	n	n	−	n	−	+	n	n	n	n	n	n	n	n	n	n	n	−	n	+	+	n	n	n	+	+	+	n	−	−	−	n	n	+
96	+	−	+	+	+	−	n	n	−	n	−	+	n	n	n	n	n	n	n	n	n	n	n	−	−	+	+	n	n	n	+	+	−	−	−	−	−	10	44.5	+
97	+	+	+	+	+	n	n	−	−	+	−	+	+	+	+	+	n	−	−	+	n	+	+	+	n	−	+	−	n	n	+	+	−	−	−	−	−	10	49.4	+
98	+	+	+	+	+	+	n	n	−	n	−	+	n	n	n	n	n	n	n	n	n	n	n	−	−	+	+	n	n	n	+	+	v	n	−	−	−	10	53.0	+
99	+	+	+	+	+	+	+	−	−	+	−	+	+	−	v	+	n	−	−	+	n	+	+	−	n	−	+	−	n	n	+	+	−	−	−	−	−	10	46.0	+
100	+	+	+	+	+	+	n	n	−	+	−	+	n	n	n	n	n	n	n	n	n	n	n	−	n	+	+	n	n	n	+	+	+	n	−	−	−	10	50.6	+
101	+	+	+	+	+	−	n	n	−	+	−	+	n	n	n	n	n	n	n	n	n	n	n	−	n	+	+	n	n	n	+	+	+	n	−	−	−	10	60.1	+
102	+	+	+	+	+	+	n	n	−	n	−	+	n	n	n	n	n	n	n	n	n	n	n	−	−	+	+	n	n	n	+	+	v	n	−	−	−	10	40.9	+
103	+	+	+	−	+	+	n	n	−	n	−	−	n	n	n	n	n	n	n	n	n	n	n	−	−	+	+	n	n	n	+	+	−	−	−	−	−	10	n	+
104	+	+	+	+	n	n	n	n	+	−	−	+	+	n	n	n	n	n	n	+	n	+	+	−	n	−	+	+	n	n	+	+	+	−	−	−	−	10	59.9	+
105	+	+	+	+	+	+	n	n	−	+	n	+	n	n	n	n	n	n	n	n	n	n	n	−	n	+	+	n	n	n	+	+	+	n	−	−	−	10	61.2	+
106	+	+	+	−	+	+	n	n	−	n	−	v	n	n	n	n	n	n	n	n	n	n	n	−	−	+	+	n	n	n	+	+	−	−	−	−	−	10	46.4	+
107	+	−	+	+	+	+	n	n	−	n	−	+	n	n	n	n	n	n	n	n	n	n	n	−	−	+	+	n	n	n	+	+	v	n	−	−	−	10	44.2	+
108	+	v	+	+	+	+	n	n	−	−	−	+	n	n	n	n	n	n	n	n	n	n	n	−	n	−	+	n	n	n	+	+	+	n	−	−	−	10	53.5	+
109	+	+	+	+	+	+	n	n	−	−	−	+	n	n	n	n	n	n	n	n	n	n	n	−	n	+	+	n	n	n	+	+	−	−	−	−	−	10	43.9	+

Symbols: +, positive or weak; −, negative; v, variable (+/−, w/−); n, no data.

Ln. no.	Species	Fermentation							Growth reactions and other characteristics																																	
		Glucose	Galactose	Sucrose	Maltose	Lactose	Raffinose	Trehalose	Glucose	Inulin	Sucrose	Raffinose	Melibiose	Galactose	Lactose	Trehalose	Maltose	Melezitose	Methyl-α-D-glucoside	Soluble Starch	Cellobiose	Salicin	L-Sorbose	L-Rhamnose	D-Xylose	L-Arabinose	D-Arabinose	D-Ribose	Methanol	Ethanol	Glycerol	Erythritol	Ribitol	Galactitol	D-Mannitol	D-Glucitol				
Bullera (*cont'd*)																																								
110	*B. pseudoschimicola*	−	−	−	−	−	−	−	+	−	+	+	+	+	−	+	+	+	+	+	+	+	+	+	+	+	+	+	−	−	−	+	+	+	+	+				
111	*B. pseudovariabilis*	−	−	−	−	−	−	−	+	−	+	+	+	+	+	+	+	+	−	+	+	+	−	+	+	+	+	+	−	−	−	−	−	+	+	+				
112	*B. sakaeratica*	−	−	−	−	−	−	−	+	−	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	−	−	−	+	−	+	+	+				
113	*B. schimicola*	−	−	−	−	−	−	−	+	−	+	+	+	+	−	+	+	+	+	+	+	+	+	+	+	+	+	+	−	−	−	+	+	+	+	+				
114	*B. setariae*	−	−	−	−	−	−	−	+	−	+	+	+	+	−	+	+	+	+	+	+	+	−	+	+	+	+	+	−	−	−	−	v	+	+	+				
115	*B. siamensis*	−	−	−	−	−	−	−	+	−	+	+	+	+	+	+	+	+	+	+	+	−	+	+	+	+	+	+	−	−	−	+	+	+	+	+				
116	*B. sinensis* var. *sinensis*	−	−	−	−	−	−	−	+	−	+	+	+	+	−	+	+	+	+	v	+	+	+	+	+	+	+	+	−	+	+	+	+	+	+	+				
117	*B. sinensis* var. *lactis*	−	−	−	−	−	−	−	+	−	+	+	+	+	−	+	+	+	+	v	+	+	+	+	+	+	+	+	−	+	+	+	+	+	+	+				
118	*B. taiwanensis*	−	−	−	−	−	−	−	+	−	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	−	+	+	+	+	+	+	+				
119	*B. unica*	−	−	−	−	−	−	−	+	−	+	+	+	+	+	+	+	+	+	+	+	+	−	+	+	+	+	+	−	−	−	+	+	+	+	+				
120	*B. variabilis*	−	−	−	−	−	−	−	+	−	+	+	+	+	−	+	+	+	+	+	+	+	v	+	+	+	+	+	−	−	v	−	v	+	+	+				
121	*B. waltii*	−	−	−	−	−	−	−	+	−	+	+	+	+	−	+	+	+	+	+	+	+	+	+	+	+	+	+	−	−	−	+	+	+	+	+				
122	***Bulleribasidium***																																							
123	*B. oberjochense*	−	−	−	−	−	−	−	+	−	+	+	+	+	v	+	+	+	+	+	+	+	−	+	+	+	+	+	−	−	v	−	+	+	+	+				
124	***Bulleromyces***																																							
125	*B. albus*	−	−	−	−	−	−	−	+	+	+	+	v	+	+	+	+	+	+	v	+	+	v	+	+	+	+	+	−	v	+	v	v	v	+	+				
126	***Candida***																																							
127	*C. aaseri*	v	v	−	−	−	−	−	+	−	+	−	−	+	v	+	+	+	+	−	+	+	+	−	+	+	v	+	−	+	+	+	+	−	+	+				
128	*C. aglyptinia*	+	−	+	+	−	−	+	+	−	+	−	−	+	−	+	+	+	+	−	+	+	−	−	−	−	−	−	−	−	−	+	−	+	−	+				
129	*C. akabanensis*	+	+	+	+	−	+	n	+	+	+	+	−	+	−	+	+	+	+	−	+	+	−	+	+	−	+	+	−	+	+	−	−	+	−	+				
130	*C. alai*	+	+	−	−	−	−	−	+	−	+	−	−	+	−	+	+	+	+	−	+	+	−	−	+	−	−	+	−	+	+	−	+	−	+	+				
131	*C. albicans*	+	v	v	+	−	−	v	+	−	v	−	−	+	−	v	+	v	v	+	−	−	v	−	+	v	v	v	−	+	v	−	v	−	+	v				
132	*C. alimentaria*	−	−	−	−	−	−	−	+	−	−	−	−	+	−	−	−	−	−	−	−	−	v	−	−	−	−	+	n	n	+	+	−	−	−	−				
133	*C. allociferrii*	−	−	−	−	−	−	−	+	+	+	+	+	+	−	+	+	−	+	+	+	+	+	+	+	+	+	+	−	+	+	+	+	+	+	+				
134	*C. amapae*	+	−	−	−	−	−	−	+	−	−	−	−	−	−	−	−	−	−	−	−	−	+	−	+	−	−	−	−	+	+	−	−	−	−	−				
135	*C. ambrosiae*	+	−	+	+	−	−	+	+	−	+	−	−	+	−	+	+	+	+	−	+	+	−	−	+	−	+	−	−	+	+	+	+	−	+	+				
136	*C. amphixiae*	+	+	+	−	−	−	+	+	−	+	−	−	+	−	+	+	+	+	−	+	+	+	+	+	+	+	+	−	+	+	+	+	−	+	+				
137	*C. anatomiae*	+	−	−	−	−	−	−	+	−	−	−	−	−	−	+	−	−	−	v	+	−	−	+	−	−	−	−	−	+	−	−	−	−	−	−				
138	*C. anglica*	+	v	−	−	−	−	+	+	−	−	−	−	+	−	+	−	−	−	−	−	−	+	−	−	−	−	−	−	+	+	−	+	−	+	+				
139	*C. anneliseae*	+	−	−	−	−	−	+	+	−	+	−	−	v	−	+	+	+	+	−	+	+	v	−	+	−	+	v	−	+	+	+	+	−	+	+				
140	*C. anutae*	−	−	−	−	−	−	−	+	−	−	−	−	−	−	+	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	+	−	+	−	+				
141	*C. apicola*	+	−	−	−	−	v	−	+	−	+	+	−	v	−	−	−	−	−	−	−	−	v	−	v	−	−	v	−	v	+	−	−	−	+	+				
142	*C. apis*	−	−	−	−	−	−	−	+	−	+	+	−	+	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	+	+	−	−	−	+	+				
143	*C. arabinofermentans*	+	−	−	−	−	−	+	+	−	−	−	−	−	−	+	−	−	−	−	+	+	−	−	+	+	v	+	+	+	+	+	+	−	+	+				
144	*C. arcana*	+	−	−	−	−	−	+	+	−	+	−	−	−	−	+	+	−	−	−	−	+	−	−	−	−	−	−	−	+	+	−	+	−	+	+				
145	*C. asparagi*	+	+	−	−	−	−	n	+	−	+	−	−	+	−	+	+	+	+	−	+	+	+	−	+	−	+	+	−	+	+	−	+	−	+	+				
146	*C. atakaporum*	+	−	−	−	−	−	+	+	−	+	−	−	+	−	+	+	+	+	+	+	+	n	n	+	−	+	−	−	+	+	−	+	−	+	+				
147	*C. atbi*	+	v	−	−	−	−	+	+	−	+	−	−	+	−	+	+	v	+	−	+	+	−	−	v	−	−	+	−	+	+	−	+	−	+	+				
148	*C. athensensis*	+	+	+	+	−	−	+	+	−	+	−	−	+	−	+	+	−	+	−	+	+	−	−	+	+	+	+	−	v	+	v	+	−	+	+				
149	*C. atlantica*	v	−	−	−	−	−	−	+	−	+	−	−	+	−	+	+	+	+	−	+	+	−	+	+	+	+	+	−	+	+	+	+	−	+	+				
150	*C. atmosphaerica*	+	v	v	v	−	−	+	+	−	+	−	−	+	−	+	+	−	+	−	+	−	+	−	+	+	+	+	−	+	+	+	+	−	+	+				
151	*C. auringiensis*	+	+	−	−	+	−	+	+	−	−	−	−	+	+	+	−	−	−	−	+	+	+	−	+	+	+	v	−	+	+	+	+	+	+	+				
152	*C. aurita*	+	−	−	−	−	−	−	+	−	−	−	−	+	−	+	−	−	−	−	−	−	−	−	−	−	−	−	−	+	−	−	−	−	+	+				
153	*C. azyma*	−	−	−	−	−	−	−	+	−	+	−	+	+	−	+	+	+	+	−	−	−	+	−	v	v	v	−	−	+	+	−	v	v	+	+				
154	*C. azymoides*	−	−	−	−	−	−	−	+	−	+	−	−	+	−	+	+	+	−	−	−	−	+	−	+	+	−	−	−	+	+	−	+	v	+	+				
155	*C. barrocoloradensis*	+	+	−	−	−	−	+	+	−	+	−	−	+	−	+	+	+	+	−	+	+	−	−	+	−	−	−	−	+	+	−	+	−	+	+				
156	*C. batistae*	+	−	−	−	−	−	−	+	−	−	−	−	+	−	−	−	−	−	−	−	−	v	−	−	−	−	−	−	−	+	−	−	−	+	+				
157	*C. bentonensis*	+	−	−	−	−	−	−	+	−	+	−	−	+	−	+	+	+	+	−	+	+	+	−	+	−	−	−	−	+	+	−	+	−	+	+				
158	*C. berthetii*	+	−	−	−	−	−	−	+	−	−	−	−	−	−	−	−	−	−	+	+	−	−	−	−	−	−	−	−	+	+	−	−	−	v	v				
159	*C. bituminiphila*	+	+	−	−	−	−	+	+	−	+	+	−	+	−	+	+	−	−	+	+	+	+	−	+	+	+	+	−	+	+	−	+	+	+	+				
160	*C. blankii*	v	v	+	v	−	−	−	+	−	+	v	−	+	+	+	v	+	+	+	+	+	+	−	+	+	+	v	v	−	+	v	+	v	v	+	+			
161	*C. blattariae*	+	+	−	−	−	−	+	+	−	+	−	−	+	−	+	+	+	+	−	+	+	−	+	+	+	+	+	−	−	−	+	+	−	+	+				
162	*C. bohiensis*	+	+	v	+	−	−	−	+	−	+	−	−	+	−	−	+	+	+	−	+	+	+	−	+	+	+	−	v	−	+	+	−	+	+	+				
163	*C. boidinii*	+	−	−	−	−	−	−	+	−	v	−	−	−	−	v	v	v	v	−	−	−	v	−	+	v	v	+	+		+	v	+	+	−	+	+				

Symbols: +, positive or weak; −, negative; v, variable (+/−, w/−); n, no data.

Growth reactions and other characteristics

	myo-Inositol	DL-Lactate	Succinate	Citrate	D-Gluconate	D-Glucosamine	*N*-Acetyl-D-glucosamine	Hexadecane	Nitrate	Nitrite	Vitamin-free	2-Keto-D-gluconate	5-Keto-D-gluconate	Saccharate	Xylitol	L-Arabinitol	Arbutin	Propane 1,2 diol	Butane 2,3 diol	Cadaverine	Creatinine	L-Lysine	Ethylamine	50% Glucose	10% NaCl/5% glucose	Starch formation	Urease	Gelatin liquefaction	Cycloheximide 0.01%	Cycloheximide 0.1%	Growth at 19°C	Growth at 25°C	Growth at 30°C	Growth at 35°C	Growth at 37°C	Growth at 40°C	Growth at 45°C	CoQ (Main component)	Mol% G + C (Ave.)	DBB
Bullera (*cont'd*)																																								
110	+	+	+	+	+	+	n	n	−	−	−	+	n	n	n	n	n	n	n	n	n	n	n	−	n	+	+	n	n	n	+	+	−	−	−	−	−	10	44.2	+
111	+	+	+	−	v	−	n	n	−	n	−	+	n	n	n	n	n	n	n	n	n	n	n	−	n	+	+	n	n	n	+	+	−	−	−	−	−	10	50.3	+
112	+	+	+	+	+	+	n	n	−	n	−	+	n	n	n	n	n	n	n	n	n	n	n	−	−	+	+	n	n	n	+	+	−	−	−	−	−	10	51.3	+
113	+	+	+	v	+	+	n	n	−	n	−	+	n	n	n	n	n	n	n	n	n	n	n	−	−	−	+	n	n	n	+	+	−	−	−	−	−	10	42.9	+
114	−	+	+	+	+	+	+	n	−	−	−	+	+	+	−	−	n	−	−	−	n	+	−	−	n	−	+	+	n	−	+	+	−	−	−	−	−	10	50.5	+
115	+	−	+	+	+	−	n	n	−	n	−	+	n	n	n	n	n	n	n	n	n	n	n	−	−	v	v	n	n	n	+	+	+	n	−	−	−	10	48.4	+
116	+	+	+	+	+	+	n	n	−	n	−	+	n	n	n	n	n	n	n	n	n	n	n	−	n	+	+	n	n	n	+	+	+	n	−	−	−	10	54.8	+
117	+	+	+	+	+	+	n	n	−	n	−	+	n	n	n	n	n	n	n	n	n	n	n	−	n	+	+	n	n	n	+	+	+	n	−	−	−	10	54.8	+
118	+	−	+	+	+	+	n	n	v	n	−	+	n	n	n	n	n	n	n	n	n	n	n	−	−	+	+	n	n	n	+	+	−	−	−	−	−	10	44.1	+
119	+	−	+	+	+	+	n	n	−	n	−	+	n	n	n	n	n	n	n	n	n	n	n	−	−	+	+	n	n	n	+	+	−	−	−	−	−	10	55.4	+
120	+	+	+	+	+	+	n	n	−	n	−	+	n	n	n	n	n	n	n	n	n	n	n	−	n	+	+	n	n	n	+	+	−	−	−	−	−	10	56.4	+
121	+	+	+	+	+	+	n	n	−	n	−	+	n	n	n	n	n	n	n	n	n	n	n	−	−	+	+	n	n	n	+	+	−	−	−	−	−	10	42.8	+
Bulleribasidium																																								
123	+	v	+	+	+	+	n	n	−	−	−	n	n	+	+	n	n	n	n	−	−	+	−	n	n	+	n	n	+	v	+	+	v	−	−	−	−	n	n	+
Bulleromyces																																								
125	+	+	+	+	+	v	n	n	−	−	−	+	n	n	n	n	n	n	n	n	n	n	n	−	n	+	+	n	n	n	+	+	v	n	−	−	−	10	54.2	+
Candida																																								
127	−	−	+	+	+	−	+	v	−	−	−	−	n	n	+	n	n	n	n	+	n	+	+	−	n	−	n	−	−	−	+	+	+	+	+	n	n	9	36.3	−
128	−	−	+	+	+	−	n	n	−	−	−	+	n	n	+	−	+	−	−	+	−	+	+	+	n	−	−	n	+	+	+	+	+	−	−	−	−	n	n	−
129	−	−	+	+	+	+	+	+	−	−	−	+	n	n	+	n	n	n	n	+	n	+	+	−	n	−	n	−	+	−	+	+	+	n	−	−	−	9	47.6	−
130	−	−	+	+	−	+	n	n	−	−	−	+	n	n	−	−	+	+	−	+	−	+	+	−	n	−	−	n	−	−	+	+	+	+	+	−	−	n	n	−
131	−	+	+	+	v	v	v	v	−	−	v	+	n	n	v	n	n	n	n	+	n	+	+	v	n	−	n	−	+	+	+	+	+	+	+	n	n	9	35.0	−
132	−	+	+	v	+	−	n	n	−	−	−	n	−	n	−	−	n	−	−	+	−	+	+	n	n	−	v	n	+	+	+	+	−	−	−	−	−	n	44.3	−
133	+	+	+	−	+	−	n	n	−	v	−	+	n	n	+	n	n	n	n	+	n	+	+	+	n	−	n	n	+	+	+	+	+	+	+	n	n	n	n	−
134	−	−	+	−	+	−	−	−	−	−	−	+	n	n	−	n	n	n	n	−	n	+	−	−	n	−	n	−	+	n	+	+	+	n	−	−	−	n	38.8	−
135	−	−	+	+	+	+	+	+	−	−	−	+	n	n	+	n	n	n	n	+	n	+	+	+	n	−	n	−	−	−	+	+	+	+	+	n	n	n	n	−
136	−	+	+	+	+	+	n	n	−	−	−	−	n	n	+	+	+	+	−	+	−	+	+	+	n	−	−	n	+	−	+	+	+	−	−	−	−	n	n	−
137	−	−	−	−	+	−	−	−	−	+	−	−	n	n	−	n	n	n	n	+	n	+	+	−	n	−	n	−	+	+	+	+	−	−	−	−	−	8	39.0	−
138	−	+	+	+	+	−	+	−	−	−	−	+	n	n	−	n	n	n	n	+	n	+	+	+	n	−	n	−	−	−	+	+	+	n	−	−	−	n	n	−
139	−	−	+	+	+	+	n	n	−	−	−	+	n	n	+	v	+	v	−	+	−	+	+	+	n	−	−	n	v	−	+	+	+	v	n	−	−	n	n	−
140	−	−	+	+	−	−	+	+	−	−	−	−	n	n	+	n	n	n	n	+	n	+	+	−	n	−	n	+	+	−	+	+	−	−	−	−	−	n	n	−
141	−	−	+	+	+	−	−	−	−	−	−	−	n	n	v	n	n	n	n	+	n	+	v	+	n	−	n	v	−	−	+	+	v	n	−	−	−	9	45.0	−
142	−	−	+	+	−	−	−	−	−	−	−	−	n	n	−	n	n	n	n	+	n	+	+	+	n	−	n	−	−	−	+	+	+	n	−	−	−	9	47.2	−
143	−	−	+	−	−	−	−	−	−	−	−	−	n	n	+	n	n	n	n	+	n	+	+	−	n	−	n	−	+	+	+	+	+	+	+	n	n	n	n	−
144	−	−	+	+	+	+	n	n	−	n	−	+	n	n	n	−	+	−	−	+	−	+	+	−	n	−	−	n	+	−	+	+	−	−	−	−	−	n	n	−
145	−	−	+	+	n	+	n	+	−	−	−	n	n	n	n	n	n	n	n	+	n	+	+	n	n	−	−	n	n	n	+	+	+	−	−	−	−	n	n	−
146	−	+	+	+	+	+	n	n	−	−	−	+	n	n	−	−	+	+	−	+	−	+	+	+	n	−	−	n	−	−	+	+	+	+	n	−	−	n	n	−
147	−	−	+	+	v	v	n	n	−	−	−	+	n	n	+	−	+	−	−	+	−	+	+	v	n	−	−	n	+	+	+	+	+	−	−	−	−	n	n	−
148	−	+	+	+	+	+	n	n	−	−	−	+	n	n	+	+	+	+	−	+	−	+	+	+	n	−	−	n	+	+	+	+	+	v	n	−	−	n	n	−
149	−	−	+	+	+	−	+	+	−	−	−	−	n	n	+	n	n	n	n	+	n	+	+	−	n	−	n	−	−	−	+	+	−	−	−	−	−	9	35.8	−
150	−	−	+	+	+	+	+	+	−	−	−	−	n	n	+	n	n	n	n	+	n	+	+	−	n	−	n	−	−	−	+	+	+	n	−	−	−	9	39.0	−
151	+	−	+	−	−	+	+	−	−	−	−	+	n	n	+	n	n	n	n	+	n	+	+	+	n	−	n	−	+	+	+	+	+	+	+	n	n	9	40.1	−
152	−	+	+	−	+	−	+	−	−	−	−	−	n	n	+	n	n	n	n	+	n	+	+	−	n	−	n	−	+	−	+	+	−	−	−	−	−	n	36.6	−
153	−	−	+	−	v	−	−	+	−	−	−	+	n	n	+	n	n	n	n	+	n	+	+	+	n	−	n	+	+	+	+	+	+	n	−	−	−	9	54.4	−
154	−	−	+	+	−	−	−	−	−	−	−	+	n	n	+	n	n	n	n	+	n	+	+	v	n	−	−	n	+	n	+	+	+	n	−	−	−	n	n	−
155	−	−	+	+	+	−	n	n	−	−	−	+	n	n	+	−	+	−	−	+	−	+	+	+	n	−	−	n	+	+	+	+	+	−	−	−	−	n	n	−
156	−	−	−	−	+	−	−	−	−	−	−	−	n	n	−	n	n	n	n	+	n	+	+	+	n	−	n	−	+	−	+	+	+	+	+	n	n	n	n	−
157	+	+	+	+	+	+	+	+	+	n	−	+	+	−	n	n	n	n	n	+	n	n	n	n	n	−	n	−	+	+	+	+	+	+	+	n	n	n	n	−
158	−	+	+	+	−	−	−	−	+	+	+	v	n	n	−	−	n	n	n	+	n	+	+	−	n	−	n	−	+	+	+	+	+	+	+	n	n	7	39.8	−
159	+	+	+	+	+	+	+	+	−	−	−	−	n	n	+	n	n	n	n	+	n	+	−	−	n	−	n	−	+	+	+	+	+	n	−	−	−	n	n	−
160	+	v	+	+	+	v	+	+	−	−	+	+	n	n	v	n	n	n	n	+	n	+	+	v	n	−	n	−	+	+	+	+	+	+	+	n	n	9	55.4	−
161	−	+	+	+	+	+	n	n	−	−	−	+	n	n	+	−	+	−	−	+	−	+	+	+	n	−	−	n	−	−	+	+	+	−	−	−	−	n	n	−
162	−	−	+	+	+	+	n	n	−	−	−	+	n	n	+	−	+	−	−	+	−	+	+	+	n	−	−	n	+	−	+	+	+	−	−	−	−	n	n	−
163	−	+	+	v	−	v	+	v	+	+	−	v	n	n	+	n	n	n	n	+	n	+	+	−	n	−	n	−	+	+	+	+	+	+	v	n	n	7	33.0	−

Symbols: +, positive or weak; −, negative; v, variable (+/−, w/−); n, no data.

Ln. no.	Species	Fermentation							Growth reactions and other characteristics																																	
		Glucose	Galactose	Sucrose	Maltose	Lactose	Raffinose	Trehalose	Glucose	Inulin	Sucrose	Raffinose	Melibiose	Galactose	Lactose	Trehalose	Maltose	Melezitose	Methyl-α-D-glucoside	Soluble Starch	Cellobiose	Salicin	L-Sorbose	L-Rhamnose	D-Xylose	L-Arabinose	D-Arabinose	D-Ribose	Methanol	Ethanol	Glycerol	Erythritol	Ribitol	Galactitol	D-Mannitol	D-Glucitol					
Candida *(cont'd)*																																										
164	*C. bokatorum*	+	−	v	v	−	−	+	+	−	+	−	−	+	−	+	+	+	+	−	+	+	n	n	+	−	+	−	−	+	+	−	+	−	+	+						
165	*C. boleticola*	+	−	−	−	−	−	+	+	−	−	−	−	+	−	+	−	−	−	−	v	+	+	−	+	−	v	+	−	+	+	+	+	−	+	+						
166	*C. bolitotheri*	+	+	−	−	−	−	+	+	−	−	−	−	+	−	+	−	−	−	−	+	+	n	n	+	−	−	v	−	+	+	+	+	−	+	+						
167	*C. bombi*	+	−	+	−	−	−	+	+	−	+	+	−	−	−	v	−	−	−	−	−	−	+	−	−	−	−	−	−	−	+	−	−	−	v	+						
168	*C. bombiphila*	+	n	n	n	n	n	n	+	−	−	−	−	−	−	−	−	−	−	−	−	−	+	−	−	−	−	+	−	−	+	−	−	−	+	+						
169	*C. boreocaroliniensis*	−	−	−	−	−	−	−	+	−	+	+	+	+	v	+	+	+	+	−	+	+	+	−	+	+	+	−	−	+	+	−	+	−	+	+						
170	*C. bracarensis*	+	−	−	−	−	−	+	+	−	−	−	−	−	−	+	−	−	−	−	−	−	−	−	−	−	−	−	−	v	v	−	−	−	−	−						
171	*C. bribrorum*	+	v	−	v	−	−	+	+	−	+	−	−	+	−	+	+	+	+	−	+	+	n	n	+	v	v	v	−	+	+	+	+	−	+	+						
172	*C. bromeliacearum*	+	n	n	n	n	n	n	+	−	+	−	−	−	−	+	+	+	+	−	+	+	+	−	+	−	−	−	−	+	v	v	+	−	+	+						
173	*C. buenavistaensis*	+	+	v	+	−	−	v	+	−	+	−	−	+	−	+	+	+	+	−	−	−	+	−	+	v	−	−	−	+	+	−	+	−	+	+						
174	*C. buinensis*	+	+	−	v	−	−	−	+	−	+	−	−	+	−	+	+	+	+	−	+	+	+	−	+	−	+	−	−	+	+	−	−	−	v	v						
175	*C. californica*	+	−	−	−	−	−	−	+	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	v	−	−	−	−	+	+	−	−	−	−	−						
176	*C. canberraensis*	+	+	−	−	−	−	+	+	−	+	−	−	+	−	+	+	+	+	−	+	+	+	−	+	−	−	+	−	+	+	+	+	−	+	+						
177	*C. carpophila*	+	v	v	−	−	v	v	+	v	+	v	v	+	−	+	+	v	+	v	v	v	v	−	+	+	v	v	−	+	+	−	+	v	v	v						
178	*C. caryicola*	+	−	−	−	−	−	−	+	−	+	−	−	+	−	−	+	+	+	−	−	−	−	−	−	−	+	−	−	+	+	−	+	−	+	+						
179	*C. caseinolytica*	−	−	−	−	−	−	−	+	−	−	−	−	+	−	+	−	−	−	−	−	−	+	−	+	−	−	−	−	+	+	−	−	−	+	+						
180	*C. castellii*	+	−	−	−	−	−	−	+	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	v	+	−	−	−	−						
181	*C. castrensis*	−	−	−	−	−	−	−	+	−	+	−	−	+	−	+	+	+	+	−	+	−	+	−	+	−	+	−	−	+	+	−	−	−	+	+						
182	*C. catenulata*	v	v	−	v	−	−	−	+	−	−	−	−	+	−	v	v	−	−	v	−	v	−	−	v	−	−	v	−	+	+	−	v	−	+	v						
183	*C. cellae*	+	n	n	n	n	n	n	+	−	−	−	−	+	−	−	−	−	n	−	−	−	−	−	−	−	−	+	−	−	+	−	−	−	+	+						
184	*C. cerambycidarum*	+	+	−	−	−	−	+	+	−	+	−	−	+	−	+	+	+	+	−	+	+	+	+	+	+	+	+	−	+	+	+	+	−	+	+						
185	*C. chickasaworum*	+	+	−	−	−	−	+	+	−	+	−	−	+	−	+	+	v	+	−	+	+	n	n	+	−	−	−	−	+	+	−	+	−	+	+						
186	*C. chilensis*	+	−	−	−	−	−	−	+	−	+	−	−	+	+	+	+	+	+	−	+	+	+	−	+	+	+	+	−	+	+	+	+	−	+	+						
187	*C. choctaworum*	+	v	−	−	−	−	+	+	−	−	−	−	+	−	+	−	−	−	−	+	+	n	n	+	v	+	v	−	+	+	+	+	−	+	+						
188	*C. chrysomelidarum*	+	−	−	−	−	−	−	+	−	+	−	−	−	−	+	+	+	−	−	+	+	+	−	−	−	−	−	−	+	+	−	+	−	+	+						
189	*C. cidri*	+	−	−	−	−	−	v	+	−	−	−	−	+	−	+	+	+	v	+	−	−	+	+	+	−	−	+	+	+	+	+	+	−	+	+						
190	*C. coipomoensis*	+	+	−	−	−	−	+	+	−	+	−	−	+	+	+	+	v	+	−	+	+	+	−	+	−	+	+	−	+	+	+	+	−	+	+						
191	*C. conglobata*	+	+	−	−	−	−	+	+	−	−	−	−	+	−	+	−	−	−	−	+	+	+	−	+	+	+	+	−	+	+	+	+	−	+	+						
192	*C. cretensis*	+	+	−	−	n	n	+	+	−	+	−	−	+	−	+	+	+	+	−	+	+	+	−	+	−	+	+	−	+	+	−	+	−	+	+						
193	*C. cylindracea*	+	−	−	−	−	−	−	+	−	−	−	−	+	−	−	−	−	−	−	−	−	+	−	−	−	−	−	−	+	+	−	−	−	+	+						
194	*C. dajiaensis*	+	−	+	−	−	−	−	+	−	+	−	−	−	−	+	+	+	+	−	+	+	−	−	+	+	−	−	−	−	+	−	+	−	+	+						
195	*C. davenportii*	+	−	−	−	−	n	−	+	−	+	+	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−						
196	*C. deformans*	−	−	−	−	−	−	−	+	−	−	−	−	−	−	−	−	−	−	−	+	+	−	−	−	−	−	+	−	+	+	+	−	−	+	+						
197	*C. dendrica*	+	−	−	−	−	−	−	+	−	−	−	−	−	−	−	−	−	−	−	+	+	−	−	−	−	−	−	−	+	+	−	−	−	−	−						
198	*C. dendronema*	+	+	v	−	−	−	+	+	−	+	−	−	+	−	+	+	−	+	+	+	+	+	+	+	+	+	+	−	+	+	+	+	+	+	+						
199	*C. derodonti*	+	−	−	−	−	−	−	+	−	+	−	−	−	−	+	+	−	+	−	+	+	−	−	−	−	−	+	−	+	+	−	+	−	+	+						
200	*C. diddensiae*	+	+	v	v	−	−	+	+	−	+	−	−	+	−	v	+	+	v	−	+	v	v	−	+	v	v	v	−	+	+	+	+	−	+	+						
201	*C. digboiensis*	−	−	−	−	−	−	−	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	−	+	+	+	+	+	+	+						
202	*C. diospyri*	+	+	−	−	−	−	n	+	−	+	−	−	+	−	+	+	+	+	−	+	+	+	+	+	+	+	+	−	+	+	+	+	−	+	+						
203	*C. diversa*	+	−	−	−	−	−	−	+	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	v	−	−	−	−	+	v	−	v	−	+	+						
204	*C. drosophilae*	−	−	−	−	−	−	−	+	−	−	−	−	v	−	−	−	−	−	−	−	−	+	−	v	−	−	−	−	+	+	−	−	−	v	+						
205	*C. dubliniensis*	+	+	−	+	−	−	n	+	−	+	−	−	+	−	+	+	+	+	+	−	−	−	−	+	−	−	−	−	+	+	−	+	−	+	+						
206	*C. easanensis*	−	−	−	−	−	−	−	+	−	+	−	−	−	−	+	+	+	+	+	+	+	−	+	+	+	+	−	−	+	+	−	−	−	+	+						
207	*C. elateridarum*	+	+	+	−	−	−	+	+	−	+	+	+	+	−	+	+	+	+	−	+	+	−	−	+	+	−	+	−	+	+	+	+	−	+	+						
208	*C. emberorum*	+	+	−	−	−	−	+	+	−	+	−	−	+	−	+	+	+	+	−	+	+	+	−	+	−	−	−	−	+	+	−	+	−	+	+						
209	*C. endomychidarum*	+	+	−	−	−	−	+	+	−	+	−	−	+	−	+	+	+	+	−	+	+	+	+	+	+	+	+	+	+	+	+	+	−	+	+						
210	*C. entomophila*	+	+	+	−	−	+	+	+	−	+	+	+	+	+	+	+	+	+	−	+	+	+	−	+	+	−	+	−	+	+	+	+	−	+	+						
211	*C. ergatensis*	+	+	−	−	−	−	−	+	−	+	−	−	+	v	+	+	−	+	−	+	+	+	−	+	−	+	v	−	+	+	−	+	−	+	+						
212	*C. etchellsii*	v	−	−	v	−	−	−	+	−	−	−	−	v	−	−	v	−	−	−	−	−	v	−	−	−	−	v	−	v	+	−	−	−	v	v						
213	*C. ethanolica*	v	−	−	−	−	−	−	+	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	+	v	−	−	−	−	−						
214	*C. fennica*	+	+	+	+	v	v	+	+	−	+	v	v	+	v	+	+	v	v	+	v	v	v	−	v	v	−	+	−	+	+	+	+	−	+	+						
215	*C. fermenticarens*	−	−	−	−	−	−	−	+	−	−	−	−	+	−	−	−	−	−	−	−	−	+	−	−	−	−	+	−	+	+	+	+	+	+	+						
216	*C. floccosa*	+	−	−	−	−	−	−	+	−	v	−	−	−	−	+	+	v	−	−	−	−	+	+	−	−	v	−	+	+	+	−	−	−	+	+						
217	*C. floricola*	+	−	+	+	−	+	−	+	−	+	+	−	+	−	−	+	−	+	−	−	−	−	+	−	v	−	−	+	−	v	+	−	−	−	+	+						

Symbols: +, positive or weak; −, negative; v, variable (+/−, w/−); n, no data.

Growth reactions and other characteristics

	myo-Inositol	DL-Lactate	Succinate	Citrate	D-Gluconate	D-Glucosamine	*N*-Acetyl-D-glucosamine	Hexadecane	Nitrate	Nitrite	Vitamin-free	2-Keto-D-gluconate	5-Keto-D-gluconate	Saccharate	Xylitol	L-Arabinitol	Arbutin	Propane 1,2 diol	Butane 2,3 diol	Cadaverine	Creatinine	L-Lysine	Ethylamine	50% Glucose	10% NaCl/5% glucose	Starch formation	Urease	Gelatin liquefaction	Cycloheximide 0.01%	Cycloheximide 0.1%	Growth at 19°C	Growth at 25°C	Growth at 30°C	Growth at 35°C	Growth at 37°C	Growth at 40°C	Growth at 45°C	CoQ (Main component)	Mol% G + C (Ave.)	DBB
Candida (*cont'd*)																																								
164	−	−	+	+	+	v	n	n	−	−	−	+	−	n	−	−	+	v	−	+	−	+	+	+	n	−	−	n	v	−	+	+	+	v	n	−	−	n	n	−
165	−	−	+	+	v	−	+	v	−	−	−	+	n	n	+	n	n	n	n	+	n	+	+	v	n	−	n	−	+	v	+	+	v	n	−	−	−	9	43.9	−
166	−	−	+	+	+	+	n	n	−	−	−	+	n	n	+	−	+	−	−	+	−	+	+	+	n	−	−	n	v	−	+	+	+	v	n	−	−	n	n	−
167	−	−	+	v	v	−	−	−	−	−	−	−	n	n	−	n	n	n	n	+	n	+	+	+	n	−	n	−	−	−	+	+	+	+	v	n	n	9	47.5	−
168	−	−	+	+	+	−	−	−	+	+	−	−	n	n	−	n	n	n	n	+	n	+	+	n	n	−	n	−	−	−	+	+	+	+	+	n	n	n	n	−
169	+	−	+	+	+	+	+	+	+	n	−	v	+	−	n	n	n	n	n	+	n	n	n	n	n	−	n	−	+	+	+	+	+	+	−	−	−	n	n	−
170	−	−	−	−	+	−	n	n	−	−	−	−	−	n	−	−	−	−	−	−	−	−	−	−	n	−	−	n	−	−	+	+	+	+	+	+	n	n	35.5	−
171	−	−	+	+	+	+	n	n	−	−	−	+	n	n	+	−	+	−	−	+	−	+	+	+	n	−	−	n	+	v	+	+	+	v	n	−	−	n	n	−
172	−	−	−	v	v	+	+	+	−	−	n	+	−	−	+	−	n	n	n	+	n	+	+	+	n	−	−	n	−	−	+	+	+	+	−	−	−	n	n	−
173	−	−	v	+	+	+	n	n	−	−	−	+	n	n	+	−	+	v	−	+	−	+	+	+	n	−	−	n	+	+	+	+	+	v	v	−	−	n	n	−
174	−	−	+	+	+	+	+	−	−	−	−	−	n	n	+	n	n	n	n	+	n	+	+	−	n	−	n	+	−	−	+	+	+	n	−	−	−	9	31.5	−
175	−	+	+	+	−	v	n	n	−	−	+	−	n	n	−	−	n	n	n	+	n	+	+	−	n	−	n	−	−	−	+	+	+	n	−	−	−	n	n	−
176	−	−	+	+	+	+	+	+	−	n	−	+	n	n	n	n	n	n	n	+	n	n	n	n	n	−	n	−	−	−	+	+	n	n	−	−	−	n	n	−
177	−	−	+	v	v	v	v	+	−	−	−	+	n	n	v	n	n	n	n	+	n	+	+	v	n	−	n	−	+	+	+	+	+	n	v	n	n	9	48.2	−
178	−	−	+	+	+	+	+	−	−	−	−	+	n	n	−	n	n	n	n	+	n	+	+	+	n	−	n	−	−	−	+	+	+	n	−	−	−	n	n	−
179	−	+	+	−	+	−	−	+	−	−	−	+	n	n	−	n	n	n	n	+	n	+	+	−	n	−	n	v	+	+	+	+	+	+	+	n	n	n	46.9	−
180	−	−	−	−	+	−	−	−	−	−	−	+	n	n	−	n	n	n	n	−	n	+	−	+	n	−	n	−	−	−	+	+	+	+	+	n	n	6	43.3	−
181	+	+	+	+	+	−	+	+	−	−	−	−	n	n	−	n	n	n	n	+	n	+	+	−	n	−	n	−	+	+	+	+	−	−	−	−	−	9	41.7	−
182	−	−	+	−	v	v	+	+	−	−	−	v	n	n	v	n	n	n	n	+	n	+	v	v	n	−	n	v	+	+	+	+	+	n	v	n	n	9	53.8	−
183	−	−	+	−	−	−	−	−	+	+	−	−	n	n	−	n	n	n	n	+	n	+	+	−	n	−	−	n	v	n	+	+	+	+	+	+	n	n	n	−
184	−	+	+	+	+	+	n	n	−	−	−	−	n	n	+	+	+	+	−	+	−	+	+	+	n	−	−	n	−	−	+	+	+	+	n	n	n	n	n	−
185	−	−	+	+	v	+	n	n	−	−	−	+	n	n	v	−	+	v	−	+	−	+	n	+	n	−	−	n	−	−	+	+	+	−	−	−	−	n	n	−
186	−	+	+	+	−	v	+	−	+	+	−	−	n	n	+	n	n	n	n	+	n	+	+	−	n	−	n	n	+	+	+	+	v	n	−	−	−	9	43.3	−
187	−	−	+	+	v	+	n	n	−	−	−	+	n	n	v	v	+	v	−	+	−	+	+	+	n	−	−	n	+	+	+	+	+	v	−	−	−	n	n	−
188	−	−	+	+	+	+	n	n	−	n	−	+	n	n	+	−	+	−	−	+	−	+	+	+	n	−	−	n	−	−	+	+	+	−	−	−	−	n	n	−
189	−	+	+	+	−	+	+	−	+	+	−	−	n	n	+	n	n	n	n	+	n	+	+	+	n	−	n	−	+	+	+	+	+	n	−	−	−	n	n	−
190	−	−	+	+	−	+	+	+	−	−	−	−	n	n	+	n	n	n	n	+	n	+	+	−	n	−	n	−	+	+	+	+	+	n	−	−	−	9	32.0	−
191	−	−	+	−	+	+	+	+	−	−	−	+	n	n	+	n	n	n	n	+	n	+	+	+	n	−	n	+	−	−	+	+	+	n	−	−	−	9	40.1	−
192	−	−	+	+	+	+	+	+	−	−	n	+	−	n	+	−	n	+	−	+	−	+	+	n	n	−	−	n	+	+	+	+	+	−	−	−	−	n	n	−
193	−	+	+	v	+	−	−	−	−	−	−	+	n	n	−	n	n	n	n	+	n	+	+	−	n	−	n	v	+	+	+	+	+	n	−	−	−	9	62.7	−
194	−	+	+	−	−	−	−	n	−	−	n	−	−	n	+	+	+	+	+	−	−	+	n	−	n	−	−	n	−	−	+	+	+	n	−	−	−	n	n	−
195	−	−	−	−	n	−	n	n	−	−	n	n	n	n	−	n	n	n	n	−	n	+	−	+	n	−	n	n	−	−	+	+	n	n	−	−	−	n	n	−
196	−	+	+	+	+	n	n	n	−	−	−	−	n	n	n	n	n	n	n	+	n	+	+	+	n	−	n	n	+	+	+	+	+	n	−	−	−	9	47.2	−
197	−	+	+	−	+	−	+	−	−	−	−	−	n	n	−	n	n	n	n	+	n	+	+	−	n	−	n	−	+	+	+	+	+	n	−	−	−	7	42.0	−
198	−	−	+	+	+	−	+	+	−	−	−	−	n	n	+	n	n	n	n	+	n	+	+	+	n	−	n	v	−	−	+	+	+	n	v	n	n	9	38.5	−
199	−	−	+	+	−	+	n	n	−	n	−	+	n	n	−	−	+	+	−	+	−	+	+	−	n	−	−	n	−	−	+	+	+	−	−	−	−	n	n	−
200	−	−	v	v	+	v	+	+	−	−	−	v	n	n	v	n	n	n	n	+	n	+	+	v	n	−	n	−	−	−	+	+	+	+	+	n	n	9	37.5	−
201	+	n	−	−	−	−	n	n	−	n	−	n	n	n	+	n	+	n	n	+	n	+	+	−	n	−	−	n	−	−	+	+	+	+	+	+	n	n	n	−
202	−	−	+	+	n	+	n	+	−	−	−	n	n	n	n	n	n	n	n	+	n	+	+	n	n	−	−	n	n	n	+	+	+	+	−	−	−	n	n	−
203	−	−	+	+	−	−	−	−	−	−	−	−	n	n	−	n	n	n	n	+	n	+	+	−	n	−	n	n	−	−	+	+	+	n	v	n	n	7	35.5	−
204	−	−	+	−	−	−	−	+	−	−	−	−	n	n	v	n	n	n	n	v	n	+	v	v	n	−	n	+	+	+	+	+	+	n	−	−	−	n	n	−
205	−	+	+	+	−	v	+	+	−	−	−	+	n	n	+	−	−	−	−	+	−	+	+	+	n	−	−	n	+	+	+	+	+	+	+	v	n	n	n	−
206	−	+	+	+	+	−	−	−	−	−	−	−	−	−	+	v	n	+	−	+	n	+	+	n	n	−	−	−	n	−	+	+	+	+	+	+	n	7	44.4	−
207	−	+	+	+	+	+	n	n	−	−	−	+	n	n	+	+	+	+	−	+	−	+	+	+	n	−	−	n	+	−	+	+	+	+	n	−	−	n	n	−
208	−	−	+	+	+	+	n	n	−	−	−	+	n	n	−	n	+	−	−	+	−	+	+	+	n	−	−	n	−	−	+	+	+	+	n	−	−	n	n	−
209	−	+	+	+	+	+	n	n	−	−	−	−	n	n	n	n	+	+	−	+	−	+	+	+	n	−	−	n	−	−	+	+	+	−	−	−	−	n	n	−
210	−	−	+	−	−	+	+	+	−	−	−	−	n	n	+	n	n	n	n	+	n	+	+	−	n	−	n	−	+	+	+	+	+	+	+	n	n	8	56.3	−
211	−	−	+	v	−	+	+	+	−	−	−	−	n	n	+	n	n	n	n	+	n	+	+	−	n	−	n	−	−	−	+	+	−	−	−	−	−	n	36.5	−
212	−	v	v	v	v	−	−	−	+	+	−	v	n	n	v	n	n	n	n	+	n	+	+	+	n	−	n	−	−	−	+	+	v	n	−	−	−	9	52.5	−
213	−	v	+	−	−	−	n	n	−	−	+	−	n	n	−	n	n	n	n	+	n	+	+	−	n	−	n	−	−	−	+	+	+	+	+	n	n	7	29.3	−
214	−	−	+	+	+	v	+	v	−	−	v	+	n	n	v	n	n	n	n	+	n	+	+	+	n	−	n	+	−	−	+	+	+	n	−	−	−	8	36.3	−
215	−	−	+	+	+	−	+	−	−	−	−	−	n	n	+	n	n	n	n	+	n	+	+	+	n	−	n	−	+	−	+	+	+	n	−	−	−	9	n	−
216	−	+	v	+	−	+	+	−	−	−	−	−	n	n	v	−	n	+	+	+	−	+	+	−	n	−	n	n	n	n	+	+	+	n	−	−	−	n	n	−
217	−	−	+	−	v	−	−	−	−	−	−	−	n	n	v	n	n	n	n	+	n	+	+	+	n	−	n	−	−	−	+	+	+	n	−	−	−	9	51.7	−

Symbols: +, positive or weak; −, negative; v, variable (+/−, w/−); n, no data.

Ln. no.	Species	Fermentation							Growth reactions and other characteristics																											
		Glucose	Galactose	Sucrose	Maltose	Lactose	Raffinose	Trehalose	Glucose	Inulin	Sucrose	Raffinose	Melibiose	Galactose	Lactose	Trehalose	Maltose	Melezitose	Methyl-α-D-glucoside	Soluble Starch	Cellobiose	Salicin	L-Sorbose	L-Rhamnose	D-Xylose	L-Arabinose	D-Arabinose	D-Ribose	Methanol	Ethanol	Glycerol	Erythritol	Ribitol	Galactitol	D-Mannitol	D-Glucitol
Candida *(cont'd)*																																				
218	*C. floridensis*	−	−	−	−	−	−	−	+	−	+	+	+	+	v	+	+	+	+	−	+	+	+	−	+	+	v	−	−	+	v	−	−	−	+	+
219	*C. floris*	v	n	n	n	n	n	n	+	−	−	−	−	v	−	−	−	−	−	−	−	−	v	−	−	−	−	−	−	−	+	−	−	−	+	+
220	*C. flosculorum*	+	n	n	n	n	n	n	+	−	+	−	−	−	−	−	+	+	−	−	+	+	+	−	+	−	−	−	−	−	+	−	−	−	−	−
221	*C. fluviatilis*	+	−	−	v	−	−	+	+	−	+	−	−	+	+	+	+	+	+	+	+	+	−	−	+	−	−	−	−	+	+	−	+	−	+	+
222	*C. fragi*	+	−	+	+	−	−	−	+	−	+	−	−	+	−	−	+	+	−	−	+	+	+	−	+	−	−	+	−	+	+	−	+	−	+	+
223	*C. freyschussii*	+	−	v	−	−	−	−	+	−	+	−	−	−	−	+	+	+	+	−	+	+	−	+	+	−	−	−	−	+	+	−	−	−	+	+
224	*C. friedrichii*	+	v	−	−	−	−	+	+	−	+	+	+	+	−	+	+	+	+	−	+	+	+	−	+	+	v	+	−	+	+	+	+	+	+	+
225	*C. frijolesensis*	+	+	+	+	−	−	+	+	−	+	−	−	+	−	+	+	+	+	−	−	−	−	−	+	−	−	−	−	+	−	−	+	−	+	+
226	*C. fructus*	+	−	−	−	−	−	+	+	−	−	−	−	−	−	+	−	−	−	−	−	−	+	−	+	−	−	+	−	+	+	−	+	−	+	+
227	*C. fukazawae*	+	−	−	−	−	−	−	+	−	+	−	−	−	−	+	+	−	+	+	+	+	−	−	+	−	−	+	−	+	+	+	+	−	+	+
228	*C. fungicola*	−	−	−	−	−	−	−	+	−	+	−	−	−	−	+	+	+	+	+	+	+	−	−	−	−	−	+	−	−	+	−	+	−	+	+
229	*C. galacta*	−	−	−	−	−	−	−	+	−	−	−	−	+	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	+	+	−	−	−	+	+
230	*C. galis*	−	−	−	−	−	−	−	+	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	+	+	−	−	−	−	−
231	*C. galli*	−	−	−	−	−	−	−	+	−	−	−	−	+	−	v	−	−	−	−	−	v	v	−	−	−	−	v	−	+	+	+	v	−	+	+
232	*C. gatunensis*	+	−	−	−	−	−	+	+	−	+	−	−	+	−	+	+	−	+	−	+	+	−	−	+	−	−	−	−	+	+	−	+	−	+	+
233	*C. gelsemii*	+	n	n	n	n	n	n	+	−	+	−	−	v	−	v	+	+	−	n	v	v	−	−	−	−	−	−	−	n	+	−	−	−	−	+
234	*C. geochares*	+	−	+	−	−	−	−	+	−	−	−	−	+	−	−	−	−	−	−	+	+	+	−	−	−	−	+	−	+	+	−	+	−	+	+
235	*C. germanica*	+	+	−	−	−	−	v	+	−	+	−	−	+	−	+	+	−	+	−	+	+	−	−	+	+	+	−	−	+	+	+	+	−	+	+
236	*C. ghanaensis*	−	−	−	−	−	−	−	+	−	+	−	−	+	−	−	+	+	+	−	−	+	−	−	+	−	−	−	−	+	−	+	−	−	+	+
237	*C. gigantensis*	+	+	+	+	−	−	+	+	−	+	−	−	+	−	+	+	+	+	−	−	−	−	−	+	−	−	−	−	+	+	−	+	−	+	+
238	*C. glabrata*	+	−	−	−	−	−	v	+	−	−	−	−	−	−	v	−	−	−	−	−	−	−	−	−	−	−	−	−	v	v	−	−	−	−	−
239	*C. glaebosa*	−	−	−	−	−	−	−	+	−	+	+	+	+	+	+	+	−	+	−	v	+	−	−	+	−	−	−	−	+	+	−	+	−	+	+
240	*C. glucosophila*	+	−	−	−	−	−	n	+	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	+	−	−	−	−	−	+	−	−	−	−	−
241	*C. gorgasii*	+	+	−	−	−	−	+	+	−	+	−	−	+	+	+	+	+	+	−	+	+	−	+	+	+	+	+	−	+	+	+	+	−	+	+
242	*C. gotoi*	+	+	+	−	−	−	−	+	−	+	+	−	+	−	+	+	+	+	+	+	+	−	+	+	+	−	+	−	+	+	+	+	+	+	+
243	*C. grinbergsii*	+	−	+	−	−	−	+	+	−	+	−	−	+	−	+	−	−	−	−	+	+	+	−	+	+	+	v	−	+	+	+	+	−	+	+
244	*C. gropengiesseri*	+	−	−	−	−	−	−	+	−	+	+	−	v	−	−	−	−	−	−	v	v	+	−	v	−	v	v	−	v	+	−	−	−	+	+
245	*C. guaymorum*	+	+	v	v	−	−	+	+	−	+	−	−	+	−	+	+	+	+	−	+	+	−	−	+	−	−	−	−	+	+	−	+	−	+	+
246	*C. haemulonii*	+	−	+	−	−	−	+	+	−	+	+	−	+	−	+	+	+	−	−	−	−	−	+	−	−	−	−	−	−	+	−	+	−	+	+
247	*C. hawaiiana*	+	n	n	n	n	n	n	+	−	+	−	−	+	−	+	+	+	−	−	+	+	+	−	+	−	v	v	−	v	+	−	+	−	+	+
248	*C. heliconiae*	+	n	n	n	n	n	n	+	−	+	−	−	+	−	−	+	+	+	−	+	+	+	−	+	v	+	−	−	+	+	−	+	−	+	+
249	*C. hispaniensis*	−	−	−	−	−	−	−	+	−	−	−	−	−	−	+	−	−	−	−	−	−	+	−	−	−	−	−	−	v	+	−	−	−	+	+
250	*C. hollandica*	−	−	−	−	−	−	−	+	−	−	−	−	+	−	−	−	−	−	−	−	−	+	−	−	−	−	−	n	n	+	+	+	−	+	−
251	*C. homilentoma*	+	+	−	+	−	−	+	+	−	+	−	−	+	−	+	+	+	+	+	+	+	−	+	+	+	−	+	−	+	+	+	+	−	+	+
252	*C. humilis*	+	+	−	−	−	−	+	+	−	−	−	−	+	−	+	−	−	−	−	−	−	−	−	−	−	−	−	−	v	+	−	−	−	−	−
253	*C. hungarica*	v	−	−	−	−	−	−	+	−	+	−	−	+	+	+	+	+	+	+	+	+	+	−	+	v	+	+	+	+	+	−	+	−	+	+
254	*C. hyderabadensis*	+	+	+	−	−	−	n	+	−	+	n	n	+	−	−	n	n	n	−	−	−	+	n	n	−	n	n	−	n	n	n	+	−	+	+
255	*C. incommunis*	+	−	v	−	−	−	−	+	−	+	−	−	v	−	+	+	v	+	−	+	+	+	−	v	−	−	−	−	+	+	+	−	−	+	+
256	*C. inconspicua*	v	−	−	−	−	−	−	+	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	+	+	−	−	−	−	−
257	*C. infanticola*	−	−	−	−	−	−	−	+	−	−	−	−	+	−	−	−	−	−	−	−	−	+	−	−	−	−	−	−	−	+	−	−	−	+	+
258	*C. insectalens*	−	−	−	−	−	−	−	+	−	−	−	−	+	−	+	−	−	−	−	+	+	−	−	−	−	v	−	−	+	−	−	+	−	+	+
259	*C. insectamans*	+	−	−	−	−	−	−	+	−	−	−	−	−	−	+	+	+	+	+	+	+	−	−	+	−	−	+	−	+	v	−	+	−	+	+
260	*C. insectorum*	+	+	v	−	−	−	+	+	−	+	+	v	+	v	+	+	+	+	−	+	+	+	+	+	+	v	+	−	+	+	+	+	−	+	+
261	*C. insectosa*	+	+	−	+	−	−	+	+	−	+	v	−	+	v	+	+	+	+	v	+	+	−	−	+	−	v	+	−	+	+	−	+	−	+	+
262	*C. intermedia*	+	+	+	v	−	v	v	+	v	+	+	−	+	+	+	+	+	v	v	+	+	+	v	+	v	v	v	−	+	v	−	v	v	+	+
263	*C. ipomoeae*	v	−	−	−	−	−	−	+	−	+	−	−	+	−	+	+	+	+	−	+	+	+	−	+	−	−	−	−	+	+	−	+	−	+	+
264	*C. ishiwadae*	+	v	v	+	−	−	+	+	−	+	−	−	v	−	+	+	v	v	+	+	+	+	+	+	+	v	+	−	+	+	+	+	v	+	+
265	*C. jeffriesii*	+	+	−	+	−	−	+	+	−	+	−	−	+	−	+	+	+	+	+	+	+	−	−	+	−	−	+	−	+	+	+	+	−	+	+
266	*C. jianshihensis*	−	−	−	−	−	−	−	+	−	−	−	−	−	−	−	−	−	−	−	+	+	−	−	+	−	−	−	−	−	+	−	+	−	+	+
267	*C. kipukae*	+	n	n	n	n	n	n	+	−	+	−	−	+	−	+	+	+	+	−	+	+	+	−	+	−	−	−	−	+	+	−	+	−	+	+
268	*C. kofuensis*	+	−	−	−	−	−	−	+	−	+	−	−	+	−	+	+	+	+	−	+	+	+	−	+	−	−	n	−	+	+	−	+	−	+	+
269	*C. krabiensis*	−	−	−	−	−	−	−	+	−	−	−	−	−	−	+	−	−	+	−	−	−	+	−	+	−	+	+	+	+	+	+	+	−	+	+
270	*C. kruisii*	+	+	−	−	−	−	+	+	−	+	−	−	+	−	+	+	+	+	+	+	+	+	−	+	+	−	v	−	+	+	−	+	−	+	+
271	*C. kunorum*	+	+	−	+	+	−	+	+	−	+	−	−	+	−	+	+	+	+	−	+	+	−	−	+	−	+	+	−	+	+	−	+	−	+	+

Symbols: +, positive or weak; −, negative; v, variable (+/−, w/−); n, no data.

	Growth reactions and other characteristics																																							
	myo-Inositol	DL-Lactate	Succinate	Citrate	D-Gluconate	D-Glucosamine	*N*-Acetyl-D-glucosamine	Hexadecane	Nitrate	Nitrite	Vitamin-free	2-Keto-D-gluconate	5-Keto-D-gluconate	Saccharate	Xylitol	L-Arabinitol	Arbutin	Propane 1,2 diol	Butane 2,3 diol	Cadaverine	Creatinine	L-Lysine	Ethylamine	50% Glucose	10% NaCl/5% glucose	Starch formation	Urease	Gelatin liquefaction	Cycloheximide 0.01%	Cycloheximide 0.1%	Growth at 19°C	Growth at 25°C	Growth at 30°C	Growth at 35°C	Growth at 37°C	Growth at 40°C	Growth at 45°C	CoQ (Main component)	Mol% G + C (Ave.)	DBB
Candida (*cont'd*)																																								
218	+	−	+	v	v	+	+	−	+	n	−	−	+	−	n	n	n	n	n	+	n	n	n	n	n	−	n	+	+	+	+	+	+	+	+	n	n	n	n	−
219	−	−	−	−	+	−	−	−	−	−	−	n	n	n	−	n	n	n	n	+	n	+	+	n	n	−	−	n	+	n	+	+	+	+	+	n	n	n	n	−
220	−	−	−	−	−	−	−	−	−	−	−	n	n	n	+	n	n	n	n	+	n	+	+	n	n	−	−	n	−	−	+	+	+	+	+	n	n	n	n	−
221	−	v	+	+	v	+	+	+	−	−	−	+	n	n	+	n	n	n	n	+	n	+	+	−	n	−	n	−	+	+	+	+	+	+	+	n	n	9	39.9	−
222	−	−	+	+	+	+	+	−	−	−	−	+	n	n	+	n	n	n	n	+	n	+	+	−	n	−	n	−	−	−	+	+	+	n	−	−	−	9	37.1	−
223	−	+	+	+	+	−	−	−	−	−	−	−	n	n	+	n	n	n	n	+	n	+	+	−	n	−	n	−	−	−	+	+	+	+	+	n	n	7	44.5	−
224	−	+	+	+	+	v	+	−	−	−	−	+	n	n	+	n	n	n	n	+	n	+	+	+	n	−	n	−	−	−	+	+	v	n	−	−	−	9	33.3	−
225	−	+	−	−	−	+	n	n	−	n	−	+	n	n	+	−	+	−	−	+	−	+	+	+	n	−	−	n	+	+	+	+	+	+	−	−	−	n	n	−
226	−	−	+	+	+	+	+	−	−	−	−	+	n	n	+	n	n	n	n	+	n	+	+	−	n	−	n	−	−	−	+	+	+	n	−	−	−	8	48.8	−
227	−	+	+	+	+	+	+	+	−	−	−	+	n	n	+	n	n	n	n	+	n	+	+	−	n	−	n	−	−	−	+	+	+	n	−	−	−	9	45.1	−
228	−	−	+	+	−	−	+	+	−	−	−	+	n	n	−	n	n	n	n	+	n	+	+	−	n	−	n	−	+	−	+	+	+	n	−	−	−	9	38.9	−
229	−	−	+	+	+	−	n	n	−	−	−	−	n	n	−	n	n	n	n	+	n	+	+	+	n	−	n	−	−	−	+	+	+	n	−	−	−	8	50.2	−
230	−	+	+	−	−	−	−	v	−	−	−	−	n	n	v	n	n	n	n	v	n	+	+	−	n	−	n	−	−	−	+	+	+	n	−	−	−	n	n	−
231	−	+	+	+	+	−	−	+	−	−	+	+	n	n	v	−	v	+	v	+	−	+	+	−	n	−	n	+	+	+	+	+	+	−	−	−	−	n	n	−
232	−	−	+	+	+	+	n	n	−	−	−	+	n	n	+	−	+	−	−	+	−	+	+	−	n	−	−	n	+	−	+	+	+	+	n	−	−	n	n	−
233	−	−	v	−	+	v	+	+	−	−	−	−	n	n	−	n	n	n	n	+	n	+	+	−	n	−	n	+	n	−	+	+	v	n	n	n	n	n	n	−
234	−	−	+	+	+	−	−	+	−	−	−	−	n	n	−	n	n	n	n	+	n	+	+	+	n	−	n	−	−	−	+	+	+	n	+	n	n	9	54.1	−
235	−	−	+	−	+	+	+	+	−	−	+	+	n	n	+	n	n	n	n	+	n	+	+	+	n	−	n	−	−	−	+	+	+	+	+	n	n	n	n	−
236	−	−	+	+	−	−	+	+	−	−	−	−	n	n	−	n	n	n	n	+	n	+	+	−	n	−	n	−	+	−	+	+	+	+	+	n	n	n	n	−
237	−	−	+	+	+	+	n	n	−	−	−	+	n	n	+	−	−	−	−	+	−	+	+	+	n	−	−	n	−	−	+	+	+	−	−	−	−	n	n	−
238	−	v	−	−	+	−	−	−	−	−	−	v	n	n	−	n	n	n	n	−	n	−	−	v	n	−	n	−	−	−	+	+	+	+	+	n	n	6	39.4	−
239	−	+	+	+	−	v	+	v	−	−	−	+	n	n	+	n	n	n	n	+	n	+	+	−	n	−	n	n	v	−	+	+	−	−	−	−	−	9	42.2	−
240	−	−	−	−	n	n	n	n	+	−	−	n	n	n	n	n	n	n	n	−	n	−	+	+	n	−	n	n	−	−	+	+	+	+	+	n	n	9	36.6	−
241	−	+	+	+	+	+	n	n	−	−	n	+	n	n	+	n	+	+	−	+	−	+	+	−	n	−	−	n	−	−	+	+	+	+	n	n	n	n	n	−
242	−	+	+	+	−	−	+	+	−	−	+	+	n	n	+	n	n	n	n	+	n	+	+	+	n	−	n	−	−	−	+	+	+	+	+	n	n	8	41.6	−
243	−	+	+	−	−	+	+	+	−	n	v	+	+	−	n	n	n	n	n	+	n	n	n	n	n	−	n	−	+	+	+	+	n	n	−	−	−	n	n	−
244	−	−	v	+	+	−	−	+	−	v	−	v	n	n	v	n	n	n	n	+	n	+	+	+	n	−	n	n	v	−	+	+	+	n	v	n	n	9	56.4	−
245	−	−	+	+	+	+	n	n	−	−	−	+	n	n	−	n	+	−	−	+	−	+	+	+	n	−	−	n	−	−	+	+	+	v	n	−	−	n	n	−
246	−	−	+	+	+	+	+	+	−	−	+	+	n	n	−	n	n	n	n	+	n	+	+	+	n	−	n	+	+	−	+	+	+	n	−	−	−	9	46.5	−
247	−	−	+	+	+	+	+	+	−	−	−	+	n	n	+	n	n	n	n	+	n	+	+	+	n	n	n	−	n	−	+	+	+	n	−	−	−	n	n	−
248	−	−	−	−	+	v	+	−	−	−	n	−	−	n	−	n	n	n	n	+	n	+	+	−	n	n	−	n	+	+	+	+	+	+	−	−	−	n	n	−
249	−	+	+	−	−	−	−	+	−	n	−	−	−	−	n	n	n	n	n	+	n	n	n	n	n	−	n	+	+	+	+	+	+	n	v	n	n	n	n	−
250	−	+	+	+	+	−	n	n	−	n	−	n	−	n	−	−	n	+	−	+	−	+	−	n	n	−	n	n	+	+	+	+	+	−	−	−	−	n	n	−
251	−	−	+	+	v	+	−	−	−	−	v	+	n	n	+	n	n	n	n	+	n	+	+	+	n	−	n	−	+	+	+	+	+	n	v	n	n	8	48.7	−
252	−	+	−	−	−	−	−	−	−	−	−	−	n	n	−	n	n	n	n	−	n	−	−	−	n	−	n	−	+	−	+	+	+	n	−	−	−	6	47.1	−
253	−	+	+	−	v	+	+	−	+	+	v	−	n	n	+	−	n	−	−	+	−	+	+	−	n	−	n	n	+	+	+	+	+	−	−	−	−	9	n	−
254	n	+	+	+	n	−	n	n	−	−	n	n	n	n	+	n	n	−	−	n	−	+	+	n	n	n	−	n	+	+	+	+	n	n	n	n	n	n	n	−
255	+	−	+	+	+	+	+	+	+	+	−	+	n	n	+	n	n	n	n	+	n	+	+	−	n	−	n	−	+	+	+	+	+	n	v	n	n	8	48.9	−
256	−	+	+	+	−	+	v	−	−	−	−	−	n	n	−	n	n	n	n	+	n	+	+	−	n	−	n	−	−	−	+	+	+	+	+	n	n	8	36.5	−
257	−	−	+	−	−	−	−	+	−	n	−	−	−	−	n	n	n	n	n	+	n	n	n	n	n	−	n	−	+	+	+	+	+	+	+	n	n	n	n	−
258	−	v	+	−	−	+	+	−	−	−	v	−	n	n	−	n	n	n	n	+	n	+	+	−	n	−	n	−	−	−	+	+	+	+	+	n	n	9	44.9	−
259	−	−	+	+	−	−	−	−	−	−	−	+	n	n	−	n	n	n	n	+	n	+	+	−	n	−	n	−	−	−	+	+	+	+	+	n	n	9	35.9	−
260	−	−	+	+	+	v	+	+	−	−	−	v	n	n	+	n	n	n	n	+	n	+	+	−	n	−	n	v	v	v	+	+	+	n	v	n	n	9	39.5	−
261	−	−	+	+	v	v	+	+	−	−	−	+	n	n	v	n	n	n	n	+	n	+	+	−	n	−	n	+	+	+	+	+	+	n	−	−	−	n	44.5	−
262	−	−	+	+	v	v	+	+	−	−	v	+	n	n	v	n	n	n	n	+	n	+	+	v	n	−	n	−	v	−	+	+	+	n	−	−	−	9	44.1	−
263	−	−	+	+	−	−	+	v	−	−	−	+	n	n	v	n	n	n	n	+	n	+	+	+	n	−	n	−	−	−	+	+	+	n	v	n	n	n	n	−
264	−	v	+	+	+	+	+	−	+	+	−	+	n	n	v	n	n	n	n	+	n	+	+	+	n	−	n	−	+	+	+	+	+	n	−	−	−	8	36.7	−
265	−	+	+	+	+	+	n	n	−	−	−	+	n	n	+	n	n	+	−	+	−	+	+	−	n	−	−	n	−	−	+	+	+	−	−	−	−	n	n	−
266	−	+	−	−	−	−	−	n	+	n	n	−	−	n	n	n	n	+	+	+	−	+	n	−	n	−	−	n	−	−	+	+	+	−	−	−	−	n	n	−
267	−	−	+	+	+	+	+	+	−	−	−	+	n	n	+	n	n	n	n	+	n	+	+	+	n	−	n	+	−	−	+	+	+	n	−	−	−	n	n	−
268	−	−	+	+	+	+	n	n	−	−	−	+	n	n	+	n	n	n	n	+	n	+	+	+	n	−	n	−	−	−	+	+	+	n	−	−	−	9	46.3	−
269	−	−	+	+	−	n	−	n	+	+	−	−	−	n	n	n	n	n	n	+	n	+	+	−	n	−	−	+	+	+	+	+	+	+	+	+	n	7	n	−
270	−	−	+	+	+	+	+	+	−	−	−	+	n	n	+	n	n	n	n	+	n	+	+	v	n	−	n	−	+	+	+	+	+	n	−	−	−	9	44.8	−
271	−	−	+	+	+	+	n	n	−	−	−	+	n	n	+	n	+	+	−	+	−	+	+	+	n	−	−	n	−	−	+	+	+	−	−	−	−	n	n	−

Symbols: +, positive or weak; −, negative; v, variable (+/−, w/−); n, no data.

Ln. no.	Species	Fermentation							Growth reactions and other characteristics																																	
		Glucose	Galactose	Sucrose	Maltose	Lactose	Raffinose	Trehalose	Glucose	Inulin	Sucrose	Raffinose	Melibiose	Galactose	Lactose	Trehalose	Maltose	Melezitose	Methyl-α-D-glucoside	Soluble Starch	Cellobiose	Salicin	L-Sorbose	L-Rhamnose	D-Xylose	L-Arabinose	D-Arabinose	D-Ribose	Methanol	Ethanol	Glycerol	Erythritol	Ribitol	Galactitol	D-Mannitol	D-Glucitol					
Candida (*cont'd*)																																										
272	*C. labiduridarum*	+	+	+	+	−	−	+	+	−	+	−	−	+	−	+	+	+	+	−	v	−	v	−	+	+	−	−	−	+	+	−	+	−	+	+						
273	*C. lactis-condensi*	+	−	+	−	−	+	−	+	−	+	v	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−						
274	*C. lassenensis*	−	−	−	−	−	−	−	+	−	−	−	−	−	−	−	−	−	−	+	−	−	−	−	−	−	+	+	−	+	+	+	+	−	+	+						
275	*C. leandrae*	+	n	n	n	n	n	n	+	+	+	+	−	+	−	+	+	−	+	−	v	v	+	−	+	−	−	v	−	+	n	−	+	−	+	+						
276	*C. lessepsii*	+	+	−	−	−	−	+	+	−	+	−	−	+	−	+	+	+	+	−	+	+	−	−	+	+	+	+	−	−	+	+	+	−	+	+						
277	*C. lignohabitans*	+	+	−	−	−	−	+	+	−	−	−	−	+	−	+	−	−	−	−	+	+	+	−	+	+	+	+	−	+	+	+	+	+	+	+						
278	*C. lignosa*	+	+	−	+	−	−	+	+	−	+	v	−	+	v	+	+	+	+	+	+	+	+	−	+	v	v	+	−	+	v	+	+	+	+	+						
279	*C. linzhiensis*	+	+	−	−	−	−	n	+	−	−	+	+	+	+	+	+	−	+	−	+	+	+	−	+	−	+	−	−	+	+	+	+	+	−	+						
280	*C. litsaeae*	+	+	+	+	−	+	+	+	−	+	+	−	+	+	+	+	+	+	+	+	+	+	−	−	+	+	+	+	−	+	+	+	+	−	+						
281	*C. llanquihuensis*	+	−	−	−	−	−	+	+	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	+	−	−	+	−	+	+	+	+	−	+						
282	*C. lycoperdinae*	+	+	−	−	−	−	+	+	−	+	−	−	+	−	+	+	−	+	−	+	+	−	−	−	+	−	+	−	−	−	+	−	+	−	+						
283	*C. lyxosophila*	+	+	−	+	−	−	−	+	−	+	−	−	+	−	+	+	v	+	+	+	+	−	−	+	−	−	v	−	+	+	−	+	−	+	+						
284	*C. magnoliae*	+	−	+	−	−	−	−	+	−	v	v	−	+	−	−	−	−	−	−	−	v	+	−	−	−	−	+	−	+	+	−	−	−	+	+						
285	*C. maltosa*	+	v	+	v	−	−	+	+	−	+	−	−	+	−	+	+	+	+	−	v	v	v	−	+	−	−	−	−	+	+	−	v	−	+	+						
286	*C. marilandica*	−	−	−	−	−	−	−	+	−	+	+	+	+	−	+	+	+	+	−	+	+	+	−	+	+	+	+	−	+	−	+	+	−	+	+						
287	*C. marionensis*	+	+	−	−	−	−	+	+	−	−	−	−	+	−	+	−	−	−	−	+	+	+	−	+	+	+	+	−	v	−	−	+	−	+	+						
288	*C. maris*	−	−	−	−	−	−	−	+	−	−	−	−	−	−	−	−	−	−	−	−	−	−	+	v	−	−	−	+	+	v	−	v	−	+	+						
289	*C. maritima*	+	−	v	−	−	v	−	+	−	+	v	−	−	−	+	+	+	+	v	+	+	−	+	+	v	v	−	−	+	+	−	−	−	+	+						
290	*C. maxii*	+	−	−	−	−	−	+	+	−	+	−	−	+	−	+	+	+	+	−	+	+	−	−	−	−	+	+	−	+	+	+	+	−	+	+						
291	*C. melibiosica*	+	+	v	v	−	v	v	+	−	+	v	+	+	−	+	+	+	v	−	+	+	v	−	+	−	−	v	−	+	v	−	v	−	+	+						
292	*C. membranifaciens*	+	v	+	v	−	+	+	+	+	+	+	+	+	−	+	+	+	v	v	+	+	v	v	+	+	+	+	−	+	+	+	+	+	+	+						
293	*C. mesenterica*	v	−	−	−	−	−	−	+	−	+	−	−	−	−	+	+	v	+	−	+	+	+	−	v	−	v	v	−	+	+	+	v	−	+	+						
294	*C. metapsilosis*	+	−	−	−	−	−	n	+	−	+	−	−	+	−	+	+	+	+	v	−	−	+	−	+	+	−	+	−	+	v	+	−	+	−	+						
295	*C. methanosorbosa*	+	+	−	−	−	−	+	+	−	−	−	−	+	−	+	−	−	−	−	v	+	+	+	+	+	−	−	+	+	+	−	+	−	+	+						
296	*C. michaelii*	+	+	+	+	−	−	+	+	−	+	−	−	+	−	+	+	+	+	−	+	+	−	+	+	+	−	−	−	+	+	+	+	−	+	+						
297	*C. milleri*	+	+	+	−	−	+	+	+	v	+	+	−	+	−	+	−	−	−	−	−	−	−	−	−	−	−	−	−	−	v	v	−	−	−	−						
298	*C. mogii*	+	−	+	v	−	−	+	+	v	+	+	−	+	−	+	+	−	−	v	−	−	−	−	+	+	v	+	−	+	+	−	v	v	+	v						
299	*C. montana*	−	−	−	−	−	−	−	+	−	−	−	−	−	−	−	−	−	−	−	+	+	−	+	−	−	−	−	−	+	+	−	−	−	+	−						
300	*C. mucifera*	−	−	−	−	−	−	−	+	−	−	n	−	+	−	+	+	−	−	−	−	−	+	+	+	+	+	+	+	−	+	+	+	+	−	−						
301	*C. multigemmis*	+	−	−	−	−	−	v	+	−	+	−	−	+	−	+	+	−	−	−	−	−	+	−	+	v	−	v	−	−	+	−	v	−	−	+						
302	*C. musae*	+	−	−	−	−	−	+	+	−	+	−	−	v	−	+	+	−	−	−	−	−	+	−	+	−	−	v	−	+	+	−	+	−	+	+						
303	*C. mycetangii*	+	−	+	−	−	+	−	+	v	+	+	−	−	−	+	+	+	+	v	+	+	−	+	+	−	+	v	−	+	+	−	−	−	+	+						
304	*C. naeodendra*	+	+	−	−	−	−	+	+	−	+	−	−	+	−	+	+	+	+	+	+	+	+	+	+	+	+	+	−	+	+	+	+	−	+	+						
305	*C. nakhonratchasimensis*	+	−	+	−	−	−	n	+	−	+	+	−	−	−	+	+	+	+	+	+	+	−	+	+	−	−	−	−	+	+	−	−	−	+	+						
306	*C. nanaspora*	+	+	−	−	−	−	+	+	−	−	−	−	+	−	+	−	−	−	−	−	−	−	+	+	+	v	+	+	+	+	+	+	−	+	+						
307	*C. natalensis*	+	+	v	−	−	−	−	+	−	+	−	−	+	−	+	+	−	−	+	+	+	+	−	v	−	−	+	−	+	+	−	v	−	+	+						
308	*C. neerlandica*	+	−	−	+	−	−	+	+	−	+	−	−	+	−	+	+	−	−	+	+	+	−	−	+	−	−	+	−	+	+	−	+	−	+	+						
309	*C. nemodendra*	−	−	−	−	−	−	−	+	−	−	−	−	+	−	+	−	−	−	−	v	v	+	−	+	+	v	+	+	+	+	+	+	+	+	+						
310	*C. neomexicana*	+	+	−	−	−	−	+	+	−	−	−	−	+	+	+	−	−	−	−	+	+	+	−	+	+	+	+	−	+	+	+	+	+	+	+						
311	*C. nitratophila*	+	v	−	−	−	−	+	+	−	−	−	−	+	−	+	−	−	−	−	−	v	−	+	+	+	−	+	+	+	+	−	+	−	+	+						
312	*C. nivariensis*	+	−	−	−	−	−	+	+	−	−	−	−	−	−	−	−	−	−	v	−	−	−	−	−	−	−	−	−	−	−	+	−	−	−	−						
313	*C. norvegica*	+	−	−	−	−	−	−	+	−	−	−	−	−	−	−	−	−	−	−	+	+	−	v	v	−	v	−	−	+	+	−	−	−	+	v						
314	*C. novakii*	+	−	−	−	−	−	−	+	−	−	−	−	+	−	+	−	−	−	−	+	+	+	−	+	+	−	+	−	+	+	+	+	−	+	+						
315	*C. odintsovae*	+	−	+	−	−	+	−	+	v	+	+	−	v	−	+	+	+	+	−	+	+	v	+	+	+	−	v	−	+	+	−	v	−	+	+						
316	*C. oleophila*	+	+	v	v	−	−	v	+	−	+	−	−	+	−	+	+	+	v	v	+	+	+	−	+	−	v	v	−	+	+	−	v	−	+	+						
317	*C. ontarioensis*	+	+	+	−	−	−	+	+	−	+	v	−	+	+	+	+	+	+	+	+	+	−	−	+	+	v	+	−	+	+	+	+	−	+	+						
318	*C. orba*	−	−	−	−	−	−	−	+	−	−	−	−	−	−	−	−	−	−	−	+	+	−	−	−	−	−	−	−	+	+	−	−	−	v	v						
319	*C. oregonensis*	+	−	−	+	−	−	−	+	−	+	v	−	−	−	+	+	+	+	+	+	+	−	+	+	−	v	v	−	+	+	−	−	v	−	+	+					
320	*C. orthopsilosis*	+	−	−	−	−	−	n	+	−	+	−	−	+	−	+	+	+	+	v	−	−	+	−	+	+	−	−	−	v	+	−	+	−	+	+						
321	*C. ortonii*	+	−	−	−	−	−	−	+	−	+	−	−	−	−	−	+	+	−	−	+	+	−	−	−	−	−	−	−	+	+	−	−	+	−	+						
322	*C. oslonensis*	−	−	−	−	−	−	−	+	−	−	−	−	+	−	−	−	−	−	−	−	−	+	−	v	−	−	v	n	n	+	v	+	−	−	+						
323	*C. ovalis*	+	−	−	−	−	−	+	+	−	−	−	−	−	−	+	−	−	−	−	+	+	+	−	+	+	+	+	+	+	+	+	+	−	+	+						
324	*C. pallodes*	+	+	−	+	−	−	+	+	−	+	−	−	+	−	+	+	+	+	−	+	+	−	−	+	−	−	v	−	v	+	−	+	−	+	+						
325	*C. palmioleophila*	−	−	−	−	−	−	−	+	−	+	+	+	+	−	+	+	+	+	+	−	−	−	−	+	−	−	−	−	+	+	−	+	−	+	+						

Symbols: +, positive or weak; −, negative; v, variable (+/−, w/−); n, no data.

Growth reactions and other characteristics

	myo-Inositol	DL-Lactate	Succinate	Citrate	D-Gluconate	D-Glucosamine	*N*-Acetyl-D-glucosamine	Hexadecane	Nitrate	Nitrite	Vitamin-free	2-Keto-D-gluconate	5-Keto-D-gluconate	Saccharate	Xylitol	L-Arabinitol	Arbutin	Propane 1,2 diol	Butane 2,3 diol	Cadaverine	Creatinine	L-Lysine	Ethylamine	50% Glucose	10% NaCl/5% glucose	Starch formation	Urease	Gelatin liquefaction	Cycloheximide 0.01%	Cycloheximide 0.1%	Growth at 19°C	Growth at 25°C	Growth at 30°C	Growth at 35°C	Growth at 37°C	Growth at 40°C	Growth at 45°C	CoQ (Main component)	Mol% G + C (Ave.)	DBB
Candida (*cont'd*)																																								
272	−	+	−	+	−	+	n	n	−	−	−	+	n	n	−	v	+	−	−	+	−	+	+	+	n	−	−	n	+	+	+	+	+	v	−	−	−	n	n	−
273	−	−	−	−	−	−	−	−	+	+	−	−	n	n	−	n	n	n	n	−	n	v	−	+	n	−	n	−	v	−	+	+	+	n	−	−	−	8	42.8	−
274	+	−	+	−	+	−	−	−	−	−	−	+	n	n	+	n	n	n	n	+	n	+	−	−	n	−	n	+	+	−	+	+	+	+	+	n	n	n	n	−
275	−	−	+	+	v	v	+	+	−	−	−	+	−	n	+	n	n	n	n	+	n	+	+	+	n	n	−	n	−	−	+	+	+	+	−	−	−	n	n	−
276	−	−	+	+	+	+	n	n	−	n	−	−	n	n	+	n	+	+	−	+	−	+	+	+	n	−	−	n	+	−	+	+	+	+	n	n	n	n	n	−
277	−	+	+	v	+	+	+	+	−	n	−	+	+	−	n	n	n	n	n	+	n	n	n	n	n	−	n	−	+	+	+	+	+	+	+	n	n	n	n	−
278	−	+	+	+	−	v	+	+	−	−	−	+	n	n	v	n	n	n	n	+	n	+	+	−	n	−	n	−	+	+	+	+	+	n	−	−	−	n	44.1	−
279	−	−	+	−	n	−	n	−	−	−	+	n	n	n	n	n	n	n	n	+	n	−	+	n	n	−	−	n	n	n	+	+	−	−	−	−	−	8	n	−
280	−	−	+	+	−	+	+	+	−	−	−	+	n	n	+	n	n	n	n	+	n	+	+	−	n	−	n	+	+	−	+	+	+	+	+	n	n	n	n	−
281	−	+	+	+	−	−	−	−	−	−	−	−	n	n	+	n	n	n	n	+	n	+	+	−	n	−	n	−	+	+	+	+	+	n	−	−	−	7	40.5	−
282	−	−	+	+	+	+	n	n	−	−	−	+	n	n	−	−	+	−	−	+	−	+	+	v	n	−	−	n	−	−	+	+	+	−	−	−	−	n	n	−
283	−	+	+	+	−	+	+	−	−	−	−	+	n	n	v	n	n	n	n	+	n	+	+	−	n	−	n	−	v	−	+	+	+	n	−	−	−	9	38.1	−
284	−	−	+	v	+	−	−	−	+	+	−	v	n	n	+	n	n	n	n	+	n	+	+	+	n	−	n	v	−	−	+	+	+	n	v	n	n	9	60.0	−
285	−	v	+	v	v	v	+	+	−	−	−	+	n	n	v	n	n	n	n	+	n	+	+	v	n	−	n	−	+	+	+	+	+	+	+	n	n	9	36.5	−
286	+	−	−	−	+	+	+	+	+	n	+	+	+	−	n	n	n	n	n	+	n	n	n	n	n	−	n	−	+	+	+	+	+	+	+	n	n	n	n	−
287	−	−	v	v	+	+	+	+	−	n	−	+	+	−	n	n	n	n	n	+	n	n	n	n	n	−	n	−	+	+	+	+	+	+	+	n	n	n	n	−
288	−	−	+	−	−	−	−	−	−	−	−	−	n	n	+	n	n	n	n	+	n	+	+	−	n	−	n	−	+	−	+	+	+	+	+	n	n	7	48.1	−
289	−	v	+	+	+	v	−	−	−	−	−	v	n	n	+	n	n	n	n	+	n	+	+	−	n	−	n	−	−	−	+	+	v	n	−	−	−	7	46.1	−
290	−	−	+	+	+	+	n	n	−	n	−	+	n	n	+	n	+	−	−	+	−	+	+	+	n	−	−	n	−	−	+	+	+	−	−	−	−	n	n	−
291	−	−	+	+	v	v	+	+	−	−	v	+	n	n	+	n	n	n	n	+	n	+	+	v	n	−	n	−	−	−	+	+	+	+	+	n	n	9	55.5	−
292	−	v	+	+	+	v	+	+	−	−	−	+	n	n	+	n	n	n	n	+	n	v	+	+	n	−	n	−	−	−	+	+	+	n	v	n	n	9	33.4	−
293	−	−	+	v	−	v	+	−	−	−	−	+	n	n	v	n	n	n	n	+	n	+	+	−	n	−	n	−	−	−	+	+	−	n	−	−	−	9	47.6	−
294	−	−	+	+	+	−	n	n	−	−	−	+	n	n	+	n	−	v	−	+	−	+	+	−	n	−	−	n	+	−	+	+	+	+	+	+	n	n	n	−
295	−	−	−	−	+	+	+	+	+	+	+	−	n	n	+	n	n	n	n	+	n	+	+	−	n	−	n	−	+	−	+	+	+	+	+	n	n	7	n	−
296	−	+	+	+	+	−	n	n	−	−	−	−	n	n	+	n	+	+	+	+	−	+	+	+	n	−	−	n	−	−	+	+	+	+	n	n	n	n	n	−
297	−	v	v	−	−	−	−	−	−	−	−	−	n	n	−	n	n	n	n	−	n	−	−	−	n	−	n	−	v	v	+	+	+	n	−	−	−	6	47.2	−
298	−	−	+	v	+	+	+	−	−	−	−	−	n	n	+	n	n	n	n	+	n	+	+	+	n	−	n	−	−	−	+	+	+	+	+	n	n	9	45.2	−
299	−	−	+	+	−	−	−	−	−	−	−	+	n	n	−	n	n	n	n	+	n	+	+	−	n	−	n	−	−	−	+	+	+	n	−	−	−	7	35.6	−
300	+	−	+	−	+	+	+	+	−	−	−	+	n	n	+	n	n	n	n	+	n	+	+	+	n	−	n	−	+	+	+	+	+	n	−	−	−	n	n	−
301	−	−	+	+	v	v	n	+	−	−	−	+	n	n	+	n	n	n	n	+	n	+	+	v	n	−	n	+	−	−	+	+	+	n	−	−	−	9	35.4	−
302	−	−	+	+	v	v	+	+	−	−	−	+	n	n	+	n	n	n	n	+	n	+	+	−	n	−	n	−	−	−	+	+	+	n	−	−	−	8	47.9	−
303	−	+	+	+	v	−	−	−	−	−	−	−	n	n	+	n	n	n	n	+	n	+	+	−	n	−	n	+	v	v	+	+	+	+	+	n	n	n	n	−
304	−	−	+	+	+	+	+	+	−	−	−	−	n	n	+	n	n	n	n	+	n	+	+	+	n	−	n	−	−	−	+	+	+	+	+	n	n	9	n	−
305	−	+	+	+	+	−	−	−	+	+	−	−	−	−	+	−	n	+	−	+	n	+	+	n	n	−	−	−	n	n	+	+	+	−	−	−	−	7	39.2	−
306	−	−	+	−	−	+	+	+	+	+	−	−	n	n	+	n	n	n	n	+	n	+	+	−	n	−	n	−	+	+	+	+	+	+	+	n	n	7	36.6	−
307	−	+	+	+	+	−	+	+	−	−	−	+	n	n	+	n	n	n	n	+	n	+	+	−	n	−	n	−	+	−	+	+	−	−	−	−	−	9	37.1	−
308	−	+	+	+	+	−	+	+	−	−	−	+	n	n	+	n	n	n	n	+	n	+	+	−	n	−	n	−	−	−	+	+	+	n	−	−	−	n	n	−
309	−	v	+	−	−	−	−	+	−	−	v	−	n	n	+	n	n	n	n	+	n	+	+	−	n	−	n	−	+	v	+	+	+	n	−	−	−	7	41.4	−
310	−	+	+	−	+	+	+	−	−	n	−	+	+	−	n	n	n	n	n	+	n	n	n	n	n	−	n	−	+	+	+	+	+	n	−	−	−	n	n	−
311	−	−	+	−	−	+	+	−	+	+	−	−	n	n	+	n	n	n	n	+	n	+	+	−	n	−	n	−	+	+	+	+	+	n	−	−	−	7	36.6	−
312	−	−	−	−	+	−	n	n	−	n	−	−	−	n	−	−	−	−	−	−	−	−	−	−	n	−	−	n	−	−	+	+	+	+	+	+	n	n	34.1	−
313	−	+	+	v	v	−	−	−	+	+	−	−	n	n	v	n	n	n	n	+	n	+	+	−	n	−	n	−	v	v	+	+	+	n	−	−	−	7	41.2	−
314	−	+	+	+	+	+	+	+	+	+	−	+	n	n	+	n	n	n	n	+	n	+	+	−	n	−	n	−	+	+	+	+	+	n	−	−	−	9	37.5	−
315	−	v	+	v	+	−	+	+	−	−	v	+	n	n	+	n	n	n	n	+	n	+	+	−	n	−	n	−	−	−	+	+	+	+	+	n	n	7	37.2	−
316	−	v	+	+	v	v	+	v	−	−	−	+	n	n	v	n	n	n	n	+	n	+	+	v	n	−	n	−	+	+	+	+	+	n	−	−	−	9	42.2	−
317	−	−	+	+	+	v	+	+	−	−	−	−	n	n	+	n	n	n	n	+	n	+	+	+	n	−	n	v	+	+	+	+	+	n	−	−	−	n	n	−
318	−	+	+	−	−	−	−	−	−	−	−	−	n	n	n	n	n	n	n	+	n	+	+	−	n	−	n	−	−	−	+	+	+	n	−	−	−	n	33.7	−
319	−	−	+	+	+	+	+	+	−	−	−	+	n	n	v	n	n	n	n	+	n	+	+	−	n	−	n	−	v	−	+	+	+	n	−	−	−	9	48.1	−
320	−	−	+	+	+	−	n	n	−	−	−	+	n	n	+	n	−	+	−	+	−	+	+	+	n	−	−	n	+	−	+	+	+	+	+	+	n	n	n	−
321	−	−	−	−	−	−	−	−	−	−	−	−	n	n	−	n	n	n	n	+	n	+	+	−	n	−	n	−	+	+	+	+	+	n	−	−	−	n	n	−
322	−	+	+	+	+	−	n	n	−	−	−	n	−	n	−	−	n	−	−	+	−	+	+	n	n	n	−	n	+	+	+	+	+	−	−	−	−	n	45.8	−
323	−	+	+	+	+	−	−	−	−	−	−	−	n	n	+	n	n	n	n	+	n	+	+	−	n	−	n	−	+	+	+	+	+	n	−	−	−	7	35.8	−
324	−	v	+	+	+	+	n	n	−	−	−	+	n	n	+	−	+	v	−	+	−	+	+	v	n	−	−	n	−	−	+	+	+	+	n	−	−	n	n	−
325	−	+	+	+	+	+	+	+	−	+	−	+	n	n	+	n	n	n	n	+	n	+	+	−	n	−	n	−	+	+	+	+	+	+	+	n	n	9	39.6	−

Symbols: +, positive or weak; −, negative; v, variable (+/−, w/−); n, no data.

Ln. no.	Species	Fermentation: Glucose	Galactose	Sucrose	Maltose	Lactose	Raffinose	Trehalose	Growth reactions and other characteristics: Glucose	Inulin	Sucrose	Raffinose	Melibiose	Galactose	Lactose	Trehalose	Maltose	Melezitose	Methyl-α-D-glucoside	Soluble Starch	Cellobiose	Salicin	L-Sorbose	L-Rhamnose	D-Xylose	L-Arabinose	D-Arabinose	D-Ribose	Methanol	Ethanol	Glycerol	Erythritol	Ribitol	Galactitol	D-Mannitol	D-Glucitol
Candida *(cont'd)*																																			
326	*C. paludigena*	v	−	−	−	−	−	−	+	−	+	v	−	+	+	+	+	+	+	−	+	+	+	−	+	+	−	−	−	+	−	−	−	−	v	−
327	*C. panamensis*	+	+	−	−	−	−	+	+	−	+	−	−	+	−	+	+	−	+	−	+	+	−	−	+	−	−	−	−	+	+	−	+	−	+	+
328	*C. panamericana*	+	+	−	−	−	−	+	+	−	+	−	−	+	−	+	+	+	+	−	+	+	n	n	+	−	−	−	−	−	+	−	+	−	+	+
329	*C. parapsilosis*	+	v	v	v	−	−	v	+	−	+	−	−	+	−	+	+	+	+	−	−	−	v	−	+	+	−	v	−	+	+	−	v	−	+	+
330	*C. pararugosa*	−	−	−	−	−	−	−	+	−	−	−	−	+	−	−	−	−	−	−	−	−	+	−	v	v	v	−	−	+	+	−	−	−	v	v
331	*C. pattaniensis*	+	−	+	−	−	−	n	+	−	+	−	−	−	−	+	+	+	+	+	+	+	−	+	+	+	−	−	−	+	+	−	−	−	+	+
332	*C. peltata*	+	+	−	−	−	−	−	+	−	+	−	−	+	−	+	+	+	+	+	+	+	+	+	+	+	+	+	−	+	+	v	+	v	+	+
333	*C. peoriensis*	+	−	+	−	−	−	+	+	−	+	+	−	−	−	+	+	+	+	−	+	+	+	+	+	−	−	−	−	+	+	−	+	−	+	+
334	*C. petrohuensis*	−	−	−	−	−	−	−	+	−	+	−	−	−	−	v	+	−	+	−	+	v	+	−	+	v	−	−	−	+	+	−	+	−	+	+
335	*C. picachoensis*	+	−	−	−	−	−	−	+	−	+	−	−	+	−	+	+	+	+	−	−	+	−	−	−	−	−	+	−	−	+	−	+	−	+	+
336	*C. piceae*	+	−	−	−	−	−	+	+	v	−	−	−	v	−	+	−	−	−	−	+	+	v	−	+	+	+	+	+	+	+	−	+	−	+	+
337	*C. picinguabensis*	+	n	n	n	n	n	n	+	−	+	−	−	−	−	+	+	+	+	−	−	−	+	−	+	−	−	−	−	−	+	−	−	+	−	+
338	*C. pignaliae*	+	−	−	−	−	−	+	+	−	+	+	−	−	−	+	+	+	+	−	−	+	+	+	+	+	−	v	+	+	+	−	+	−	+	+
339	*C. pimensis*	+	−	−	−	−	−	−	+	−	+	−	−	+	−	+	+	+	+	−	−	+	−	−	−	−	−	+	−	−	−	+	−	+	−	+
340	*C. pini*	+	−	−	−	−	−	v	+	−	−	−	−	−	−	+	−	−	−	−	−	−	−	−	+	+	−	+	+	+	−	+	+	−	+	+
341	*C. pinicola*	+	+	−	−	−	−	+	+	−	−	−	−	+	+	+	−	−	−	−	+	+	+	−	+	+	+	−	−	v	+	+	−	−	+	+
342	*C. plutei*	−	−	−	−	−	−	−	+	−	+	−	−	−	−	+	+	+	+	+	+	+	+	−	+	−	−	−	−	−	+	−	+	−	+	+
343	*C. polysorbophila*	+	+	+	+	−	−	+	+	−	+	+	−	+	−	+	+	+	−	+	+	+	+	−	+	+	+	+	+	−	+	+	−	+	+	+
344	*C. pomicola*	+	−	−	−	−	−	v	+	−	+	−	−	+	−	+	+	+	+	+	+	+	v	+	+	+	+	+	+	−	+	+	+	−	+	+
345	*C. ponderosae*	−	−	−	−	−	−	−	+	−	−	−	−	+	−	−	−	−	−	−	+	+	−	−	+	−	−	−	−	−	+	+	−	−	−	v
346	*C. populi*	+	−	−	−	−	−	+	+	−	+	−	−	−	−	+	+	+	v	−	+	+	−	+	+	+	+	+	+	−	+	+	−	+	−	+
347	*C. powellii*	+	−	−	+	−	−	−	+	−	−	−	−	+	−	−	+	−	−	−	−	−	+	−	−	−	−	+	+	−	−	+	−	−	+	+
348	*C. prunicola*	+	−	−	−	−	−	+	+	−	−	−	−	+	−	+	−	−	−	−	−	−	+	−	+	−	−	−	−	−	+	+	−	+	−	+
349	*C. pseudoglaebosa*	+	−	−	−	−	−	−	+	−	+	+	+	+	+	+	+	+	+	−	+	+	+	−	+	−	−	−	−	−	−	−	−	−	+	+
350	*C. pseudointermedia*	+	+	+	+	−	−	+	+	v	+	+	−	+	v	+	+	+	+	v	+	+	+	−	+	v	v	v	−	+	−	−	−	+	+	+
351	*C. pseudolambica*	+	−	−	−	−	−	−	+	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	v	−	−	−	−	+	−	−	−	−	−	−
352	*C. pseudorhagii*	+	+	+	−	−	+	+	+	−	+	+	−	+	−	+	+	+	+	−	+	+	v	+	+	+	v	+	−	+	+	+	+	−	+	+
353	*C. psychrophila*	−	−	−	−	−	−	−	+	−	−	−	−	+	−	+	−	−	−	−	−	−	v	−	+	+	−	−	−	+	+	+	+	v	−	+
354	*C. pyralidae*	+	−	−	−	−	−	+	+	−	−	−	−	+	−	−	−	−	−	−	−	−	+	−	+	+	−	+	−	+	+	−	−	−	+	+
355	*C. qinlingensis*	+	−	−	−	−	−	n	+	−	+	−	−	+	−	+	−	+	−	+	+	+	+	−	+	+	−	−	−	+	+	+	−	−	+	+
356	*C. quercitrusa*	+	v	v	v	−	−	−	+	−	+	−	−	+	−	v	+	+	+	−	−	−	+	−	v	−	−	+	−	+	+	−	+	−	+	+
357	*C. quercuum*	+	−	−	−	−	−	−	+	−	+	−	−	−	−	−	+	+	+	−	+	+	−	−	+	−	−	−	−	+	+	−	−	−	+	+
358	*C. railenensis*	+	+	−	−	−	−	+	+	−	+	−	−	+	−	+	+	+	v	−	+	+	+	−	+	−	−	−	−	−	+	+	−	v	−	+	+
359	*C. rancensis*	+	−	−	−	−	−	−	+	−	+	−	−	v	−	+	+	+	+	−	+	+	+	−	+	−	−	v	−	+	+	+	−	v	−	+	+
360	*C. restingae*	+	−	−	−	−	−	−	+	v	+	+	−	+	−	+	+	+	+	−	+	+	+	−	+	−	−	−	−	+	+	−	+	−	+	+
361	*C. rhagii*	+	v	+	−	−	v	+	+	−	+	+	−	+	−	+	+	+	v	−	+	+	v	v	+	v	−	v	−	+	+	v	+	−	+	+
362	*C. riodocensis*	v	n	n	n	n	n	n	+	−	−	−	−	v	−	−	−	−	n	−	−	−	+	−	−	−	−	−	−	−	+	−	−	−	+	+
363	*C. rugopelliculosa*	+	−	−	−	−	−	−	+	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	+	−	−	−	−	−
364	*C. rugosa*	−	−	−	−	−	−	−	+	−	−	−	−	v	−	−	−	−	−	−	−	−	v	−	v	−	−	−	−	+	+	−	v	−	v	v
365	*C. sagamina*	+	−	−	−	−	−	−	+	−	+	−	−	−	−	+	+	+	+	+	+	+	−	−	+	−	+	−	−	+	+	−	+	−	+	+
366	*C. saitoana*	−	−	−	−	−	−	−	+	−	+	−	−	+	−	+	+	+	+	−	−	−	+	−	+	−	−	−	−	+	+	−	−	−	+	+
367	*C. sake*	v	v	v	v	−	−	v	+	−	v	−	−	+	−	+	v	v	v	−	v	v	v	−	v	−	−	v	−	v	v	−	v	−	v	v
368	*C. salmanticensis*	+	+	+	+	−	+	+	+	+	+	+	+	+	v	+	+	+	+	−	+	+	+	−	+	v	+	−	−	+	v	−	+	−	+	v
369	*C. santamariae*	+	−	−	−	−	−	v	+	−	−	−	−	v	−	+	−	−	−	−	+	v	v	−	v	−	v	v	−	+	+	−	+	−	+	+
370	*C. santjacobensis*	+	+	−	−	−	−	+	+	−	+	+	+	+	−	+	+	+	+	−	+	+	+	v	+	+	+	+	−	+	+	+	+	−	+	+
371	*C. sanyiensis*	+	−	−	−	−	−	−	+	−	−	−	−	−	−	−	−	−	−	−	+	+	−	−	+	−	−	−	−	−	−	−	−	−	−	+
372	*C. saopaulonensis*	+	n	n	n	n	n	n	+	−	+	−	−	+	−	+	+	+	+	−	−	−	+	−	+	−	−	−	−	−	+	−	−	+	−	+
373	*C. savonica*	+	+	−	−	−	−	+	+	−	−	−	−	+	−	+	−	−	−	−	+	+	−	−	+	−	+	−	−	−	+	+	−	+	−	+
374	*C. schatavii*	+	+	−	−	−	−	+	+	−	−	−	−	+	−	+	−	−	−	−	−	−	−	−	+	−	v	+	−	+	+	+	+	−	+	+
375	*C. scorzettiae*	−	−	−	−	−	−	−	+	−	−	−	−	+	+	+	+	−	−	−	+	+	−	−	+	−	−	−	−	−	+	+	−	+	−	+
376	*C. sequanensis*	+	+	−	−	−	−	−	+	−	−	−	−	+	−	+	+	−	−	−	+	+	−	−	+	+	−	+	−	+	+	+	+	−	+	+
377	*C. sergipensis*	v	−	−	n	n	−	n	+	−	+	v	−	+	−	−	v	−	n	−	−	+	+	−	−	v	−	−	−	+	+	−	+	+	+	+
378	*C. shehatae*	+	+	−	+	−	−	+	+	−	+	v	−	+	v	+	+	+	+	+	+	+	v	−	+	v	v	+	−	+	+	v	+	−	+	+
379	*C. silvae*	+	−	−	−	−	−	−	+	−	−	−	−	v	−	−	−	−	−	−	−	−	−	−	−	−	v	−	−	+	v	−	v	−	+	+

Symbols: +, positive or weak; −, negative; v, variable (+/−, w/−); n, no data.

Growth reactions and other characteristics

	myo-Inositol	DL-Lactate	Succinate	Citrate	D-Gluconate	D-Glucosamine	*N*-Acetyl-D-glucosamine	Hexadecane	Nitrate	Nitrite	Vitamin-free	2-Keto-D-gluconate	5-Keto-D-gluconate	Saccharate	Xylitol	L-Arabinitol	Arbutin	Propane 1,2 diol	Butane 2,3 diol	Cadaverine	Creatinine	L-Lysine	Ethylamine	50% Glucose	10% NaCl/5% glucose	Starch formation	Urease	Gelatin liquefaction	Cycloheximide 0.01%	Cycloheximide 0.1%	Growth at 19°C	Growth at 25°C	Growth at 30°C	Growth at 35°C	Growth at 37°C	Growth at 40°C	Growth at 45°C	CoQ (Main component)	Mol% G + C (Ave.)	DBB
Candida (*cont'd*)																																								
326	+	−	+	+	+	+	+	−	−	−	−	+	n	n	−	n	n	n	n	+	n	+	+	−	n	−	n	−	+	+	+	+	+	n	−	−	−	9	41.5	−
327	−	−	+	+	+	+	n	n	−	−	−	+	n	n	−	−	+	−	−	+	−	+	+	+	n	−	−	n	−	−	+	+	+	−	−	−	−	n	n	−
328	−	−	+	+	+	+	n	n	−	−	v	+	n	n	−	n	+	−	−	+	−	+	+	+	n	−	−	n	−	−	+	+	+	+	n	−	−	n	n	−
329	−	−	+	+	v	v	+	+	−	−	−	+	n	n	v	n	n	n	n	+	n	+	+	+	n	−	n	−	v	−	+	+	+	+	+	n	n	9	40.5	−
330	−	+	+	−	−	−	−	−	−	−	−	−	n	n	v	n	n	n	n	+	n	+	+	−	n	−	n	−	−	−	+	+	+	n	v	n	n	9	48.3	−
331	−	+	+	+	+	−	−	−	−	−	−	−	−	−	+	+	n	+	+	+	n	+	+	n	n	−	−	−	n	−	+	+	+	+	−	−	−	7	43.5	−
332	−	−	+	+	−	+	+	−	−	−	−	−	n	n	+	n	n	n	n	+	n	+	+	−	n	−	n	−	+	+	+	+	+	+	+	n	n	7	n	−
333	−	+	+	+	+	−	−	−	+	+	−	−	n	n	+	n	n	n	n	+	n	+	−	−	n	−	n	−	−	−	+	+	+	n	−	−	−	n	n	−
334	−	v	+	v	−	v	+	−	−	−	−	−	n	n	−	n	n	n	n	+	n	+	+	−	n	−	n	−	+	+	+	+	−	−	−	−	−	9	44.0	−
335	−	−	+	v	+	+	n	n	−	−	n	−	n	n	+	−	+	−	−	+	−	−	+	+	n	−	−	n	−	−	+	+	+	−	−	−	−	n	n	−
336	−	−	v	−	−	−	−	−	−	−	−	−	n	n	+	n	n	n	n	+	n	+	+	−	n	−	n	−	+	+	+	+	+	n	−	−	−	n	n	−
337	−	+	+	+	v	−	−	+	−	−	n	+	−	n	+	n	n	n	n	+	n	+	+	+	n	−	n	n	+	−	+	+	+	+	−	−	−	n	n	−
338	−	−	+	−	+	−	−	+	+	+	−	−	n	n	+	n	n	n	n	+	n	+	+	−	n	−	n	−	+	+	+	+	v	n	−	−	−	7	42.7	−
339	−	−	+	+	+	+	n	n	−	−	n	−	n	n	+	−	+	−	−	+	−	−	+	−	n	−	−	n	−	−	+	+	+	−	−	−	−	n	n	−
340	−	−	−	+	−	−	−	+	−	−	−	−	n	n	+	n	n	n	n	+	n	+	+	−	n	−	n	−	+	+	+	+	−	−	−	−	−	7	37.3	−
341	−	−	+	+	+	+	+	−	−	n	−	+	+	−	n	n	n	n	n	+	n	n	n	n	n	−	n	−	+	+	+	+	+	n	−	−	−	n	n	−
342	−	−	+	+	−	−	n	n	−	n	−	+	n	n	−	−	+	−	−	+	−	+	+	−	n	−	−	n	−	−	+	+	+	−	−	−	−	n	n	−
343	+	+	+	+	+	+	+	−	−	n	−	−	+	−	n	n	n	n	n	+	n	n	n	n	n	−	n	−	+	+	+	+	+	n	−	−	−	n	n	−
344	−	−	+	+	+	+	+	−	+	+	−	−	n	n	+	n	n	n	n	+	n	+	+	+	n	−	n	−	+	+	+	+	+	n	−	−	−	n	n	−
345	−	+	+	+	+	−	−	−	−	−	−	−	n	n	−	n	n	n	n	+	n	+	+	−	n	−	n	−	−	−	+	+	+	n	−	−	−	n	n	−
346	−	−	+	+	+	+	+	−	+	+	−	−	n	n	+	n	n	n	n	+	n	+	+	−	n	−	n	−	+	+	+	+	+	n	−	−	−	8	38.2	−
347	−	−	+	+	−	−	−	−	−	−	−	−	n	n	v	n	n	n	n	+	n	+	+	+	n	−	n	−	−	−	+	+	+	+	+	n	n	n	n	−
348	−	−	−	+	+	+	+	−	−	+	−	+	n	n	+	n	n	n	n	+	n	−	+	−	n	−	n	−	−	−	+	+	+	+	+	n	n	n	n	−
349	−	+	+	+	−	+	+	+	−	−	−	+	n	n	+	n	n	n	n	+	n	+	+	−	n	−	n	−	−	−	+	+	+	n	−	−	−	9	34.0	−
350	−	+	+	+	+	+	+	+	−	−	−	+	n	n	+	n	n	n	n	+	n	+	+	+	n	−	n	−	v	−	+	+	+	n	v	n	n	9	44.9	−
351	−	+	+	−	−	v	−	−	−	−	+	−	n	n	−	n	n	n	n	+	n	+	+	−	n	−	n	−	−	−	+	+	+	n	−	−	−	7	31.1	−
352	−	v	+	−	+	+	+	+	−	n	+	+	−	−	n	n	n	n	n	+	n	n	n	n	n	−	n	+	−	−	+	+	+	n	v	n	n	n	n	−
353	−	−	−	−	−	−	n	n	−	−	−	+	n	n	+	n	n	n	n	−	n	−	−	+	n	−	n	n	−	−	−	−	−	−	−	−	−	9	36.1	−
354	−	−	+	+	+	+	+	+	−	−	+	+	n	n	+	n	n	n	n	+	n	+	+	−	n	−	n	−	−	−	+	+	+	+	+	n	n	n	n	−
355	−	+	+	+	n	−	n	−	−	−	−	n	n	n	n	n	n	n	n	+	n	+	+	n	n	−	−	n	n	n	+	+	+	−	−	−	−	n	n	−
356	−	+	+	v	+	+	+	v	−	−	−	+	n	n	+	n	n	n	n	+	n	+	+	v	n	−	n	−	+	−	+	+	+	n	−	−	−	9	40.7	−
357	−	+	+	+	+	−	−	−	−	−	−	−	n	n	+	n	n	n	n	+	n	+	+	−	n	−	n	−	−	−	+	+	+	n	−	−	−	7	38.9	−
358	−	+	+	+	+	+	+	+	−	−	−	+	n	n	+	n	n	n	n	+	n	+	+	+	n	−	n	−	+	+	+	+	+	n	−	−	−	n	41.8	−
359	−	−	+	−	+	−	+	+	−	−	−	+	n	n	+	n	n	n	n	+	n	+	+	+	n	−	n	+	−	−	+	+	v	n	−	−	−	n	45.9	−
360	−	−	v	v	−	+	+	+	−	−	−	+	n	n	+	n	n	n	n	+	n	+	+	−	n	−	n	−	−	−	+	+	+	n	v	n	n	n	n	−
361	−	v	+	−	v	+	+	+	−	−	v	+	n	n	+	n	n	n	n	+	n	+	+	v	n	−	n	−	−	−	+	+	+	n	−	−	−	8	42.4	−
362	−	−	−	−	−	−	−	−	−	−	−	−	n	n	−	n	n	n	n	+	n	+	+	−	n	−	−	n	v	n	+	+	+	+	+	−	−	n	n	−
363	−	+	+	−	−	+	−	−	−	−	+	−	n	n	−	n	n	n	n	+	n	+	+	−	n	−	n	−	−	−	+	+	+	+	+	n	n	7	30.0	−
364	−	v	v	v	v	−	+	−	−	−	−	−	n	n	v	n	n	n	n	+	n	+	+	+	n	−	n	−	−	−	+	+	+	+	+	n	n	9	50.5	−
365	−	−	+	+	+	+	+	+	−	−	−	+	n	n	−	n	n	n	n	+	n	+	+	−	n	−	n	−	+	+	+	+	+	n	−	−	−	9	40.5	−
366	−	+	+	−	−	−	+	−	−	−	+	+	n	n	−	n	n	n	n	+	n	+	+	−	n	−	n	−	−	−	+	+	+	n	−	−	−	9	36.9	−
367	−	v	+	v	v	v	+	v	−	−	v	v	n	n	−	n	n	n	n	v	n	v	v	−	n	−	n	−	−	−	v	v	v	n	−	−	−	9	39.2	−
368	−	+	+	v	+	+	+	−	−	−	−	+	n	n	+	n	n	n	n	+	n	+	+	+	n	−	n	−	+	+	+	+	+	n	−	−	−	9	45.5	−
369	−	v	+	+	+	+	+	−	−	−	−	+	n	n	v	n	n	n	n	+	n	+	+	v	n	−	n	−	v	v	+	+	+	n	−	−	−	9	38.8	−
370	+	v	+	+	−	+	+	−	−	−	−	+	n	n	−	n	n	n	n	+	n	+	+	−	n	−	n	−	+	+	+	+	v	n	−	−	−	9	48.5	−
371	−	+	+	−	−	−	−	n	+	n	n	−	−	n	n	n	n	+	+	−	−	−	−	−	n	−	−	n	−	−	+	+	+	−	−	−	−	n	n	−
372	−	+	+	+	+	−	−	+	−	−	n	+	−	n	+	n	n	n	n	+	n	+	+	v	n	n	−	n	−	−	+	+	+	+	−	−	−	n	n	−
373	−	−	+	+	−	−	+	−	−	−	+	+	n	n	+	n	n	n	n	+	n	+	+	−	n	−	n	−	+	−	+	+	+	n	−	−	−	9	48.0	−
374	−	−	+	+	+	+	+	+	−	−	−	+	n	n	+	n	n	n	n	+	n	+	+	v	n	−	n	−	+	+	+	+	+	n	v	n	n	n	44.2	−
375	−	+	+	+	+	−	+	+	−	−	n	+	−	n	−	n	n	+	+	+	−	+	+	n	n	−	−	n	+	−	+	+	+	−	−	−	−	n	n	−
376	−	−	+	−	+	−	+	+	−	−	−	+	n	n	+	n	n	n	n	+	n	+	+	+	n	−	n	+	−	−	+	+	−	−	−	−	−	8	39.6	−
377	−	−	−	−	−	−	−	−	−	−	n	n	n	n	+	n	n	n	n	+	n	+	+	−	n	−	−	n	−	−	+	+	+	+	n	n	n	n	n	−
378	−	−	+	+	v	v	+	+	−	−	−	+	n	n	v	n	n	n	n	+	n	+	+	−	n	−	n	−	v	v	n	n	+	n	−	−	−	9	43.6	−
379	−	v	+	v	v	−	−	−	−	−	−	−	n	n	−	n	n	n	n	+	n	+	+	−	n	−	n	−	−	−	+	+	+	n	v	n	n	7	41.7	−

Symbols: +, positive or weak; −, negative; v, variable (+/−, w/−); n, no data.

Ln. no.	Species	Fermentation: Glucose	Galactose	Sucrose	Maltose	Lactose	Raffinose	Trehalose	Growth: Glucose	Inulin	Sucrose	Raffinose	Melibiose	Galactose	Lactose	Trehalose	Maltose	Melezitose	Methyl-α-D-glucoside	Soluble Starch	Cellobiose	Salicin	L-Sorbose	L-Rhamnose	D-Xylose	L-Arabinose	D-Arabinose	D-Ribose	Methanol	Ethanol	Glycerol	Erythritol	Ribitol	Galactitol	D-Mannitol	D-Glucitol
Candida *(cont'd)*																																				
380	*C. silvanorum*	+	+	+	+	−	+	+	+	−	+	+	+	+	−	+	+	+	+	+	+	+	−	+	+	+	−	+	−	+	+	+	+	−	+	+
381	*C. silvatica*	−	−	−	−	−	−	−	+	−	−	−	−	−	−	+	−	−	−	−	−	−	−	−	−	−	−	−	−	+	+	−	+	−	+	+
382	*C. silvicultrix*	+	+	+	+	−	+	−	+	−	+	+	+	+	−	+	+	+	+	+	+	+	−	−	+	+	+	+	−	+	+	+	+	−	+	+
383	*C. sinolaborantium*	+	+	−	−	−	−	+	+	−	+	−	−	+	+	+	+	+	−	+	+	+	+	+	+	+	+	+	−	+	+	+	+	+	+	+
384	*C. sithepensis*	+	−	−	−	−	−	+	+	−	−	−	−	+	−	+	−	−	−	+	+	+	−	+	+	−	+	+	+	+	+	+	+	−	+	+
385	*C. smithsonii*	+	+	−	−	−	−	+	+	−	+	−	−	+	−	+	+	+	−	+	+	+	−	−	+	−	−	v	−	−	+	+	+	−	+	+
386	*C. sojae*	+	+	+	−	−	−	n	+	−	+	−	−	+	−	+	+	+	+	+	+	v	+	−	+	−	−	v	−	+	+	+	+	−	+	+
387	*C. solani*	+	−	−	−	−	−	−	+	−	+	−	−	−	−	+	+	+	+	−	+	+	v	−	+	−	−	−	−	+	+	−	−	−	+	v
388	*C. sonorensis*	+	−	−	−	−	−	−	+	−	−	−	−	−	−	−	−	−	−	−	+	+	−	−	+	+	−	v	+	+	+	−	+	−	+	+
389	*C. sophiae-reginae*	+	+	−	−	−	−	+	+	−	+	−	−	+	−	+	+	+	+	−	−	−	+	−	−	−	−	+	−	+	+	+	+	−	+	+
390	*C. sorbophila*	+	n	n	n	n	n	n	+	−	−	−	−	+	−	−	−	−	−	−	−	−	+	−	+	v	−	−	−	v	−	−	−	−	+	+
391	*C. sorbosivorans*	+	−	+	−	−	−	−	+	−	+	+	−	+	−	−	−	−	−	−	v	+	+	−	−	−	−	v	−	v	+	−	−	−	+	+
392	*C. sorboxylosa*	+	−	−	−	−	−	−	+	−	−	−	−	−	−	−	−	−	−	−	−	−	+	−	+	−	−	−	−	+	+	−	−	−	−	−
393	*C. spandovensis*	+	+	+	−	−	v	−	+	−	+	+	−	+	−	−	−	−	−	−	−	−	+	−	v	+	−	−	−	+	+	−	+	+	+	+
394	*C. spencermartinsiae*	+	+	+	+	−	+	v	+	−	+	−	−	+	−	+	+	+	−	+	+	+	+	+	+	+	+	+	−	+	+	+	+	−	+	+
395	*C. stellata*	+	−	+	−	−	+	−	+	−	+	+	−	−	−	−	−	−	−	−	−	−	v	−	−	−	−	−	−	−	−	−	−	−	−	−
396	*C. stellimalicola*	+	n	n	n	n	n	n	+	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	+	−	+	−	−	+	+	−	−	−	+	+
397	*C. stri*	+	+	−	−	−	−	+	+	−	+	−	−	+	−	+	+	+	+	−	+	+	−	−	−	−	−	−	−	+	+	−	+	−	+	+
398	*C. subhashii*	−	−	−	−	−	−	−	+	−	+	−	−	+	−	−	+	+	+	−	+	+	−	−	+	+	−	−	n	n	−	−	+	−	−	−
399	*C. succiphila*	+	+	−	−	−	−	+	+	v	−	−	−	+	−	+	−	−	−	−	+	+	+	+	+	+	+	+	+	+	+	+	+	v	+	+
400	*C. suecica*	v	−	−	−	−	−	−	+	−	+	−	−	−	−	+	+	−	+	−	v	v	+	−	+	−	−	−	−	+	+	−	+	−	+	+
401	*C. suzukii*	−	−	−	−	−	−	−	+	−	−	−	−	+	−	+	−	−	−	−	−	−	+	+	+	+	−	+	+	+	+	+	+	−	+	+
402	*C. takamatsizukensis*	+	+	−	−	−	−	+	+	n	+	−	−	+	−	+	+	−	−	−	+	+	+	+	+	+	+	+	−	+	+	+	+	−	+	+
403	*C. taliae*	+	+	−	−	−	−	+	+	−	+	−	−	+	−	+	+	+	+	−	+	+	n	n	+	−	+	−	−	+	+	+	+	−	+	+
404	*C. tammaniensis*	+	+	−	−	−	−	+	+	−	+	−	−	+	−	+	+	+	+	−	+	+	−	+	+	+	+	+	−	+	+	+	+	−	+	+
405	*C. tanzawaensis*	+	−	−	−	−	−	+	+	−	+	−	−	+	−	+	+	+	+	−	+	+	−	−	−	−	−	−	−	+	+	−	+	−	+	+
406	*C. tartarivorans*	+	+	+	+	−	+	+	+	−	+	+	+	+	+	+	+	+	+	+	+	+	+	−	+	+	+	+	−	+	+	+	+	+	+	+
407	*C. taylori*	+	+	+	+	+	−	+	+	−	+	−	−	+	−	+	+	+	+	−	+	+	+	+	+	+	+	+	−	+	+	+	+	−	+	+
408	*C. temnochilae*	+	+	−	−	−	−	+	+	−	+	−	−	+	−	+	+	+	+	−	+	+	−	+	+	+	+	+	−	+	+	+	+	−	+	+
409	*C. tenuis*	v	v	v	v	−	−	v	+	−	+	−	−	+	v	+	+	v	+	v	+	+	v	+	+	v	+	+	−	+	+	v	+	−	+	v
410	*C. tepae*	−	−	−	−	−	−	−	+	−	+	−	−	v	−	v	+	−	−	−	v	v	+	−	+	−	−	−	−	v	v	−	−	−	v	+
411	*C. terraborum*	+	+	+	+	−	−	+	+	−	+	−	−	+	−	+	+	+	+	−	+	+	n	n	+	−	−	−	−	+	+	−	+	−	+	+
412	*C. tetrigidarum*	+	+	+	+	−	−	+	+	−	+	−	−	+	−	+	+	+	+	−	−	−	−	−	+	+	−	−	−	+	+	−	+	−	+	+
413	*C. thaimueangensis*	−	−	−	−	−	−	−	+	−	−	−	−	−	−	−	−	−	n	n	−	n	−	−	+	−	−	−	−	+	+	−	n	−	−	n
414	*C. tibetensis*	+	−	−	−	−	−	n	+	−	+	−	−	+	−	+	+	+	+	−	+	+	−	−	+	+	+	+	−	+	+	−	+	−	+	+
415	*C. tilneyi*	+	n	n	n	n	n	n	+	−	−	−	−	+	−	−	−	−	−	−	−	−	+	−	−	−	−	−	−	−	+	−	+	−	+	+
416	*C. tolerans*	+	n	n	n	n	n	n	+	−	+	v	−	+	−	+	+	−	−	−	−	−	+	−	+	+	−	+	−	+	+	−	+	+	+	+
417	*C. torresii*	+	−	−	−	−	−	+	+	−	−	−	−	+	−	+	−	−	−	−	+	+	v	−	+	+	−	+	−	+	+	−	v	−	+	+
418	*C. transvaalensis*	+	+	−	−	−	−	−	+	−	+	+	+	+	−	+	+	+	+	−	+	+	+	−	+	+	+	+	−	+	+	+	+	+	+	+
419	*C. tritomae*	+	+	−	+	−	−	+	+	−	+	−	−	+	−	+	+	+	+	v	+	+	−	−	+	−	−	+	−	+	+	−	+	−	+	+
420	*C. tropicalis*	+	+	v	+	−	−	+	+	−	v	−	−	+	−	+	+	v	v	+	v	v	v	−	+	−	−	v	−	+	v	−	v	−	+	+
421	*C. trypodendroni*	v	−	−	−	−	−	−	+	−	+	−	−	+	−	+	+	+	+	−	+	+	−	+	+	+	+	v	−	+	+	+	+	−	+	+
422	*C. tsuchiyae*	+	−	+	+	−	+	+	+	−	+	+	−	−	−	+	+	+	+	+	−	−	+	−	−	−	−	−	−	+	+	−	+	−	+	+
423	*C. tumulicola*	+	+	−	−	−	−	−	+	n	+	−	−	+	+	+	+	v	+	−	+	+	+	−	+	+	+	+	−	+	+	+	+	−	+	+
424	*C. ubatubensis*	+	n	n	n	n	n	n	+	−	+	−	−	+	−	+	+	+	+	−	+	+	+	+	+	−	−	+	−	+	+	+	+	−	+	+
425	*C. ulmi*	+	−	−	−	−	−	−	+	−	+	−	−	−	−	+	+	+	+	−	+	+	−	+	+	−	−	−	−	+	+	−	+	−	+	+
426	*C. vaccinii*	+	−	+	−	−	v	−	+	−	+	+	−	v	−	−	−	−	−	−	+	+	+	−	−	−	−	−	−	−	+	−	−	−	+	+
427	*C. vadensis*	−	−	−	−	−	−	−	+	−	+	−	−	+	−	+	+	+	+	−	+	+	−	−	+	−	−	v	−	+	+	−	+	−	+	+
428	*C. valdiviana*	+	−	−	−	−	−	−	+	−	+	+	+	+	v	+	+	+	+	−	+	+	+	−	+	+	v	−	−	+	+	−	+	v	+	+
429	*C. vanderwaltii*	−	−	−	−	−	−	−	+	−	v	−	−	+	−	+	−	−	−	−	−	−	+	−	+	+	+	+	−	−	+	−	+	+	+	+
430	*C. vartiovaarae*	+	−	+	v	−	−	−	+	−	+	−	−	−	−	+	+	+	+	−	+	+	−	−	+	−	−	−	−	+	+	−	−	−	+	+
431	*C. versatilis*	+	+	v	v	v	v	v	+	−	−	v	v	+	−	+	v	−	−	−	+	v	−	−	−	−	−	−	−	+	+	−	−	−	+	−
432	*C. viswanathii*	+	+	v	+	−	−	+	+	−	+	−	−	+	−	+	+	+	+	+	+	+	−	−	+	v	−	−	−	+	+	−	+	−	+	+
433	*C. wickerhamii*	+	−	−	−	−	−	v	+	−	−	−	−	+	−	v	−	−	−	−	+	+	−	+	+	+	v	v	−	+	+	−	+	−	+	+

Symbols: +, positive or weak; −, negative; v, variable (+/−, w/−); n, no data.

Growth reactions and other characteristics

	myo-Inositol	DL-Lactate	Succinate	Citrate	D-Gluconate	D-Glucosamine	*N*-Acetyl-D-glucosamine	Hexadecane	Nitrate	Nitrite	Vitamin-free	2-Keto-D-gluconate	5-Keto-D-gluconate	Saccharate	Xylitol	L-Arabinitol	Arbutin	Propane 1,2 diol	Butane 2,3 diol	Cadaverine	Creatinine	L-Lysine	Ethylamine	50% Glucose	10% NaCl/5% glucose	Starch formation	Urease	Gelatin liquefaction	Cycloheximide 0.01%	Cycloheximide 0.1%	Growth at 19°C	Growth at 25°C	Growth at 30°C	Growth at 35°C	Growth at 37°C	Growth at 40°C	Growth at 45°C	CoQ (Main component)	Mol% G + C (Ave.)	DBB
Candida *(cont'd)*																																								
380	−	−	+	+	+	−	+	+	−	−	v	−	n	n	+	n	n	n	n	+	n	+	+	+	n	−	n	−	+	−	+	+	+	+	+	n	n	8	41.1	−
381	−	−	+	−	−	+	+	−	−	−	−	−	n	n	−	n	n	n	n	+	n	+	+	−	n	−	n	−	−	−	+	+	+	+	+	n	n	9	55.6	−
382	−	+	+	+	+	−	−	−	−	−	+	−	n	n	+	n	n	n	n	+	n	+	+	+	n	−	n	−	−	−	+	+	+	+	+	n	n	7	36.6	−
383	−	+	+	+	+	−	n	n	−	−	−	+	n	n	+	n	+	+	−	+	−	+	+	+	n	−	−	n	+	+	+	+	+	−	−	−	−	n	n	−
384	−	+	+	+	+	n	−	n	−	−	−	n	n	n	n	n	n	n	n	+	n	+	+	+	n	−	−	+	+	+	+	+	+	+	+	+	n	7	n	−
385	−	+	+	+	v	+	n	n	−	−	−	−	n	n	+	v	+	v	−	+	−	+	+	+	n	−	−	n	+	+	+	+	+	−	−	−	−	n	n	−
386	−	v	+	+	−	+	+	+	−	−	−	+	n	n	−	n	n	n	n	+	n	+	+	−	n	−	n	−	+	+	+	+	+	+	+	n	n	9	31.0	−
387	−	+	+	−	+	−	−	−	−	−	−	+	n	n	+	n	n	n	n	+	n	+	+	−	n	−	n	−	−	−	+	+	+	n	−	−	−	7	41.9	−
388	−	+	+	−	−	−	−	−	−	−	−	−	n	n	+	n	n	n	n	+	n	+	+	−	n	−	n	−	+	+	+	+	+	+	+	n	n	7	36.1	−
389	−	−	+	+	−	−	+	−	−	−	−	+	n	n	+	n	n	n	n	+	n	+	+	−	n	−	n	−	−	−	+	+	−	−	−	−	−	9	39.3	−
390	−	+	+	−	−	−	−	+	−	−	−	+	n	n	+	n	n	n	n	+	n	+	+	−	n	−	n	+	+	+	+	+	+	n	v	n	n	9	50.0	−
391	−	v	+	+	v	−	−	−	+	+	−	v	n	n	+	n	n	n	n	+	n	+	+	v	n	−	n	v	+	+	+	+	+	+	+	n	n	n	n	−
392	−	+	+	+	−	−	−	−	−	−	−	−	n	n	+	n	n	n	n	+	n	+	+	v	n	−	n	−	−	−	+	+	+	n	v	n	n	7	40.3	−
393	−	+	+	+	−	−	−	−	−	−	−	v	n	n	+	n	n	n	n	+	n	+	+	+	n	−	n	−	−	−	+	+	v	n	−	−	−	9	52.7	−
394	−	−	−	+	+	+	+	−	−	n	−	−	−	−	n	n	n	n	n	n	n	n	n	n	n	−	−	n	n	n	+	+	+	+	+	n	n	n	n	−
395	−	−	−	−	−	−	−	−	−	−	−	−	n	n	−	n	n	n	n	−	n	+	−	v	n	−	n	−	−	−	+	+	+	n	−	−	−	8	42.0	−
396	−	+	+	−	+	−	+	−	−	−	−	−	n	n	−	n	n	n	n	+	n	+	+	−	n	−	n	−	−	−	+	+	+	+	+	n	n	7	40.7	−
397	−	−	+	+	+	−	n	n	−	−	−	+	n	n	−	−	+	−	−	+	−	+	+	−	n	−	−	n	+	+	+	+	+	−	−	−	−	n	n	−
398	−	−	−	−	−	−	n	n	−	−	+	n	−	n	−	−	+	−	−	+	−	+	+	n	n	n	n	n	n	n	+	+	+	+	+	+	−	n	n	−
399	−	v	v	−	v	+	+	−	−	−	−	v	n	n	+	n	n	n	n	−	n	−	+	−	n	−	n	−	+	v	+	+	+	+	+	n	n	7	40.6	−
400	−	−	−	v	−	−	v	−	−	−	−	+	n	n	−	n	n	n	n	−	n	−	−	−	n	−	n	−	−	−	+	+	−	−	−	−	−	9	42.6	−
401	−	+	+	−	−	+	+	−	+	+	−	−	n	n	+	+	n	+	−	+	−	+	+	−	n	−	−	n	+	+	+	+	+	−	−	−	−	n	n	−
402	−	−	+	+	+	+	+	−	−	−	−	+	−	n	+	+	+	−	−	+	−	+	+	−	n	−	−	n	+	+	+	+	+	−	−	−	−	9	36.7	−
403	−	−	+	+	+	+	n	n	−	−	−	+	n	n	+	n	+	−	−	+	−	+	+	+	n	−	−	n	−	−	+	+	+	+	n	−	−	n	n	−
404	−	+	+	+	+	+	+	+	−	−	−	+	n	n	+	n	n	n	n	+	n	+	+	−	n	−	n	−	+	+	+	+	+	n	−	−	−	n	n	−
405	−	−	+	+	+	−	+	−	−	−	−	+	n	n	−	n	n	n	n	+	n	+	+	−	n	−	n	−	+	−	+	+	+	n	−	−	−	9	44.6	−
406	+	−	+	+	+	+	+	+	−	−	−	+	n	n	+	n	n	n	n	+	n	+	+	−	n	−	n	−	+	+	+	+	+	+	+	n	n	n	40.1	−
407	−	−	+	+	+	+	+	−	−	n	−	+	−	−	n	n	n	n	n	n	n	n	n	n	n	−	−	n	n	n	+	+	n	n	−	−	−	n	n	−
408	−	v	+	+	+	+	n	n	−	n	−	+	n	n	+	n	+	v	−	+	−	+	+	+	n	−	−	n	+	+	+	+	+	−	−	−	−	n	n	−
409	−	v	+	+	v	v	+	v	−	−	−	+	n	n	v	n	n	n	n	+	n	+	+	−	n	−	n	v	v	v	+	+	v	n	−	−	−	9	43.8	−
410	−	+	v	v	−	−	+	−	−	−	−	−	n	n	−	n	n	n	n	v	n	+	+	−	n	−	n	−	+	+	+	+	−	−	−	−	−	9	40.0	−
411	−	−	+	+	+	+	n	n	−	n	−	+	n	n	−	n	+	+	−	+	−	+	+	+	n	−	−	n	−	−	+	+	+	−	−	−	−	n	n	−
412	−	+	−	+	+	−	n	n	−	n	−	+	n	n	−	−	−	−	−	+	−	+	+	+	n	−	−	n	+	+	+	+	+	+	+	−	−	n	n	−
413	−	+	+	−	−	n	n	n	−	−	−	−	n	n	n	n	n	n	n	+	n	+	+	n	−	−	−	n	−	−	+	+	+	+	+	n	n	7	n	−
414	−	−	+	+	n	+	n	+	−	−	+	n	n	n	n	n	n	n	n	+	n	+	+	n	n	−	−	n	n	n	+	+	−	−	−	−	−	9	n	−
415	−	−	+	+	+	−	−	+	−	−	−	+	n	n	v	n	n	n	n	+	n	+	+	+	n	−	n	+	−	−	+	+	+	n	−	−	−	n	n	−
416	−	+	+	+	+	+	+	+	−	−	+	+	n	n	+	n	n	n	n	+	n	+	+	+	n	−	n	−	+	−	+	+	+	+	+	n	n	n	n	−
417	−	−	+	+	+	v	+	−	−	−	−	+	n	n	+	n	n	n	n	+	n	+	+	+	n	−	n	−	−	−	+	+	+	n	−	−	−	9	51.8	−
418	+	+	+	+	−	+	+	−	−	n	−	+	+	−	n	n	n	n	n	+	n	n	n	n	n	−	n	−	+	+	+	+	+	n	−	−	−	n	n	−
419	−	v	+	+	+	+	n	n	−	−	−	+	n	n	+	−	+	v	−	+	−	+	+	v	n	−	−	n	−	−	+	+	+	+	n	−	−	n	n	−
420	−	v	+	v	v	v	+	+	−	−	v	+	n	n	v	n	n	n	n	+	n	+	+	v	n	−	n	−	+	+	+	+	+	+	+	n	n	9	34.7	−
421	−	−	+	+	+	−	+	−	−	−	−	+	n	n	−	n	n	n	n	+	n	+	+	−	n	−	n	−	−	−	+	+	+	n	−	−	−	n	n	−
422	−	−	+	+	+	+	−	−	−	−	−	+	n	n	+	n	n	n	n	+	n	+	+	+	n	−	n	−	+	−	+	+	−	−	−	−	−	9	47.5	−
423	−	v	+	+	+	+	+	−	−	−	−	+	−	n	+	+	+	+	−	+	−	+	+	−	n	−	−	n	+	+	+	+	+	+	+	n	n	9	43.1	−
424	−	−	−	−	+	−	+	+	−	n	n	−	−	n	+	+	n	n	n	+	n	+	+	−	n	n	−	n	−	−	+	+	+	+	−	−	−	n	n	−
425	−	−	+	−	+	−	−	−	+	+	−	−	n	n	−	n	n	n	n	+	n	+	+	−	n	−	n	−	−	−	+	+	+	+	+	n	n	n	n	−
426	−	−	+	+	+	−	−	+	+	+	−	+	n	n	+	n	n	n	n	+	n	+	+	+	n	−	n	−	+	−	+	+	+	n	v	n	n	9	52.0	−
427	−	−	+	+	+	+	+	+	−	n	n	+	−	n	−	n	n	−	−	+	−	+	+	n	n	−	−	n	+	−	+	+	+	−	−	−	−	n	n	−
428	+	−	+	+	+	+	+	+	+	+	−	+	n	n	−	n	n	n	n	+	n	+	+	−	n	−	n	−	+	+	+	+	+	n	v	n	n	9	55.3	−
429	−	−	+	+	−	−	−	−	+	+	−	v	n	n	+	n	n	n	n	+	n	+	+	+	n	−	n	+	+	+	+	+	+	n	−	−	−	9	49.7	−
430	−	+	+	v	+	−	−	−	+	+	+	+	n	n	+	n	n	n	n	+	n	+	+	−	n	−	n	−	−	−	+	+	+	n	−	−	−	7	48.8	−
431	−	−	+	−	−	−	−	−	+	+	−	+	n	n	v	n	n	n	n	+	n	v	v	+	n	−	n	−	v	v	+	+	+	n	−	−	−	9	48.9	−
432	−	+	+	+	+	+	+	+	−	−	−	+	n	n	v	n	n	n	n	+	n	+	+	v	n	−	n	v	+	+	+	+	+	+	+	n	n	9	45.9	−
433	−	−	+	+	v	v	+	−	+	+	−	v	n	n	−	n	n	n	n	+	n	+	+	−	n	−	n	−	+	+	+	+	+	n	−	−	−	7	38.1	−

Symbols: +, positive or weak; −, negative; v, variable (+/−, w/−); n, no data.

Ln. no.	Species	Fermentation: Glucose	Galactose	Sucrose	Maltose	Lactose	Raffinose	Trehalose	Growth reactions and other characteristics: Glucose	Inulin	Sucrose	Raffinose	Melibiose	Galactose	Lactose	Trehalose	Maltose	Melezitose	Methyl-α-D-glucoside	Soluble Starch	Cellobiose	Salicin	L-Sorbose	L-Rhamnose	D-Xylose	L-Arabinose	D-Arabinose	D-Ribose	Methanol	Ethanol	Glycerol	Erythritol	Ribitol	Galactitol	D-Mannitol	D-Glucitol
	Candida *(cont'd)*																																			
434	*C. wounanorum*	+	+	−	−	−	−	+	+	−	+	−	−	+	−	+	+	+	+	−	+	+	n	n	+	−	−	−	−	+	+	−	+	−	+	+
435	*C. wyomingensis*	+	−	−	−	−	−	−	+	−	−	−	−	−	−	+	−	−	−	−	+	+	−	+	+	−	+	v	−	+	+	−	v	−	+	+
436	*C. xylopsoci*	+	−	−	−	−	−	+	+	−	−	−	−	+	−	v	−	−	−	−	+	−	−	−	+	−	−	−	−	+	+	−	−	−	+	+
437	*C. yuanshanicus*	+	−	−	−	−	−	−	+	−	+	−	−	−	−	+	+	+	+	−	+	+	−	−	+	+	−	−	−	−	+	−	−	−	+	−
438	*C. yuchorum*	+	+	−	−	−	−	+	+	−	+	−	−	+	−	+	+	−	+	−	+	+	n	n	+	−	−	−	−	−	+	−	+	−	+	+
439	*C. zemplinina*	+	−	+	−	−	+	n	+	−	v	v	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−
440	*C. zeylanoides*	−	−	−	−	−	−	−	+	−	−	−	−	−	−	v	−	−	−	−	v	+	+	−	−	−	−	−	−	v	+	−	v	−	+	+
441	***Cephaloascus***																																			
442	*C. albidus*	+	+	−	−	−	−	−	+	−	−	+	+	+	−	+	−	−	−	−	+	+	+	−	+	+	v	−	−	+	+	−	+	−	+	+
443	*C. fragrans*	−	−	−	−	−	−	−	+	−	−	−	−	+	−	v	−	−	−	v	−	−	v	−	+	+	−	−	−	+	+	−	+	−	+	+
444	***Chionosphaera***																																			
445	*C. apobasidialis*	−	−	−	−	−	−	−	+	−	−	−	−	−	−	+	+	−	−	+	−	−	v	−	v	v	−	−	−	+	−	−	+	−	+	v
446	*C. cuniculicola*	−	−	−	−	−	−	−	+	+	−	−	+	+	−	v	−	−	−	v	−	v	+	−	−	+	n	−	+	+	+	−	v	−	+	+
447	***Citeromyces***																																			
448	*C. matritensis*	+	−	+	v	−	+	v	+	v	+	+	−	−	−	+	+	−	+	−	−	−	+	−	−	−	v	−	−	+	+	−	v	−	+	+
449	*C. siamensis*	+	−	+	+	−	v	v	+	−	+	+	−	−	−	+	+	−	+	−	−	−	−	−	−	−	−	−	−	−	+	+	−	+	−	+	+
450	***Clavispora***																																			
451	*C. lusitaniae*	+	v	v	v	−	−	v	+	−	v	−	−	v	−	+	v	v	v	−	+	v	+	+	+	−	v	v	−	+	+	−	v	−	+	v
452	*C. opuntiae*	+	+	+	+	−	−	+	+	−	+	−	−	+	−	+	+	+	+	−	+	+	+	−	+	−	−	−	−	+	+	−	+	−	+	+
453	***Colacogloea***																																			
454	*C. papilionacea*	−	−	−	−	−	−	−	+	−	−	−	−	+	−	+	+	−	−	−	−	−	−	−	−	−	−	−	−	−	+	+	−	−	+	−
455	*C. peniophorae*	−	−	−	−	−	−	−	+	−	−	−	−	−	−	+	−	−	−	−	−	−	−	−	−	−	−	v	−	−	v	−	−	−	+	+
456	***Cryptococcus***																																			
457	*C. adeliensis*	−	−	−	−	−	−	−	+	−	+	+	−	+	+	+	+	+	−	+	+	+	−	+	+	+	−	−	−	+	−	−	−	v	+	+
458	*C. aerius*	−	−	−	−	−	−	−	+	−	+	+	+	+	v	+	+	+	+	+	+	+	v	+	+	+	v	+	−	+	v	v	v	+	+	+
459	*C. albidosimilis*	−	−	−	−	−	−	−	+	−	+	−	v	+	+	+	+	+	+	v	+	+	v	+	+	+	v	v	−	+	v	v	+	−	+	+
460	*C. albidus* var. *albidus*	−	−	−	−	−	−	−	+	−	+	+	−	v	v	+	+	+	v	+	+	+	v	v	+	+	v	+	−	+	v	−	v	v	+	+
461	*C. albidus* var. *kuetzingii*	−	−	−	−	−	−	−	+	−	+	+	−	−	−	+	−	−	−	−	+	+	−	−	+	+	+	+	−	+	v	−	+	−	+	+
462	*C. albidus* var. *ovalis*	−	−	−	−	−	−	−	+	−	+	+	−	v	v	+	+	+	v	−	+	+	v	v	+	+	v	+	−	+	v	−	v	v	+	+
463	*C. allantoinivorans*	−	−	−	−	−	−	−	+	−	+	+	+	+	+	+	+	+	+	+	+	+	v	+	+	+	+	+	−	+	+	+	+	+	+	+
464	*C. amylolentus*	−	−	−	−	−	−	−	+	−	+	+	+	+	−	+	v	v	v	v	+	+	v	+	+	+	+	+	−	+	+	+	+	−	+	+
465	*C. amylolyticus*	−	−	−	−	−	−	−	+	−	+	+	+	+	+	+	+	+	+	+	+	+	−	+	+	+	+	+	−	−	+	−	+	+	+	+
466	*C. antarcticus* var. *antarcticus*	−	−	−	−	−	−	−	+	−	+	+	−	−	−	+	+	+	+	+	+	+	−	+	+	−	+	−	−	−	−	−	−	−	+	+
467	*C. antarcticus* var. *circumpolaris*	−	−	−	−	−	−	−	+	−	+	−	−	−	−	+	+	+	+	+	+	−	−	+	+	−	+	−	−	+	−	−	−	−	+	+
468	*C. armeniacus*	−	−	−	−	−	−	−	+	−	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	−	−	+	−	+	+	+	+
469	*C. arrabidensis*	−	−	−	−	−	−	−	+	−	+	+	+	+	+	+	+	+	+	−	+	+	+	+	+	+	+	+	−	+	+	−	+	+	+	+
470	*C. aureus*	−	−	−	−	−	−	−	+	+	+	+	+	+	+	+	+	+	+	+	+	+	−	v	+	+	+	+	−	−	+	−	+	+	+	+
471	*C. bhutanensis*	−	−	−	−	−	−	−	+	−	+	+	−	+	+	+	v	+	+	+	+	+	+	−	+	+	+	+	−	+	−	−	−	−	+	+
472	*C. carnescens*	−	−	−	−	−	−	−	+	−	+	+	+	+	+	+	+	+	+	+	+	+	v	+	+	+	+	+	−	−	+	+	+	+	+	+
473	*C. chernovii*	−	−	−	−	−	−	−	+	−	+	+	−	+	+	+	+	+	+	+	+	+	+	+	+	+	+	−	−	+	−	−	+	+	+	+
474	*C. cistialbidi*	−	−	−	−	−	−	−	+	−	+	+	+	+	+	+	+	+	+	−	+	+	−	+	+	+	+	+	−	−	+	v	+	+	+	+
475	*C. curvatus*	−	−	−	−	−	−	−	+	−	+	+	−	+	+	+	+	v	v	v	+	+	v	+	+	v	+	+	−	+	+	+	+	v	v	+
476	*C. cylindricus*	−	−	−	−	−	−	−	+	−	+	+	+	+	−	+	+	+	+	+	+	+	v	v	+	+	+	−	−	+	−	−	+	−	+	+
477	*C. daszewskae*	−	−	−	−	−	−	−	+	−	+	+	+	+	+	+	+	+	v	+	+	v	+	+	+	+	+	+	−	+	+	+	+	+	+	+
478	*C. diffluens*	−	−	−	−	−	−	−	+	−	+	+	−	v	v	+	+	+	+	+	+	+	+	+	+	+	v	v	−	+	v	v	−	v	−	+
479	*C. dimennae*	−	−	−	−	−	−	−	+	−	+	+	−	+	+	+	−	−	−	−	+	+	+	+	+	+	+	+	−	+	v	−	+	+	+	+
480	*C. festucosus*	−	−	−	−	−	−	−	+	−	+	v	−	v	v	+	+	+	+	+	+	+	−	+	+	+	+	+	n	+	+	−	v	+	+	+
481	*C. flavescens*	−	−	−	−	−	−	−	+	−	+	+	+	+	+	+	+	+	+	v	+	+	v	+	+	+	v	+	−	+	v	+	+	+	+	+
482	*C. flavus*	−	−	−	−	−	−	−	+	+	+	+	+	+	+	+	+	+	+	+	+	+	−	+	+	+	+	+	−	−	−	−	+	+	+	+
483	*C. fragicola*	−	−	−	−	−	−	−	+	v	+	+	+	+	v	+	v	+	+	+	v	+	+	+	+	+	+	+	−	+	+	+	+	+	v	+
484	*C. friedmannii*	−	−	−	−	−	−	−	+	−	+	−	−	−	−	+	+	+	+	+	+	+	−	−	+	+	−	−	−	−	−	−	−	−	−	−
485	*C. fuscescens*	−	−	−	−	−	−	−	+	−	−	−	−	−	−	−	−	−	−	−	+	+	−	−	+	+	−	+	−	−	−	−	−	−	−	−
486	*C. gastricus*	−	−	−	−	−	−	−	+	−	−	−	−	+	v	+	+	+	v	+	+	+	−	v	+	+	−	−	−	+	−	−	v	−	+	+
487	*C. gilvescens*	−	−	−	−	−	−	−	+	−	−	−	−	+	+	+	+	+	−	+	+	+	−	+	+	+	−	−	−	+	+	−	−	−	+	+

Symbols: +, positive or weak; −, negative; v, variable (+/−, w/−); n, no data.

	Growth reactions and other characteristics																																							
	myo-Inositol	DL-Lactate	Succinate	Citrate	D-Gluconate	D-Glucosamine	*N*-Acetyl-D-glucosamine	Hexadecane	Nitrate	Nitrite	Vitamin-free	2-Keto-D-gluconate	5-Keto-D-gluconate	Saccharate	Xylitol	L-Arabinitol	Arbutin	Propane 1,2 diol	Butane 2,3 diol	Cadaverine	Creatinine	L-Lysine	Ethylamine	50% Glucose	10% NaCl/5% glucose	Starch formation	Urease	Gelatin liquefaction	Cycloheximide 0.01%	Cycloheximide 0.1%	Growth at 19°C	Growth at 25°C	Growth at 30°C	Growth at 35°C	Growth at 37°C	Growth at 40°C	Growth at 45°C	CoQ (Main component)	Mol% G + C (Ave.)	DBB
Candida (*cont'd*)																																								
434	−	−	+	+	−	+	n	n	−	n	−	+	n	n	−	n	+	−	−	+	−	+	+	+	n	−	−	n	−	−	+	+	+	−	−	−	−	n	n	−
435	−	v	+	−	−	+	+	−	+	+	−	v	n	n	−	n	n	n	n	+	n	+	+	−	n	−	n	−	+	+	+	+	+	n	−	−	−	n	n	−
436	−	−	+	+	+	+	+	+	−	−	+	+	n	n	−	n	n	n	n	+	n	+	+	+	n	−	n	+	−	−	+	+	+	+	+	n	n	n	n	−
437	−	−	−	+	−	+	−	n	−	−	n	−	−	n	+	n	n	+	+	−	−	+	n	−	n	−	−	n	−	−	+	+	+	+	+	−	−	n	n	−
438	−	−	+	+	+	−	n	n	−	−	−	+	n	n	−	n	+	−	−	+	−	+	+	+	n	−	−	n	−	−	+	+	+	+	n	−	−	n	n	−
439	−	−	−	−	−	−	−	−	−	−	−	v	n	n	−	n	n	n	n	−	n	+	−	+	n	−	n	−	−	−	+	+	+	n	v	n	n	n	n	−
440	−	−	+	v	v	v	+	−	−	−	−	+	n	n	−	n	n	n	n	+	n	+	+	v	n	−	n	−	+	+	+	+	+	n	−	−	−	9	50.5	−
Cephaloascus																																								
442	−	+	+	+	−	−	+	−	−	−	−	−	−	−	n	n	n	n	n	+	−	+	+	n	+	−	n	−	n	n	+	+	+	n	−	−	−	9	37.8	−
443	−	v	+	+	−	−	v	−	−	−	+	−	−	−	n	n	n	n	n	+	−	+	+	n	v	−	n	−	n	n	+	+	+	n	−	−	−	9	39.9	−
Chionosphaera																																								
445	−	−	+	+	−	−	−	−	−	−	−	n	n	n	n	n	n	n	n	n	n	n	+	−	n	−	v	n	n	n	+	+	v	n	−	−	−	10	51.6	+
446	+	−	−	−	n	−	−	n	−	n	+	n	n	n	−	n	n	n	n	n	n	n	n	n	−	n	+	n	n	n	+	+	+	n	v	n	n	n	n	+
Citeromyces																																								
448	−	v	−	v	+	v	+	−	+	n	+	+	+	−	n	n	n	n	n	n	n	n	n	n	+	−	n	−	n	n	+	+	+	n	−	−	−	8	45.4	−
449	−	v	−	−	+	v	+	−	+	n	+	+	−	−	n	n	n	n	n	n	n	n	n	n	+	−	n	−	n	n	+	+	+	n	v	n	n	8	42.0	−
Clavispora																																								
451	−	v	+	v	v	v	v	v	−	−	−	+	n	n	+	n	n	n	n	+	n	+	+	v	n	−	n	−	+	n	+	+	+	+	+	n	n	8	45.4	−
452	−	+	+	+	v	v	+	+	−	n	−	+	n	n	v	n	n	n	n	+	n	−	+	−	n	−	n	−	−	−	+	+	+	+	+	n	n	8	43.6	−
Colacogloea																																								
454	−	−	+	−	−	−	n	n	−	−	−	n	n	n	−	n	n	n	n	n	n	n	n	n	n	−	n	n	−	−	+	+	+	−	−	−	−	n	n	+
455	−	v	+	v	−	+	n	n	−	−	+	n	n	n	v	n	n	n	n	n	n	n	n	n	n	−	n	n	v	−	+	+	+	−	−	−	−	10	n	+
Cryptococcus																																								
457	+	−	v	+	v	−	n	n	+	n	+	n	n	+	+	n	n	n	n	+	n	v	−	n	n	+	+	n	−	−	+	+	+	−	−	−	−	n	n	+
458	+	−	+	v	+	v	n	n	+	n	+	n	n	+	v	n	n	n	n	+	n	+	v	n	n	v	+	n	v	−	+	+	v	−	−	−	−	10	52.7	+
459	+	v	+	+	+	−	n	n	+	n	−	n	n	+	+	n	n	n	n	+	n	v	+	n	n	+	+	n	v	−	+	+	+	−	−	−	−	n	55.0	+
460	+	+	+	+	+	−	n	n	+	n	−	n	n	+	+	n	n	n	n	+	n	v	−	n	n	+	+	n	−	−	+	+	+	v	−	−	−	10	52.4	+
461	+	+	+	+	+	−	−	−	+	n	−	+	+	+	n	n	n	n	n	n	n	n	n	−	−	+	+	−	n	n	+	+	n	−	−	−	−	n	52.5	+
462	+	+	+	+	+	−	n	n	+	n	−	n	n	+	+	n	n	n	n	+	n	+	−	n	n	+	+	n	n	n	+	+	+	+	−	−	−	n	n	+
463	+	+	+	+	+	+	n	n	−	n	−	+	n	n	n	n	n	n	n	n	+	n	n	−	−	+	+	n	n	n	+	+	+	n	−	−	−	n	n	+
464	+	v	+	v	+	v	+	−	−	n	−	−	n	n	n	n	n	n	n	n	−	n	n	+	v	+	+	n	n	n	+	+	+	−	−	−	−	9	55.2	+
465	+	−	+	+	+	+	n	n	−	n	−	n	n	n	n	n	n	n	n	n	−	n	n	n	−	+	+	n	n	n	+	+	−	−	−	−	−	n	n	+
466	+	−	+	−	−	−	n	n	+	n	+	n	n	n	+	n	n	n	n	+	n	+	+	n	n	+	+	n	−	−	+	−	−	−	−	−	−	n	55.0	+
467	+	+	+	−	−	−	n	n	+	n	+	n	n	n	−	n	n	n	n	+	n	+	−	n	n	+	+	n	−	−	n	−	−	−	−	−	−	n	n	+
468	+	−	+	+	+	+	n	n	−	n	−	n	n	n	n	n	n	n	n	n	−	n	n	n	−	+	+	n	n	n	+	+	−	−	−	−	−	n	n	+
469	+	+	+	+	+	+	n	n	−	n	−	n	n	+	+	n	n	n	n	+	n	−	+	n	n	−	+	n	+	+	+	−	−	−	−	−	−	n	n	+
470	+	−	+	+	+	+	+	−	−	n	−	+	n	n	n	n	n	n	n	n	n	n	n	−	−	+	+	n	n	n	+	+	+	n	−	−	−	10	55.0	+
471	−	−	+	+	−	−	n	n	+	n	−	n	n	+	+	n	n	n	n	+	n	+	+	n	n	+	+	n	−	−	+	+	−	−	−	−	−	n	54.2	+
472	+	+	+	+	+	+	+	−	−	n	−	+	n	n	n	n	n	n	n	n	−	n	n	−	−	+	+	n	n	n	+	+	−	−	−	−	−	10	n	+
473	+	−	+	+	+	+	n	n	+	n	−	n	n	−	+	n	n	n	n	+	n	+	+	n	n	+	+	n	−	−	+	+	+	−	−	−	−	n	n	+
474	+	−	+	+	v	+	n	n	−	n	−	n	n	n	n	n	n	n	n	n	−	n	n	n	−	+	+	n	n	n	+	+	−	−	−	−	−	n	n	+
475	v	+	+	+	+	v	+	−	−	v	v	n	+	−	+	n	n	n	n	+	−	+	+	−	−	v	+	−	n	n	+	+	+	v	v	n	n	10	57.3	+
476	+	v	+	−	+	+	n	n	+	n	−	n	n	+	v	n	n	n	n	+	n	+	+	n	n	+	+	n	+	−	+	+	v	−	−	−	−	n	n	+
477	+	+	+	+	+	+	+	−	−	−	−	+	+	+	+	n	n	n	n	+	−	+	v	−	n	v	+	−	n	n	+	+	+	v	n	n	n	10	59.4	+
478	+	v	+	+	+	−	n	n	+	n	−	n	n	−	+	n	n	n	n	+	n	v	v	n	n	+	+	n	v	−	+	+	+	−	−	−	−	10	54.0	+
479	+	+	+	+	+	−	−	−	−	n	−	+	n	n	n	n	n	n	n	n	+	n	n	−	−	+	+	n	n	n	+	+	+	n	−	n	n	9	53.1	+
480	+	+	+	+	n	−	+	n	−	−	−	+	+	n	+	n	n	n	n	+	−	+	+	+	+	+	+	n	n	n	+	+	−	−	−	−	−	n	n	+
481	+	v	+	v	+	v	−	−	−	n	+	+	n	n	n	n	n	n	n	n	−	n	n	v	−	+	+	n	n	n	+	+	+	n	v	n	n	10	58.1	+
482	+	+	+	+	+	+	+	−	−	n	−	+	n	n	n	n	n	n	n	n	−	n	n	−	−	−	+	n	n	n	+	+	+	n	−	−	−	10	52.3	+
483	+	+	+	+	+	+	+	−	−	v	−	+	+	+	+	n	n	n	n	−	+	+	v	−	−	+	+	−	n	n	+	+	+	−	−	−	−	10	58.8	+
484	−	−	−	+	+	−	n	n	+	n	+	n	n	−	−	n	n	n	n	+	n	+	−	n	n	+	+	n	−	−	+	−	−	−	−	−	−	n	n	+
485	+	−	+	+	+	−	n	n	+	n	−	n	n	+	−	n	n	n	n	−	n	−	−	n	n	+	+	n	−	−	+	+	−	−	−	−	−	n	52.4	+
486	+	−	+	−	+	−	n	n	−	n	−	n	n	v	v	n	n	n	n	+	n	+	−	n	n	+	+	n	−	−	+	+	−	−	−	−	−	n	58.3	+
487	+	−	+	−	+	−	n	n	−	n	−	n	n	−	−	n	n	n	n	+	n	+	−	n	n	+	+	n	+	−	+	+	−	−	−	−	−	9	n	+

Symbols: +, positive or weak; −, negative; v, variable (+/−, w/−); n, no data.

Ln. no.	Species	Fermentation: Glucose	Galactose	Sucrose	Maltose	Lactose	Raffinose	Trehalose	Growth reactions and other characteristics: Glucose	Inulin	Sucrose	Raffinose	Melibiose	Galactose	Lactose	Trehalose	Maltose	Melezitose	Methyl-α-D-glucoside	Soluble Starch	Cellobiose	Salicin	L-Sorbose	L-Rhamnose	D-Xylose	L-Arabinose	D-Arabinose	D-Ribose	Methanol	Ethanol	Glycerol	Erythritol	Ribitol	Galactitol	D-Mannitol	D-Glucitol
	Cryptococcus (*cont'd*)																																			
488	*C. haglerorum*	−	−	−	−	−	−	−	+	+	+	+	−	+	+	+	+	+	+	−	+	+	−	+	+	+	+	+	−	+	+	+	+	−	+	+
489	*C. heimaeyensis*	−	−	−	−	−	−	−	+	−	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	−	−	+	+	+	+	+	+
490	*C. heveanensis*	−	−	−	−	−	−	−	+	−	+	+	−	+	+	+	+	+	+	−	+	+	+	+	+	+	+	+	−	+	−	+	+	+	+	+
491	*C. huempii*	−	−	−	−	−	−	−	+	−	−	−	−	+	+	+	+	+	−	+	+	+	+	+	+	+	+	+	−	+	−	−	+	+	+	+
492	*C. humicola*	−	−	−	−	−	−	−	+	v	+	v	+	+	+	+	+	+	+	−	+	+	+	+	+	+	+	+	−	+	+	+	+	+	+	+
493	*C. laurentii*	−	−	−	−	−	−	−	+	−	+	+	+	+	+	+	+	+	+	+	+	+	v	+	+	+	+	+	−	+	v	+	+	v	+	+
494	*C. liquefaciens*	−	−	−	−	−	−	−	+	−	+	+	−	+	+	+	+	+	+	v	+	+	v	+	+	+	v	+	−	+	−	−	+	+	+	+
495	*C. longus*	−	−	−	−	−	−	−	+	−	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	−	+	+	+	+	+	+	+
496	*C. luteolus*	−	−	−	−	−	−	−	+	−	+	+	+	+	−	+	+	+	+	−	+	+	v	+	+	+	v	v	−	v	v	+	v	+	+	+
497	*C. magnus*	−	−	−	−	−	−	−	+	−	+	+	−	+	+	+	+	+	+	+	+	+	v	v	+	+	v	v	−	v	v	v	v	+	+	+
498	*C. marinus*	−	−	−	−	−	−	−	+	−	−	−	−	−	−	+	−	−	−	−	v	v	+	+	+	+	+	+	−	+	+	+	+	−	+	+
499	*C. musci*	−	−	−	−	−	−	−	+	v	+	v	+	+	+	+	+	+	+	+	+	+	v	+	+	+	+	+	−	+	v	+	+	+	v	v
500	*C. mycelialis*	−	−	−	−	−	−	−	+	−	+	+	−	v	+	+	+	+	+	+	+	+	−	+	+	+	v	+	−	v	+	−	−	v	+	+
501	*C. nemorosus*	−	−	−	−	−	−	−	+	−	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	−	+	+	+	+	+	+	+
502	*C. nyarrowii*	−	−	−	−	−	−	−	+	−	+	−	−	+	−	+	+	+	+	+	+	+	+	+	+	+	+	+	−	+	+	−	+	+	+	+
503	*C. oeirensis*	−	−	−	−	−	−	−	+	−	+	+	−	+	+	+	+	+	+	v	+	+	+	+	+	+	v	+	−	+	v	−	v	v	+	+
504	*C. paraflavus*	−	−	−	−	−	−	−	+	−	+	+	+	+	+	+	+	+	+	+	+	+	−	+	+	+	+	+	−	−	−	−	+	−	+	−
505	*C. peneaus*	−	−	−	−	−	−	−	+	−	+	+	+	+	+	+	+	+	+	v	+	+	+	+	+	+	+	+	−	−	v	+	+	+	+	+
506	*C. perniciosus*	−	−	−	−	−	−	−	+	−	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	−	−	+	+	+	+	+	−
507	*C. phenolicus*	−	−	−	−	−	−	−	+	−	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	−	−	−	−	+	+	+	+
508	*C. podzolicus*	−	−	−	−	−	−	−	+	−	+	+	+	+	+	+	+	+	+	+	+	+	v	+	+	+	+	+	−	+	−	v	−	+	+	+
509	*C. pseudolongus*	−	−	−	−	−	−	−	+	−	+	−	+	+	+	+	+	−	+	−	+	+	+	+	+	+	+	+	−	+	+	+	+	+	+	+
510	*C. ramirezgomezianus*	−	−	−	−	−	−	−	+	−	+	+	+	+	+	+	+	+	+	−	+	+	+	+	+	+	+	+	−	+	+	+	+	+	+	+
511	*C. saitoi*	−	−	−	−	−	−	−	+	−	+	+	−	v	v	+	+	+	+	+	+	+	−	+	+	+	−	v	−	+	v	−	−	−	+	+
512	*C. silvicola*	−	−	−	−	−	−	−	+	−	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	−	+	+	−	+	+	+	+
513	*C. skinneri*	−	−	−	−	−	−	−	+	−	−	−	−	v	−	+	−	−	v	−	+	+	v	+	+	+	+	v	−	+	v	−	+	v	+	+
514	*C. surugaensis*	−	−	−	−	−	−	−	+	−	+	+	+	+	−	+	+	+	+	+	+	+	+	+	+	+	+	+	−	+	+	+	+	+	+	+
515	*C. taeanensis*	−	−	−	−	−	−	−	+	−	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	−	−	+	+	+	+	+	+
516	*C. tephrensis*	−	−	−	−	−	−	−	+	−	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	−	−	v	+	+	+	+	+
517	*C. terreus*	−	−	−	−	−	−	−	+	−	−	−	−	+	+	+	v	v	v	v	+	+	+	+	+	+	v	+	−	v	v	−	v	+	+	+
518	*C. terricola*	−	−	−	−	−	−	−	+	v	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	−	+	−	−	−	+	+	+
519	*C. uzbekistanensis*	−	−	−	−	−	−	−	+	−	+	+	−	−	−	+	+	+	+	v	+	+	+	+	+	+	v	v	−	+	−	−	−	−	+	+
520	*C. victoriae*	−	−	−	−	−	−	−	+	−	+	+	+	+	+	+	+	+	v	+	+	+	v	v	+	+	+	+	−	−	+	+	+	+	+	+
521	*C. vishniacii*	−	−	−	−	−	−	−	+	−	+	+	−	−	−	+	v	v	v	v	v	v	−	v	v	v	−	−	−	−	−	−	−	−	−	−
522	*C. watticus*	−	−	−	−	−	−	−	+	+	+	+	+	+	+	+	−	−	+	+	−	+	−	+	+	−	−	+	−	−	−	−	−	−	+	−
523	*C. wieringae*	−	−	−	−	−	−	−	+	−	+	+	−	+	+	+	+	+	+	v	+	+	v	+	+	+	+	v	−	+	v	−	+	+	+	+
524	***Cryptotrichosporon***																																			
525	*C. anacardii*	−	−	−	−	−	−	−	+	−	−	−	−	+	−	+	+	+	−	+	+	+	+	+	+	+	+	+	−	−	−	−	+	−	+	+
526	***Cuniculitrema***																																			
527	*C. polymorpha*	−	−	−	−	−	−	−	+	−	+	+	+	−	+	+	+	+	+	+	+	+	+	+	+	v	−	+	−	+	−	v	+	+	+	+
528	***Curvibasidium***																																			
529	*C. cygneicollum*	−	−	−	−	−	−	−	+	−	−	−	−	+	−	v	−	−	−	−	+	+	+	−	+	+	+	v	−	+	v	−	+	+	+	v
530	*C. pallidicorallinum*	−	−	−	−	−	−	−	+	v	−	+	v	+	v	−	−	v	−	−	+	+	+	−	+	+	+	v	−	+	+	−	+	+	+	+
531	***Cyniclomyces***																																			
532	*C. guttulatus*	+	−	+	−	−	+	−	+	+	+	+	−	−	−	+	−	v	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−
533	***Cyrenella***																																			
534	*C. elegans*	−	−	−	−	−	−	−	+	−	+	+	−	+	−	+	+	+	−	+	+	+	+	+	+	+	−	−	−	−	+	−	+	−	+	+
535	***Cystobasidium***																																			
536	*C. fimetarium*	−	−	−	−	−	−	−	+	−	v	−	−	−	+	+	−	−	−	−	+	+	−	−	+	+	+	+	−	+	+	−	+	−	v	v
537	***Cystofilobasidium***																																			
538	*C. bisporidii*	−	−	−	−	−	−	−	+	v	+	+	+	+	−	+	+	+	−	+	+	v	+	+	+	+	+	+	−	+	+	−	+	v	+	+
539	*C. capitatum*	−	−	−	−	−	−	−	+	−	+	+	−	+	+	+	+	+	−	+	+	+	+	v	+	+	+	+	−	+	+	−	+	+	+	+
540	*C. ferigula*	−	−	−	−	−	−	−	+	−	−	−	−	v	−	+	−	−	−	−	+	+	+	+	+	+	+	+	−	+	+	−	v	−	+	+
541	*C. infirmominiatum*	−	−	−	−	−	−	−	+	−	+	+	−	v	v	+	+	+	−	+	+	+	+	+	+	+	+	+	−	+	+	−	+	v	+	+

Symbols: +, positive or weak; −, negative; v, variable (+/−, w/−); n, no data.

	Growth reactions and other characteristics																																							
	myo-Inositol	DL-Lactate	Succinate	Citrate	D-Gluconate	D-Glucosamine	*N*-Acetyl-D-glucosamine	Hexadecane	Nitrate	Nitrite	Vitamin-free	2-Keto-D-gluconate	5-Keto-D-gluconate	Saccharate	Xylitol	L-Arabinitol	Arbutin	Propane 1,2 diol	Butane 2,3 diol	Cadaverine	Creatinine	L-Lysine	Ethylamine	50% Glucose	10% NaCl/5% glucose	Starch formation	Urease	Gelatin liquefaction	Cycloheximide 0.01%	Cycloheximide 0.1%	Growth at 19°C	Growth at 25°C	Growth at 30°C	Growth at 35°C	Growth at 37°C	Growth at 40°C	Growth at 45°C	CoQ (Main component)	Mol% G + C (Ave.)	DBB
Cryptococcus (*cont'd*)																																								
488	+	+	+	+	+	+	+	+	−	n	−	−	−	+	+	n	n	n	n	+	−	+	+	n	−	−	+	n	n	n	+	+	+	n	−	−	−	n	n	+
489	+	−	+	+	+	+	n	n	−	n	−	+	n	n	n	n	n	n	n	n	−	n	n	−	−	+	+	n	n	n	+	+	−	−	−	−	−	n	n	+
490	+	+	+	+	+	−	−	−	−	n	−	+	n	n	n	n	n	n	n	n	−	n	n	−	v	+	+	n	n	n	+	+	+	n	−	−	−	10	50.5	+
491	−	+	+	+	+	+	+	−	+	+	−	+	n	+	+	n	n	n	n	+	−	+	+	−	+	+	+	−	n	n	+	+	−	−	−	−	−	8	52.7	+
492	+	+	+	+	+	+	+	−	−	v	−	n	+	+	+	n	n	n	n	+	−	+	+	−	−	v	+	−	n	n	+	+	+	v	−	−	−	9	62.3	+
493	+	+	+	+	+	+	+	−	−	n	−	+	n	n	n	n	n	n	n	n	+	n	n	v	−	+	+	n	n	n	+	+	n	+	v	n	n	10	57.9	+
494	+	+	+	+	+	−	n	n	+	+	−	n	n	+	+	n	n	n	n	+	n	+	v	n	n	+	+	n	v	−	+	+	+	−	−	−	−	n	52.5	+
495	+	+	+	+	+	+	+	+	−	−	−	+	+	+	+	n	n	n	n	+	+	+	+	−	n	+	+	−	n	n	+	+	+	−	−	−	−	9	60.6	+
496	+	+	+	+	+	+	+	−	−	n	−	+	n	n	n	n	n	n	n	n	−	n	n	−	−	+	+	n	n	n	+	+	−	−	−	−	−	10	58.7	+
497	+	−	+	+	+	v	n	n	v	n	−	n	n	+	+	n	n	n	n	+	n	v	+	n	n	+	+	n	−	−	+	+	v	−	−	−	−	10	52.7	+
498	+	−	−	−	+	+	+	−	−	−	−	n	n	−	+	n	n	n	n	+	−	+	+	−	+	−	+	−	n	n	+	+	−	−	−	−	−	10	62.6	+
499	+	+	v	v	v	+	+	+	−	−	−	+	+	+	+	n	n	n	n	+	+	+	v	−	−	+	+	−	n	n	+	+	+	−	−	−	−	9	61.0	+
500	+	−	+	v	+	−	+	n	−	−	−	+	+	n	v	n	n	n	n	+	−	+	+	−	n	+	+	n	n	n	+	+	−	−	−	−	−	n	55.6	+
501	+	−	+	+	+	+	n	n	−	n	−	+	n	n	n	n	n	n	n	n	−	n	n	v	−	+	+	n	n	n	+	+	−	−	−	−	−	n	n	+
502	+	−	+	+	+	−	+	+	v	+	+	+	+	n	−	n	n	n	n	+	+	+	+	−	+	+	+	n	n	n	+	−	−	−	−	−	−	n	n	+
503	+	−	+	+	+	+	n	n	+	n	−	n	n	+	+	n	n	n	n	+	n	v	+	n	n	+	+	n	v	−	+	+	−	−	−	−	−	n	n	+
504	+	+	+	+	+	+	+	n	−	n	−	+	n	n	n	n	n	n	n	n	−	n	n	−	−	+	+	n	n	n	+	+	−	−	−	−	−	n	n	+
505	+	+	+	+	+	+	+	−	−	n	−	+	n	n	n	n	n	n	n	n	−	n	n	−	−	+	+	n	n	n	+	+	+	n	−	−	−	10	51.8	+
506	+	+	+	+	+	+	n	n	−	n	−	+	n	n	n	n	n	n	n	n	−	n	n	−	−	+	+	n	n	n	+	+	−	−	−	−	−	n	n	+
507	+	−	+	+	+	+	n	n	+	n	+	n	n	+	+	n	n	n	n	+	n	+	+	n	n	+	+	n	+	−	+	+	+	−	−	−	−	n	n	+
508	+	v	+	+	+	+	+	−	−	n	v	+	n	n	n	n	n	n	n	n	+	n	n	−	−	v	+	n	n	n	+	+	v	n	−	−	−	10	62.8	+
509	+	+	+	+	+	+	+	n	−	−	−	+	+	+	+	n	n	n	n	+	−	+	+	−	n	+	+	−	n	n	+	+	+	−	−	−	−	9	59.1	+
510	+	+	+	+	+	+	+	−	−	−	−	+	+	+	+	n	n	n	n	+	−	+	+	−	n	+	+	−	n	n	+	+	+	−	−	−	−	9	60.9	+
511	+	−	+	+	+	−	n	n	+	n	−	n	n	+	v	n	n	n	n	+	n	+	+	n	n	+	+	n	−	−	+	+	+	−	−	−	−	10	49.3	+
512	+	v	+	+	+	+	n	n	+	n	−	n	n	+	v	n	n	n	n	v	n	v	+	n	n	+	+	n	v	−	+	+	−	−	−	−	−	n	n	+
513	+	v	+	+	+	−	−	−	−	n	−	+	n	n	n	n	n	n	n	n	−	n	n	−	−	+	+	n	n	n	+	+	v	n	−	−	−	10	53.0	+
514	+	+	+	+	+	+	n	n	−	n	−	+	n	n	n	n	n	n	n	n	n	n	n	−	−	+	+	n	n	n	+	+	+	−	−	−	−	10	48.3	+
515	+	+	+	+	+	+	n	n	−	n	−	+	n	n	n	n	n	n	n	n	−	n	n	−	−	+	+	n	n	n	+	+	+	n	−	−	−	10	n	+
516	+	v	+	+	+	+	+	n	−	n	−	+	n	n	n	n	n	n	n	n	−	n	n	−	−	+	+	n	n	n	+	+	−	−	−	−	−	n	n	+
517	+	−	+	+	+	+	n	n	+	n	+	n	n	+	+	n	n	n	n	+	n	+	+	n	n	+	+	n	v	−	+	+	+	−	−	−	−	10	56.4	+
518	+	−	+	+	+	+	n	n	+	n	+	n	n	+	−	n	n	n	n	v	n	v	v	n	n	−	+	n	−	−	+	+	−	−	−	−	−	10	50.8	+
519	+	v	+	+	+	−	n	n	+	n	−	n	n	+	+	n	n	n	n	+	n	v	v	n	n	+	+	n	−	−	+	+	+	n	v	n	n	n	n	+
520	+	−	+	+	+	+	n	n	−	n	v	+	n	n	n	n	n	n	n	n	−	n	n	−	−	+	+	n	n	n	+	v	−	−	−	−	−	n	50.3	+
521	−	−	+	−	−	−	n	n	v	n	+	n	n	−	−	n	n	n	n	−	n	−	−	n	n	+	v	n	−	−	v	−	−	−	−	−	−	9	54.8	+
522	+	−	+	+	−	−	+	−	+	n	−	n	n	n	n	n	n	n	n	n	n	n	n	−	−	−	+	+	n	n	+	+	−	−	−	−	−	n	n	+
523	+	v	+	+	v	−	n	n	+	n	−	n	n	+	+	n	n	n	n	v	n	v	−	n	n	+	+	n	−	−	+	+	v	−	−	−	−	n	49.1	+
Cryptotrichosporon																																								
525	+	−	+	+	+	+	n	n	−	n	−	−	n	n	n	n	n	n	n	n	n	+	n	−	n	+	+	n	n	n	+	+	+	+	+	−	−	n	n	+
Cuniculitrema																																								
527	+	−	+	+	+	+	n	n	−	−	+	n	n	−	−	n	n	n	n	−	−	+	+	n	n	+	n	n	+	+	+	+	+	−	−	−	−	10	51.3	+
Curvibasidium																																								
529	−	−	+	+	+	−	n	n	−	−	v	n	n	n	+	n	n	n	n	n	n	n	n	n	n	−	+	n	v	−	+	+	−	−	−	−	−	9	63.4	+
530	v	+	+	v	+	−	n	n	−	−	+	n	n	n	+	n	n	n	n	n	n	n	n	n	n	−	n	n	+	−	+	+	−	−	−	−	−	n	n	+
Cyniclomyces																																								
532	−	−	+	−	−	−	−	n	−	n	−	−	−	n	n	n	n	n	n	n	n	n	n	n	n	−	n	−	−	−	−	−	v	v	+	n	−	6	34.5	−
Cyrenella																																								
534	−	−	+	+	+	−	n	n	+	+	−	n	n	n	+	n	n	n	n	n	n	n	n	n	n	−	n	n	+	−	+	+	−	−	−	−	−	n	n	+
Cystobasidium																																								
536	−	+	+	−	+	−	n	n	−	−	−	n	n	n	+	n	n	n	n	n	n	n	n	n	n	−	n	n	−	−	+	+	+	−	−	−	−	n	n	+
Cystofilobasidium																																								
538	+	+	+	−	v	−	n	n	+	+	−	n	n	v	+	n	n	n	n	n	n	n	n	n	n	+	+	n	−	−	+	+	−	−	−	−	−	8	62.5	+
539	+	−	+	+	+	−	n	n	+	+	−	n	n	+	+	n	n	n	n	n	n	n	n	n	n	+	+	n	−	−	+	−	−	−	−	−	−	8	59.6	+
540	+	−	−	v	+	−	n	n	+	+	−	n	n	+	v	n	n	n	n	n	n	n	n	n	n	+	+	n	−	−	+	+	+	−	−	−	−	n	66.7	+
541	+	+	+	v	+	−	n	n	+	+	−	n	n	+	+	n	+	n	n	n	n	n	n	−	n	+	+	n	v	−	+	+	−	−	−	−	−	8	66.3	+

Symbols: +, positive or weak; −, negative; v, variable (+/−, w/−); n, no data.

Ln. no.	Species	Fermentation: Glucose	Galactose	Sucrose	Maltose	Lactose	Raffinose	Trehalose	Growth reactions and other characteristics: Glucose	Inulin	Sucrose	Raffinose	Melibiose	Galactose	Lactose	Trehalose	Maltose	Melezitose	Methyl-α-D-glucoside	Soluble Starch	Cellobiose	Salicin	L-Sorbose	L-Rhamnose	D-Xylose	L-Arabinose	D-Arabinose	D-Ribose	Methanol	Ethanol	Glycerol	Erythritol	Ribitol	Galactitol	D-Mannitol	D-Glucitol
	Cystofilobasidium (*cont'd*)																																			
542	*C. lacus-mascardii*	−	−	−	−	−	−	−	+	−	+	+	v	+	+	+	+	+	−	−	+	+	+	+	+	+	+	+	−	+	+	+	+	−	+	+
543	*C. macerans*	−	−	−	−	−	−	−	+	−	+	+	−	+	v	+	+	+	−	−	+	+	+	−	+	+	+	+	−	+	+	+	+	−	+	+
544	***Debaryomyces***																																			
545	*D. coudertii*	−	−	−	−	−	−	−	+	−	−	−	−	+	−	+	+	−	−	+	+	+	−	+	+	+	+	+	−	+	+	+	+	−	+	+
546	*D. fabryi*	v	−	v	−	−	v	v	+	−	+	+	+	+	v	+	+	+	+	+	+	+	+	−	+	+	v	+	−	+	+	+	+	v	+	+
547	*D. hansenii*	v	v	v	v	−	v	v	+	v	+	+	v	+	v	+	+	v	+	v	+	+	v	v	+	+	v	v	−	+	+	v	+	v	+	+
548	*D. maramus*	v	−	−	−	−	−	−	+	v	+	+	v	+	v	+	+	+	+	+	+	+	v	−	+	+	−	+	−	+	+	+	+	−	+	+
549	*D. mycophilus*	−	−	−	−	−	−	−	+	−	−	−	−	+	−	−	−	−	−	−	−	−	−	−	+	+	−	−	−	−	−	−	−	+	−	+
550	*D. nepalensis*	v	−	v	−	−	v	v	+	−	+	+	+	+	v	+	+	+	+	+	+	+	+	−	+	+	v	+	−	+	+	+	+	v	+	+
551	*D. prosopidis*	−	−	−	−	−	−	−	+	−	+	+	−	+	−	+	+	+	+	+	−	−	+	−	+	+	−	+	−	+	+	+	+	−	+	+
552	*D. robertsiae*	+	−	+	+	−	v	+	+	−	+	+	−	+	−	+	+	+	+	−	+	+	+	+	+	+	−	v	−	+	+	+	+	−	+	+
553	*D. singareniensis*	+	+	−	−	−	−	−	+	−	−	+	−	+	−	−	−	−	−	−	−	−	−	+	−	−	−	−	+	−	+	+	+	−	−	+	+
554	*D. subglobosus*	v	−	v	−	−	v	−	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	−	+	+	+	+	−	+	+	+	+	−	+	+
555	*D. udenii*	+	−	v	v	−	−	v	+	−	+	+	+	+	−	+	+	+	+	+	+	+	+	+	+	+	−	+	−	+	+	+	+	−	+	+
556	***Dekkera***																																			
557	*D. anomala*	+	+	+	v	v	v	v	+	−	+	v	−	+	v	+	v	v	v	−	+	+	−	−	−	−	−	−	−	−	v	+	−	−	−	−	−
558	*D. bruxellensis*	+	v	v	v	−	−	v	+	−	v	v	−	v	−	v	v	v	v	−	v	v	−	−	−	−	−	v	−	v	v	−	−	−	−	−
559	***Dioszegia***																																			
560	*D. aurantiaca*	−	−	−	−	−	−	−	+	−	+	+	+	+	−	+	+	+	+	+	+	+	+	−	+	+	+	+	+	−	−	+	+	+	+	+	+
561	*D. buhagiarii*	−	−	−	−	−	−	−	+	−	+	+	−	+	−	+	+	+	v	v	+	+	+	+	+	+	v	+	−	−	+	−	+	+	+	+
562	*D. catarinonii*	−	−	−	−	−	−	−	+	−	+	+	+	+	+	+	+	+	v	v	+	+	v	+	+	+	+	+	−	−	−	−	v	−	v	v	−
563	*D. changbaiensis*	−	−	−	−	−	−	−	+	−	+	+	+	+	−	+	+	+	−	+	+	+	−	+	+	+	+	+	−	−	−	−	−	−	+	+	+
564	*D. crocea*	−	−	−	−	−	−	−	+	−	+	+	+	+	−	+	+	+	+	+	+	+	v	+	+	+	+	+	−	−	+	v	+	+	+	+
565	*D. fristingensis*	−	−	−	−	−	−	−	+	−	+	+	+	+	−	+	+	+	+	−	+	+	−	+	+	+	+	+	−	−	−	−	+	+	+	+
566	*D. hungarica*	−	−	−	−	−	−	−	+	−	+	+	−	+	−	+	+	+	−	+	+	+	−	+	+	+	+	+	−	−	v	−	−	+	+	+
567	*D. statzelliae*	−	−	−	−	−	−	−	+	−	+	+	+	+	−	+	+	+	−	−	+	+	−	+	+	+	+	+	−	−	−	−	+	+	+	+
568	*D. takashimae*	−	−	−	−	−	−	−	+	−	+	+	+	+	+	+	+	+	v	v	+	+	−	v	+	+	+	+	−	−	−	v	−	+	+	−
569	*D. zsoltii* var. *zsoltii*	−	−	−	−	−	−	−	+	−	+	+	+	+	v	+	+	+	v	+	+	v	v	+	+	+	v	+	−	−	−	−	−	+	+	−
570	*D. zsoltii* var. *yunnanensis*	−	−	−	−	−	−	−	+	−	+	+	+	+	v	+	+	+	v	+	+	v	v	+	+	+	v	+	−	−	−	−	−	+	−	−
571	***Dipodascopsis***																																			
572	*D. anomala*	−	−	−	−	−	−	−	+	−	−	−	−	v	+	−	v	−	−	−	+	v	v	−	+	−	−	−	−	−	v	−	v	−	−	−
573	*D. tothii*	−	−	−	−	−	−	−	+	+	+	+	−	+	+	+	+	+	+	+	+	+	+	−	+	+	+	−	−	−	+	+	−	+	−	+	+
574	*D. uninucleata* var. *uninucleata*	−	−	−	−	−	−	−	+	+	+	+	+	v	−	+	+	+	+	+	−	−	+	−	+	+	+	−	−	−	+	+	−	+	−	+	+
575	*D. uninucleata* var. *wickerhamii*	−	−	−	−	−	−	−	+	−	−	−	+	v	−	+	+	+	+	+	−	−	+	+	+	+	+	−	−	−	+	+	−	+	−	+	+
576	***Dipodascus***																																			
577	*D. aggregatus*	−	−	−	−	−	−	−	+	−	−	−	−	+	−	−	−	−	−	−	−	−	+	−	+	−	−	v	−	+	+	−	v	−	+	+
578	*D. albidus*	−	−	−	−	−	−	−	+	−	−	−	−	+	−	−	−	−	−	−	−	−	+	−	+	−	−	−	−	+	+	−	−	−	+	+
579	*D. armillariae*	−	−	−	−	−	−	−	+	−	−	−	−	+	−	−	−	−	−	−	−	−	−	−	+	−	−	v	−	v	+	−	−	−	+	v
580	*D. australiensis*	−	−	−	−	−	−	−	+	−	−	−	−	+	−	−	−	−	−	v	−	−	+	−	+	−	−	−	−	+	+	−	v	−	+	+
581	*D. geniculatus*	v	−	−	−	−	−	−	+	−	−	−	−	+	−	−	+	−	−	+	−	−	+	−	+	−	−	−	−	+	+	−	−	−	+	+
582	*D. macrosporus*	−	−	−	−	−	−	−	+	−	−	−	−	+	−	−	−	−	−	−	+	−	+	−	+	−	−	−	−	+	+	−	v	−	+	+
583	***Eremothecium***																																			
584	*E. ashbyi*	v	−	v	v	−	v	v	+	−	+	+	−	−	−	+	+	−	−	−	−	−	−	−	−	−	−	−	−	−	−	+	−	−	−	−	v
585	*E. coryli*	+	−	+	+	−	v	+	+	−	+	+	−	−	−	+	+	−	v	v	−	−	−	−	−	−	−	−	−	−	+	+	−	−	−	−	−
586	*E. cymbalariae*	−	−	−	−	−	−	−	+	−	+	+	v	v	−	+	+	v	−	v	−	−	−	−	−	−	−	−	−	−	v	+	−	−	−	−	−
587	*E. gossypii*	−	−	−	−	−	−	−	+	−	+	+	−	−	−	+	+	−	−	−	v	v	−	−	−	−	−	−	−	−	v	+	−	−	−	−	v
588	*E. sinecaudum*	v	−	v	v	−	−	v	+	−	+	−	−	−	−	v	+	−	−	+	−	−	−	−	−	−	−	v	−	−	+	−	−	−	−	−	+
589	***Erythrobasidium***																																			
590	*E. hasegawianum*	−	−	−	−	−	−	−	+	−	+	−	−	+	−	+	+	+	−	−	+	+	+	−	+	+	+	+	+	−	−	+	−	+	−	+	+
591	***Fellomyces***																																			
592	*F. borneensis*	−	−	−	−	−	−	−	+	−	+	+	+	+	+	+	+	+	−	+	+	+	+	−	+	+	+	+	+	−	−	+	+	+	+	+	+
593	*F. chinensis*	−	−	−	−	−	−	−	+	−	+	+	+	+	+	+	+	+	−	−	+	+	v	−	+	+	+	+	+	−	−	+	−	+	+	+	+
594	*F. distylii*	−	−	−	−	−	−	−	+	−	+	+	+	+	+	+	+	+	−	+	+	+	+	−	+	+	+	+	+	−	−	+	+	+	+	+	+
595	*F. fuzhouensis*	−	−	−	−	−	−	−	+	−	+	v	+	+	+	+	v	v	−	−	+	+	+	−	+	+	+	+	+	−	−	+	+	+	+	+	+

Symbols: +, positive or weak; −, negative; v, variable (+/−, w/−); n, no data.

Growth reactions and other characteristics

	myo-Inositol	DL-Lactate	Succinate	Citrate	D-Gluconate	D-Glucosamine	*N*-Acetyl-D-glucosamine	Hexadecane	Nitrate	Nitrite	Vitamin-free	2-Keto-D-gluconate	5-Keto-D-gluconate	Saccharate	Xylitol	L-Arabinitol	Arbutin	Propane 1,2 diol	Butane 2,3 diol	Cadaverine	Creatinine
Cystofilobasidium (*cont'd*)																					
542	+	+	+	+	+	−	n	n	+	+	−	n	n	−	+	n	n	n	n	n	n
543	+	+	+	+	+	−	n	n	+	+	−	n	n	−	+	n	n	n	n	n	n
Debaryomyces																					
545	−	−	+	+	+	+	+	−	−	n	−	+	−	−	n	n	n	n	n	n	n
546	−	v	+	+	+	+	v	−	−	n	−	+	−	−	n	n	n	n	n	n	n
547	−	v	+	v	+	v	v	v	−	n	−	+	v	−	n	n	n	n	n	n	n
548	−	−	+	+	+	v	+	−	−	n	−	+	−	−	n	n	n	n	n	n	n
549	−	−	−	−	−	−	n	n	−	n	−	−	−	n	n	n	n	n	n	n	n
550	−	v	+	+	+	+	v	−	−	n	−	+	−	−	n	n	n	n	n	n	n
551	−	−	+	+	+	−	+	−	−	n	−	+	−	−	n	n	n	n	n	n	n
552	−	−	+	+	+	−	+	+	−	n	+	+	−	−	n	n	n	n	n	n	n
553	−	−	−	−	−	+	n	n	−	n	n	−	−	n	n	n	n	n	n	n	n
554	−	+	+	+	+	+	v	v	−	n	−	+	−	−	n	n	n	n	n	n	n
555	−	−	+	+	+	v	+	+	−	n	−	+	−	−	n	n	n	n	n	n	n
Dekkera																					
557	−	v	v	−	−	+	+	n	v	n	−	−	n	−	−	n	n	n	n	n	n
558	−	v	−	−	−	v	+	+	v	n	−	−	n	−	−	n	n	n	n	n	n
Dioszegia																					
560	−	+	+	+	+	+	+	−	−	+	−	+	+	−	+	+	n	−	−	−	n
561	−	−	+	+	+	+	+	−	−	+	+	+	+	+	+	+	n	−	−	−	n
562	v	+	+	+	+	+	+	−	−	v	−	+	+	+	+	−	n	−	−	−	n
563	−	−	+	−	+	+	+	−	−	+	+	+	+	+	+	+	n	−	−	−	n
564	−	+	+	+	+	+	+	−	−	+	−	+	+	+	+	+	n	−	−	+	n
565	−	+	+	+	+	+	+	−	−	+	−	+	+	−	+	+	n	−	−	−	n
566	+	−	+	+	+	+	+	−	−	+	−	+	+	+	+	+	n	−	−	−	n
567	−	+	+	−	+	+	+	−	−	n	−	n	n	n	n	n	n	n	n	n	n
568	v	v	+	+	+	+	+	−	−	+	−	+	+	+	+	−	n	−	−	−	n
569	−	v	+	v	+	+	+	−	−	+	−	+	+	+	+	+	n	−	−	−	n
570	−	v	+	v	+	+	+	−	−	+	−	+	+	+	+	+	n	−	−	−	n
Dipodascopsis																					
572	−	−	−	−	−	−	n	−	−	n	−	−	n	n	n	n	n	n	n	n	n
573	+	−	+	−	v	−	n	n	−	n	−	n	n	n	n	+	n	n	n	n	n
574	+	−	−	−	v	−	n	n	−	n	−	n	n	n	n	+	n	n	n	n	n
575	+	−	−	−	v	−	n	n	−	n	−	n	n	n	n	+	n	n	n	n	n
Dipodascus																					
577	−	v	+	+	−	−	n	n	−	n	−	−	n	n	−	n	−	n	n	n	n
578	−	+	+	−	−	−	n	n	−	n	−	−	n	n	−	n	−	n	n	n	n
579	−	v	+	v	−	−	n	n	−	n	+	−	n	n	−	n	−	n	n	n	n
580	−	+	+	−	−	−	n	n	−	n	−	−	n	n	−	n	−	n	n	n	n
581	−	+	+	+	−	−	n	n	−	n	−	−	n	n	n	n	−	n	n	n	n
582	−	+	+	+	−	−	n	n	n	−	+	−	n	n	−	n	−	n	n	n	n
Eremothecium																					
584	−	−	v	v	−	−	−	−	−	n	−	−	−	−	n	n	n	n	n	n	n
585	−	−	+	−	−	−	−	−	−	n	−	−	−	n	n	n	n	n	n	−	n
586	−	−	v	−	−	−	−	−	−	n	−	−	−	−	n	n	n	n	n	n	n
587	−	−	+	+	v	−	−	−	−	n	−	−	−	−	n	n	n	n	n	n	n
588	−	−	−	−	−	−	−	−	−	n	−	−	−	−	n	n	n	n	n	n	n
Erythrobasidium																					
590	−	+	+	+	−	+	n	n	+	+	−	+	n	n	n	n	+	n	n	−	−
Fellomyces																					
592	+	+	+	+	+	+	n	n	−	n	+	+	n	n	n	+	+	n	n	−	−
593	+	+	+	+	+	+	n	n	−	n	+	+	n	n	n	v	+	n	n	v	−
594	−	−	+	+	+	+	n	n	−	n	−	+	+	n	n	+	+	n	n	−	−
595	+	−	+	+	+	+	n	n	−	n	−	+	+	n	n	n	+	n	n	n	n

	L-Lysine	Ethylamine	50% Glucose	10% NaCl/5% glucose	Starch formation	Urease	Gelatin liquefaction	Cycloheximide 0.01%	Cycloheximide 0.1%	Growth at 19°C	Growth at 25°C	Growth at 30°C	Growth at 35°C	Growth at 37°C	Growth at 40°C	Growth at 45°C	CoQ (Main component)	Mol% G + C (Ave.)	DBB
Cystofilobasidium (*cont'd*)																			
542	n	n	n	n	+	+	n	+	+	+	+	−	−	−	−	−	n	n	+
543	n	n	n	n	+	+	n	v	−	+	+	−	−	−	−	−	8	61.2	+
Debaryomyces																			
545	n	n	n	+	−	n	n	n	n	+	+	−	−	−	−	−	9	37.4	−
546	n	n	−	+	−	n	n	n	n	+	+	+	n	−	−	−	9	35.3	−
547	n	n	−	+	−	n	n	n	n	+	+	+	n	−	−	−	9	36.8	−
548	n	n	−	+	−	n	n	n	n	+	+	−	−	−	−	−	9	39.1	−
549	n	n	−	−	−	n	n	n	n	+	+	+	n	−	−	−	9	38.5	−
550	n	n	−	+	−	n	n	n	n	+	+	+	n	v	−	−	9	37.8	−
551	n	n	+	+	−	n	n	n	n	+	+	+	+	+	n	−	n	37.5	−
552	n	n	−	+	−	n	n	n	n	+	+	+	n	−	−	−	9	42.7	−
553	n	n	−	n	−	n	n	n	n	+	+	+	n	−	−	−	n	n	−
554	n	n	−	+	−	n	n	n	n	+	+	+	+	+	n	n	9	35.4	−
555	n	n	−	+	−	n	n	n	n	+	+	−	−	−	−	−	9	35.8	−
Dekkera																			
557	n	n	−	n	−	n	n	+	v	+	+	+	+	+	n	n	9	40.0	−
558	n	n	−	n	−	n	n	+	v	+	+	+	+	+	n	n	9	39.4	−
Dioszegia																			
560	+	−	−	n	+	+	n	n	n	+	+	−	−	−	−	−	10	50.0	+
561	+	−	n	n	+	+	n	n	n	+	+	−	−	−	−	−	n	n	+
562	+	−	n	n	+	+	n	n	n	+	+	−	−	−	−	−	n	n	+
563	+	−	−	n	+	+	n	n	n	+	+	−	−	−	−	−	10	n	+
564	+	−	−	n	+	+	+	n	n	+	+	−	−	−	−	−	10	52.5	+
565	+	+	n	n	+	+	n	n	n	+	−	−	−	−	−	−	n	n	+
566	+	−	−	−	+	+	−	n	n	+	v	−	−	−	−	−	10	55.4	+
567	n	n	−	+	+	+	−	n	n	+	−	−	−	−	−	−	n	n	+
568	+	−	n	n	+	+	n	n	n	+	+	−	−	−	−	−	n	n	+
569	+	−	−	n	+	+	n	n	n	+	+	−	−	−	−	−	10	50.0	+
570	+	−	−	n	+	+	n	n	n	+	+	−	−	−	−	−	10	50.6	+
Dipodascopsis																			
572	n	n	−	n	+	n	n	+	+	+	+	−	−	−	−	−	9	43.5	−
573	n	n	+	n	+	n	n	+	+	+	+	n	n	−	−	−	9	n	−
574	n	n	+	n	+	n	n	+	+	+	+	+	+	+	n	n	9	n	−
575	n	n	+	n	+	n	n	+	+	+	+	+	+	+	n	n	9	n	−
Dipodascus																			
577	n	n	n	n	−	n	n	n	n	+	+	+	−	−	−	−	n	45.1	−
578	n	n	n	n	−	n	n	n	n	+	+	−	−	−	−	−	9	37.4	−
579	n	n	n	n	−	n	n	n	n	+	+	−	−	−	−	−	n	42.2	−
580	n	n	n	n	−	n	n	n	n	+	+	+	+	+	+	n	n	38.5	−
581	n	n	n	n	−	n	n	n	n	+	+	+	+	−	−	−	n	42.7	−
582	n	n	n	n	−	n	n	n	n	+	+	−	−	−	−	−	n	42.3	−
Eremothecium																			
584	n	n	n	−	−	n	+	n	n	+	+	+	+	+	n	n	6	n	−
585	−	−	−	−	−	−	v	+	n	+	+	+	+	+	+	−	5/6	43.3	−
586	n	n	n	−	−	n	−	n	n	+	+	+	+	v	n	n	7	n	−
587	n	n	n	−	−	n	v	n	n	+	+	+	+	+	n	n	6	n	−
588	n	n	n	−	−	n	−	+	n	+	+	+	+	+	+	−	9	41.8	−
Erythrobasidium																			
590	+	+	−	n	−	+	n	n	n	+	+	n	n	−	−	−	10	55.7	+
Fellomyces																			
592	+	n	−	−	+	+	n	+	+	+	+	+	n	−	−	−	10	n	+
593	v	n	−	−	v	+	n	+	+	+	+	v	n	−	−	−	10	n	+
594	+	n	−	−	−	+	−	+	+	+	+	−	−	−	−	−	10	51.4	+
595	n	−	−	+	v	+	n	n	n	+	+	n	n	−	−	−	10	54.9	+

Symbols: +, positive or weak; −, negative; v, variable (+/−, w/−); n, no data.

Ln. no.	Species	Fermentation							Growth reactions and other characteristics																																	
		Glucose	Galactose	Sucrose	Maltose	Lactose	Raffinose	Trehalose	Glucose	Inulin	Sucrose	Raffinose	Melibiose	Galactose	Lactose	Trehalose	Maltose	Melezitose	Methyl-α-D-glucoside	Soluble Starch	Cellobiose	Salicin	L-Sorbose	L-Rhamnose	D-Xylose	L-Arabinose	D-Arabinose	D-Ribose	Methanol	Ethanol	Glycerol	Erythritol	Ribitol	Galactitol	D-Mannitol	D-Glucitol					
Fellomyces (*cont'd*)																																									
596	*F. horovitziae*	−	−	−	−	−	−	−	+	−	+	+	+	+	+	+	+	+	−	−	+	−	+	−	+	+	+	+	−	−	−	−	−	−	−	−	+					
597	*F. lichenicola*	−	−	−	−	−	−	−	+	v	+	+	+	+	+	+	v	+	−	v	+	+	−	+	+	+	+	+	−	−	+	−	v	+	+	+					
598	*F. mexicanus*	−	−	−	−	−	−	−	+	−	+	+	v	+	+	+	+	+	−	−	+	−	−	+	+	+	+	+	−	−	−	−	+	+	v	+					
599	*F. ogasawarensis*	−	−	−	−	−	−	−	+	−	+	+	+	+	+	+	+	+	−	+	+	+	+	+	+	+	+	+	+	−	−	+	−	+	+	+	+					
600	*F. penicillatus*	−	−	−	−	−	−	−	+	−	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	−	−	+	+	+	+	+	+					
601	*F. polyborus*	−	−	−	−	−	−	−	+	−	+	v	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	−	−	+	+	+	+	+	+					
602	*F. sichuanensis*	−	−	−	−	−	−	−	+	+	+	+	+	+	+	+	+	+	−	v	+	+	−	+	+	+	+	+	+	−	−	+	+	+	+	+	+					
603	*F. thailandicus*	−	−	−	−	−	−	−	+	−	+	+	+	+	+	+	+	+	−	−	+	+	+	+	+	+	+	+	+	−	−	+	+	+	+	+	+					
604	***Fibulobasidium***																																									
605	*F. inconspicuum*	−	−	−	−	−	−	−	+	−	+	+	−	v	+	+	+	+	+	v	+	+	+	+	+	+	+	+	+	−	+	v	+	+	+	+	+					
606	*F. murrhardtense*	−	−	−	−	−	−	−	+	−	+	−	−	−	−	+	−	+	−	+	+	−	−	+	+	+	+	−	−	−	−	−	−	+	−	+	+					
607	***Filobasidiella***																																									
608	*F. bacillispora*	−	−	−	−	−	−	−	+	v	+	+	−	+	−	+	+	+	+	+	+	+	−	+	+	+	+	v	−	−	−	−	v	+	+	+					
609	*F. neoformans*	−	−	−	−	−	−	−	+	v	+	+	−	+	−	+	+	+	+	+	+	+	−	+	+	+	+	v	−	v	−	−	v	+	+	+					
610	***Filobasidium***																																									
611	*F. capsuligenum*	+	−	−	v	−	−	−	+	−	+	+	−	+	−	+	−	+	+	+	+	−	−	v	v	v	v	−	+	+	−	+	v	+	+						
612	*F. elegans*	−	−	−	−	−	−	−	+	−	+	−	−	−	−	+	+	−	−	+	+	−	−	+	+	−	−	−	−	−	−	−	−	v	v						
613	*F. floriforme*	−	−	−	−	−	−	−	+	−	+	+	−	+	+	+	+	+	+	+	+	v	+	+	+	+	+	+	−	+	+	−	+	+	+	+					
614	*F. globisporum*	−	−	−	−	−	−	−	+	−	−	−	−	−	+	+	+	−	−	+	+	+	−	+	+	+	−	−	−	−	−	−	−	−	−	−					
615	*F. uniguttulatum*	−	−	−	−	−	−	−	+	−	+	+	−	v	−	+	+	+	+	v	−	+	v	+	+	+	v	−	−	+	+	−	+	−	+	+					
616	***Galactomyces***																																									
617	*G. candidus*	v	v	−	−	−	−	−	+	−	−	−	−	+	−	−	−	−	−	−	−	−	−	+	−	+	−	−	−	−	+	+	−	v	−	+	+					
618	*G. citri-aurantii*	v	v	−	−	−	−	−	+	−	−	−	−	+	−	−	−	−	−	−	−	−	−	+	−	+	v	−	−	−	+	+	−	+	−	+	+					
619	*G. geotrichum*	v	−	−	−	−	−	−	+	−	−	−	−	+	−	−	−	−	−	−	−	−	−	+	−	+	−	−	−	−	+	+	−	−	−	+	+					
620	*G. pseudocandidus*	−	−	−	−	−	−	−	+	−	−	−	−	+	−	−	−	−	−	−	−	−	−	+	−	+	−	−	−	−	+	+	−	−	−	+	+					
621	*G. reessii*	−	−	−	−	−	−	−	+	−	−	−	−	+	−	−	−	−	−	−	−	−	−	+	−	+	−	−	−	−	+	+	−	−	−	+	+					
622	***Geotrichum***																																									
623	*G. carabidarum*	+	−	−	−	−	−	−	+	−	−	−	−	−	−	−	−	−	−	−	−	−	−	+	−	+	−	−	−	−	+	+	−	−	−	v	+					
624	*G. cucujoidarum*	−	−	−	−	−	−	−	+	−	−	−	−	+	−	−	−	−	−	v	+	+	−	−	v	−	−	−	−	−	+	+	−	+	−	+	+					
625	*G. europaeum*	−	−	−	−	−	−	−	+	−	−	−	−	+	−	−	−	−	−	−	−	−	−	+	−	+	−	−	−	−	+	+	−	−	−	−	+					
626	*G. fermentans*	+	+	−	−	−	−	n	+	−	−	−	−	+	−	−	−	−	−	−	+	v	−	+	−	+	v	v	+	−	+	+	−	v	−	+	+					
627	*G. histeridarum*	+	−	−	−	−	−	−	+	−	−	−	−	+	−	−	−	−	−	−	−	−	−	+	−	+	−	−	−	−	+	+	−	v	−	+	+					
628	*G. klebahnii*	v	v	−	−	−	−	n	+	−	−	−	−	+	−	−	−	−	−	−	−	−	−	+	−	+	−	−	−	−	+	+	−	v	−	+	+					
629	*G. restrictum*	−	−	−	−	−	−	−	+	−	−	−	−	+	−	−	−	−	−	−	−	−	−	+	−	+	−	−	−	−	+	+	−	−	−	+	+					
630	***Guehomyces***																																									
631	*G. pullulans*	−	−	−	−	−	−	−	+	−	+	+	+	+	+	+	+	v	+	+	+	v	v	v	+	+	v	v	−	+	v	+	+	−	+	+					
632	***Hanseniaspora***																																									
633	*H. clermontiae*	+	−	−	−	−	−	−	+	−	−	−	−	−	−	−	−	−	−	−	+	+	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−					
634	*H. guilliermondii*	+	−	−	−	−	−	−	+	−	−	−	−	−	−	−	−	−	−	−	+	+	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−					
635	*H. lachancei*	+	−	−	−	−	−	−	+	−	−	−	−	−	−	−	−	−	−	−	+	+	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−					
636	*H. meyeri*	+	−	−	−	−	−	−	+	−	−	−	−	−	−	−	−	−	−	−	+	+	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−					
637	*H. occidentalis* var. *occidentalis*	+	−	+	−	−	−	−	+	−	+	−	−	−	−	−	−	−	−	−	+	+	−	−	−	−	−	−	−	−	−	v	−	−	−	−	−					
638	*H. occidentalis* var. *citrica*	+	−	+	−	−	−	−	+	−	+	−	−	−	−	+	−	−	−	−	+	+	−	−	−	−	−	−	−	−	−	v	−	−	−	−	−					
639	*H. opuntiae*	+	−	−	−	−	−	−	+	−	−	−	−	−	−	−	−	−	−	−	+	+	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−					
640	*H. osmophila*	+	−	−	−	−	−	−	+	−	v	−	−	−	−	−	v	−	−	−	+	+	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−					
641	*H. pseudoguilliermondii*	+	−	−	−	−	−	−	+	−	−	−	−	−	−	−	−	−	−	−	+	+	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−					
642	*H. uvarum*	+	−	−	−	−	−	−	+	−	−	−	−	−	−	−	−	−	−	−	+	+	−	−	−	−	−	−	−	−	−	−	−	−	−	−	v					
643	*H. valbyensis*	+	−	−	−	−	−	−	+	−	−	−	−	−	−	−	−	−	−	−	+	+	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−					
644	*H. vineae*	+	−	−	−	−	−	−	+	−	v	−	−	−	−	−	v	−	−	−	+	+	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−					
645	***Holtermannia***																																									
646	*H. corniformis*	−	−	−	−	−	−	−	+	−	v	−	−	+	−	+	+	v	v	+	+	+	+	+	+	+	+	v	−	+	v	−	+	+	+	+					
647	***Hyphopichia***																																									
648	*H. burtonii*	+	v	+	+	−	+	+	+	−	+	+	−	+	−	+	+	v	+	+	+	+	v	−	+	v	−	+	−	+	+	+	+	−	+	+					
649	*H. heimii*	+	+	+	v	−	−	+	+	−	+	+	−	+	−	+	+	+	+	−	+	+	−	+	+	+	−	+	−	+	+	+	+	+	+	+					

Symbols: +, positive or weak; −, negative; v, variable (+/−, w/−); n, no data.

	Growth reactions and other characteristics																																							
	myo-Inositol	DL-Lactate	Succinate	Citrate	D-Gluconate	D-Glucosamine	*N*-Acetyl-D-glucosamine	Hexadecane	Nitrate	Nitrite	Vitamin-free	2-Keto-D-gluconate	5-Keto-D-gluconate	Saccharate	Xylitol	L-Arabinitol	Arbutin	Propane 1,2 diol	Butane 2,3 diol	Cadaverine	Creatinine	L-Lysine	Ethylamine	50% Glucose	10% NaCl/5% glucose	Starch formation	Urease	Gelatin liquefaction	Cycloheximide 0.01%	Cycloheximide 0.1%	Growth at 19°C	Growth at 25°C	Growth at 30°C	Growth at 35°C	Growth at 37°C	Growth at 40°C	Growth at 45°C	CoQ (Main component)	Mol% G + C (Ave.)	DBB
Fellomyces (*cont'd*)																																								
596	−	−	+	+	−	+	n	n	−	n	−	−	−	n	n	−	+	n	n	−	−	+	+	−	n	−	+	n	+	+	+	+	−	−	−	−	−	10	54.2	+
597	+	+	+	+	+	+	n	n	−	n	+	+	n	n	n	+	+	n	n	−	−	+	n	v	−	v	+	n	+	+	+	+	−	−	−	−	−	10	n	+
598	−	v	+	+	v	+	n	n	−	n	+	+	+	n	n	+	−	n	n	−	−	−	n	−	−	+	+	n	+	+	+	+	−	−	−	−	−	10	n	+
599	−	+	+	+	+	+	n	n	−	n	−	+	+	n	n	+	+	n	n	−	−	+	n	−	−	−	+	−	+	+	+	+	−	−	−	−	−	10	53.3	+
600	+	v	+	+	+	+	n	n	−	n	−	+	+	n	n	n	+	n	n	n	n	n	−	−	n	+	+	n	n	n	+	+	+	+	+	n	n	10	48.8	+
601	+	+	+	+	+	+	n	−	−	n	−	+	+	n	n	n	+	n	n	n	n	n	−	−	+	−	+	n	+	+	+	+	+	n	−	−	−	10	49.6	+
602	+	+	+	+	+	+	n	n	−	n	+	+	n	n	n	+	+	n	n	−	−	+	n	−	−	−	+	n	+	+	+	+	+	n	−	−	−	10	n	+
603	+	−	+	+	+	+	n	n	−	n	+	+	n	n	n	+	+	n	n	−	−	+	n	−	−	v	+	n	+	+	+	+	+	n	−	−	−	10	n	+
Fibulobasidium																																								
605	+	+	+	v	+	+	n	n	−	+	−	+	n	n	n	n	n	n	n	n	n	n	n	−	n	+	+	n	n	n	+	+	v	n	−	−	−	n	n	+
606	+	−	+	−	+	−	n	n	−	−	−	n	n	n	n	n	n	n	n	n	n	n	n	n	n	+	+	n	n	n	+	+	+	n	−	−	−	n	n	+
Filobasidiella																																								
608	+	−	v	−	+	v	v	−	−	−	−	v	n	v	n	n	n	n	n	n	n	+	−	n	−	+	+	n	n	n	+	+	+	+	+	−	−	n	56.8	+
609	+	−	v	v	+	v	v	−	−	−	−	v	n	v	n	n	n	n	n	n	n	v	−	n	−	+	+	n	n	n	+	+	+	+	+	+	n	10	55.0	+
Filobasidium																																								
611	+	−	+	+	v	v	v	v	−	−	−	−	n	−	n	n	n	n	n	n	−	+	+	−	n	+	+	n	n	n	+	+	+	n	v	n	n	10	49.8	+
612	−	−	v	−	−	−	n	n	−	+	−	−	n	−	n	n	n	n	n	n	−	−	−	−	−	+	−	n	n	n	+	+	−	−	−	−	−	n	n	+
613	+	−	+	+	+	+	v	−	+	+	−	+	n	+	n	n	n	n	n	n	−	+	+	−	−	+	+	n	n	n	+	+	+	n	−	−	−	10	52.0	+
614	+	−	−	v	+	−	−	n	−	n	−	+	n	−	n	n	n	n	n	n	−	−	−	−	−	+	n	n	n	n	+	+	n	n	n	n	n	n	n	+
615	+	v	+	v	+	−	+	+	−	−	−	+	n	−	n	n	n	n	n	n	−	+	−	+	n	n	+	n	n	n	+	+	+	−	−	−	−	9	49.8	+
Galactomyces																																								
617	−	+	+	v	−	−	n	n	−	n	+	n	n	n	−	n	−	n	n	n	n	n	n	n	n	−	n	n	n	n	+	+	+	+	v	−	−	n	42.0	−
618	−	+	+	+	−	−	n	n	−	n	−	n	n	n	−	n	−	n	n	n	n	n	n	n	n	−	n	n	n	n	+	+	+	−	−	−	−	n	40.9	−
619	−	v	+	v	−	−	n	n	−	n	−	n	n	n	−	n	−	n	n	n	n	n	n	n	n	−	n	n	n	n	+	+	+	−	−	−	−	n	42.3	−
620	−	+	+	v	−	−	n	n	−	n	+	n	n	n	−	n	−	n	n	n	n	n	n	n	n	−	n	n	n	n	+	+	+	v	−	−	−	n	42.4	−
621	−	+	+	v	−	−	n	n	−	n	−	n	n	n	−	n	−	n	n	n	n	n	n	n	n	−	n	n	n	n	+	+	+	v	−	−	−	n	41.0	−
Geotrichum																																								
623	−	+	+	+	−	−	n	n	−	n	−	v	n	n	−	n	−	n	n	n	n	n	n	n	n	n	n	n	n	n	+	+	+	−	−	−	−	n	n	−
624	−	+	+	v	v	−	n	n	−	n	+	v	n	n	−	n	+	n	n	n	n	n	n	n	n	n	n	n	n	n	+	+	+	+	+	n	n	n	n	−
625	−	+	+	+	−	−	n	n	−	n	+	−	n	n	−	n	−	n	n	n	n	n	n	n	n	n	n	n	n	n	+	+	+	−	−	−	−	n	43.0	−
626	−	+	+	+	−	−	n	n	−	n	+	−	n	n	v	n	+	n	n	n	n	n	n	n	n	n	n	n	n	n	+	+	+	+	v	−	−	n	45.2	−
627	−	+	+	+	v	−	n	n	−	n	−	v	n	n	v	n	−	n	n	n	n	n	n	n	n	n	n	n	n	n	+	+	+	−	−	−	−	n	n	−
628	−	+	+	v	−	−	n	n	−	n	+	−	n	n	−	n	+	n	n	n	n	n	n	n	n	n	n	n	n	n	+	+	v	−	−	−	−	n	41.1	−
629	−	−	n	n	−	−	n	n	−	n	−	n	n	n	n	n	n	n	n	n	n	n	n	n	n	−	n	n	n	n	+	+	−	−	−	−	−	n	42.7	−
Guehomyces																																								
631	+	−	+	+	+	−	−	n	+	+	v	+	+	n	+	n	n	n	n	v	n	v	v	+	+	+	n	n	n	n	+	v	−	−	−	−	−	9	57.8	+
Hanseniaspora																																								
633	−	−	−	−	+	−	n	n	−	n	−	+	n	n	n	n	n	n	n	n	n	n	n	n	n	−	n	n	+	n	+	+	n	n	−	−	−	n	36.5	−
634	−	−	−	−	v	−	n	n	−	n	−	+	n	−	n	n	n	n	n	n	n	n	n	n	n	n	n	n	+	n	+	+	+	+	+	−	−	6	33.5	−
635	−	−	−	−	+	−	n	n	−	n	−	−	n	n	n	n	n	n	n	n	n	n	n	n	n	−	n	n	+	n	+	+	+	+	+	−	−	n	35.2	−
636	−	−	−	−	+	−	n	n	−	n	−	+	n	n	n	n	n	n	n	n	n	n	n	n	n	−	n	n	+	n	+	+	+	−	−	−	−	n	37.0	−
637	−	−	−	−	−	−	n	n	−	n	−	−	n	n	n	n	n	n	n	n	n	n	n	n	n	−	n	n	−	−	+	+	+	n	−	−	−	6	35.4	−
638	−	−	−	−	−	−	n	n	−	n	−	−	n	n	n	n	n	n	n	n	n	n	n	n	n	−	n	n	−	−	+	+	+	n	−	−	−	6	n	−
639	−	−	−	−	+	−	n	n	−	n	−	+	n	n	n	n	n	n	n	n	n	n	n	n	n	−	n	n	+	n	+	+	+	+	+	−	−	n	34.5	−
640	−	−	−	−	−	−	n	n	−	n	−	−	n	n	n	n	n	n	n	n	n	n	n	n	n	−	n	n	−	−	+	+	+	−	−	−	−	6	40.1	−
641	−	−	−	−	+	−	n	n	−	n	−	+	n	n	n	n	n	n	n	n	n	n	n	n	n	−	n	n	+	n	+	+	+	+	+	−	−	n	31.5	−
642	−	−	−	−	v	−	n	n	−	n	−	+	n	n	n	n	n	n	n	n	n	n	n	n	n	−	n	n	+	n	+	+	+	n	−	−	−	6	33.9	−
643	−	−	−	−	−	−	n	n	−	n	−	−	n	n	n	n	n	n	n	n	n	n	n	n	n	−	n	n	+	n	+	+	v	n	−	−	−	6	29.4	−
644	−	−	−	−	−	−	n	n	−	n	−	−	n	n	n	n	n	n	n	n	n	n	n	n	n	−	n	n	−	−	+	+	+	n	−	−	−	6	39.7	−
Holtermannia																																								
646	+	+	+	+	+	−	n	n	−	−	v	+	n	n	n	n	n	n	n	n	n	n	n	−	n	+	+	n	n	n	+	+	v	v	v	n	n	n	n	+
Hyphopichia																																								
648	−	−	+	+	v	+	+	+	−	n	+	+	−	−	n	n	n	n	n	n	n	n	n	n	+	−	n	+	n	n	+	+	+	n	v	n	n	8	36.5	−
649	−	−	+	+	v	+	+	+	−	n	+	+	−	−	n	n	n	n	n	n	n	n	n	n	+	−	n	−	n	n	+	+	+	n	−	−	−	n	39.7	−

Symbols: +, positive or weak; −, negative; v, variable (+/−, w/−); n, no data.

Ln. no.	Species	Fermentation: Glucose	Galactose	Sucrose	Maltose	Lactose	Raffinose	Trehalose	Growth reactions and other characteristics: Glucose	Inulin	Sucrose	Raffinose	Melibiose	Galactose	Lactose	Trehalose	Maltose	Melezitose	Methyl-α-D-glucoside	Soluble Starch	Cellobiose	Salicin	L-Sorbose	L-Rhamnose	D-Xylose	L-Arabinose	D-Arabinose	D-Ribose	Methanol	Ethanol	Glycerol	Erythritol	Ribitol	Galactitol	D-Mannitol	D-Glucitol
650	***Itersonilia***																																		
651	*I. perplexans*	−	−	−	−	−	−	−	+	v	+	+	v	+	v	+	v	+	−	+	+	v	−	v	+	v	v	v	−	v	v	−	v	−	+	v
652	***Kazachstania***																																			
653	*K. aerobica*	+	+	−	v	−	−	−	+	−	−	−	−	+	−	+	−	−	−	−	−	−	−	−	−	−	−	v	−	−	+	−	−	−	v	−
654	*K. africana*	+	+	−	−	−	−	−	+	−	−	−	−	+	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	v	−	−	−	−	−
655	*K. aquatica*	+	+	−	−	−	−	−	+	−	−	−	−	+	−	+	−	−	−	−	−	−	−	−	−	−	−	−	−	+	−	−	−	−	−	−
656	*K. barnettii*	+	+	+	−	−	+	+	+	−	+	+	−	+	−	+	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−
657	*K. bovina*	+	−	−	−	−	−	−	+	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	+	−	−	−	−	−	−
658	*K. bulderi*	+	+	v	−	−	v	v	+	−	+	+	v	+	−	+	+	−	−	−	v	−	−	−	+	v	−	v	−	−	+	−	−	−	+	−
659	*K. exigua*	+	+	+	−	−	v	+	+	−	+	+	−	+	−	+	−	−	−	−	−	−	−	−	−	−	−	−	−	+	v	−	−	−	−	−
660	*K. gamospora*	+	−	+	−	−	+	−	+	+	+	−	−	−	−	+	−	−	−	−	−	−	−	n	−	−	−	−	n	+	+	−	−	−	−	−
661	*K. hellenica*	+	+	+	−	−	−	−	+	+	+	+	−	+	−	+	+	+	n	−	+	+	−	−	−	+	+	−	−	−	−	+	n	n	n	−	+
662	*K. heterogenica*	+	−	−	−	−	−	−	+	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	v	−	−	−	−	−	−
663	*K. humantica*	+	+	−	−	−	−	−	+	−	−	−	−	+	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−
664	*K. jiainica*	+	+	−	+	−	−	−	+	−	−	−	−	+	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−
665	*K. kunashirensis*	+	+	−	−	−	−	−	+	−	−	−	−	+	−	+	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	+	−	−	−	−	−
666	*K. lodderae*	+	+	v	v	−	+	+	+	−	+	+	−	+	−	+	−	−	v	−	−	v	−	−	−	−	−	−	−	−	+	+	−	−	−	−	−
667	*K. martiniae*	+	+	−	−	−	−	−	+	−	−	−	−	+	−	+	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	v	−	−	−	−	−
668	*K. naganishii*	+	+	v	−	−	+	v	+	−	+	+	−	+	−	+	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	+	−	−	−	−	−
669	*K. piceae*	+	−	−	−	−	−	−	+	−	+	+	−	+	−	+	+	+	−	+	−	+	+	+	−	−	−	−	+	−	+	+	−	−	v	+	+
670	*K. pintolopesii*	+	−	−	−	−	−	−	+	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	v	−	−	−	−	−	−
671	*K. rosinii*	+	+	−	−	−	−	−	+	−	−	−	−	+	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−
672	*K. servazzii*	+	+	−	−	−	−	−	+	−	v	−	−	+	−	+	−	−	−	−	−	−	−	−	−	−	−	−	−	−	v	+	−	−	−	−	−
673	*K. siamensis*	+	+	−	−	−	−	−	+	−	−	n	−	+	−	+	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−
674	*K. sinensis*	+	+	+	−	−	+	−	+	−	−	+	−	−	−	+	−	−	−	−	+	−	−	−	−	−	−	−	−	n	−	−	−	−	−	−	−
675	*K. slooffiae*	+	−	−	−	−	−	−	+	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−
676	*K. solicola*	+	+	−	−	−	−	−	+	−	−	−	−	+	−	+	−	−	−	−	−	−	−	−	−	−	−	−	v	+	−	+	−	−	−	−	−
677	*K. spencerorum*	+	+	−	−	−	−	v	+	−	−	−	−	+	−	+	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	+	−	−	−	v	−
678	*K. telluris*	+	−	−	−	−	−	−	+	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	+	−	−	−	−	−	−
679	*K. transvaalensis*	+	+	−	−	−	−	−	+	−	−	−	−	+	−	+	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−
680	*K. turicensis*	v	−	−	−	−	−	−	+	−	v	−	−	v	−	+	−	−	−	−	−	−	−	−	−	−	−	−	−	−	v	−	−	−	−	−	−
681	*K. unispora*	+	+	−	−	−	−	−	+	−	−	−	−	+	−	v	−	−	−	−	−	−	−	−	−	−	−	−	−	−	+	−	−	−	−	−	−
682	*K. viticola*	+	+	−	−	−	−	−	+	−	−	−	−	+	−	+	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	+	−	−	−	−	−
683	*K. yakushimaenisis*	+	+	−	−	−	−	−	+	−	−	−	−	+	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−
684	*K. zonata*	+	−	+	−	−	+	−	+	+	+	+	−	−	−	+	−	−	−	−	−	−	−	n	−	−	−	−	n	+	+	−	−	−	−	−	−
685	***Kloeckera***																																				
686	*K. lindneri*	+	−	−	−	−	−	−	+	−	−	−	−	−	−	−	−	−	−	−	+	+	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−
687	***Kluyveromyces***																																				
688	*K. aestuarii*	+	v	+	−	−	+	−	+	−	+	v	−	+	+	−	v	−	v	−	+	+	−	−	−	−	−	−	−	−	v	+	−	−	−	v	v
689	*K. dobzhanskii*	+	+	+	+	−	+	+	+	−	+	+	−	+	−	+	+	+	+	−	+	+	+	−	−	−	−	−	−	−	+	+	−	−	−	+	+
690	*K. lactis* var. *lactis*	+	+	v	v	+	v	v	+	v	+	v	−	+	+	+	v	+	v	−	+	+	v	−	v	−	−	−	−	−	+	v	−	v	−	+	+
691	*K. lactis* var. *drosophilarum*	+	+	v	v	−	v	v	+	v	+	v	−	+	+	+	v	+	v	−	+	+	v	−	v	−	−	−	−	−	+	v	−	v	−	+	+
692	*K. marxianus*	+	+	+	−	v	+	−	+	v	+	+	−	+	v	−	−	−	−	−	v	v	−	−	v	v	−	v	−	−	+	v	−	v	−	v	v
693	*K. nonfermentans*	−	−	−	−	−	−	−	+	−	−	−	−	+	+	−	−	−	−	−	v	v	−	−	−	−	−	−	−	−	+	−	−	v	−	+	−
694	*K. wickerhamii*	+	+	+	−	−	−	−	+	−	+	−	−	+	+	−	−	−	−	−	+	+	v	−	+	−	−	−	−	−	+	v	−	−	−	−	+
695	***Kockovaella***																																				
696	*K. barringtoniae*	−	−	−	−	−	−	−	+	−	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	−	+	+	+	+	+	+	+
697	*K. calophylli*	−	−	−	−	−	−	−	+	−	+	+	+	+	+	+	+	+	−	+	+	+	+	+	+	+	+	+	+	−	−	−	−	−	+	+	+
698	*K. cucphuongensis*	−	−	−	−	−	−	−	+	−	+	+	+	+	+	+	+	+	−	+	+	+	+	+	+	+	+	+	+	−	−	−	+	+	+	+	+
699	*K. imperatae*	−	−	−	−	−	−	−	+	−	+	+	+	+	+	+	+	+	−	+	+	+	v	+	+	+	+	+	+	−	−	−	v	+	+	+	+
700	*K. litseae*	−	−	−	−	−	−	−	+	−	+	+	+	+	+	+	+	+	−	+	+	+	+	+	+	+	+	+	+	−	−	+	+	+	+	+	+
701	*K. machilophila*	−	−	−	−	−	−	−	+	−	+	+	+	+	+	+	+	+	−	+	+	+	−	+	+	+	+	+	+	−	−	−	+	+	+	+	+
702	*K. phaffii*	−	−	−	−	−	−	−	+	−	+	+	−	+	+	+	+	+	−	+	+	−	−	+	+	−	+	+	+	−	−	−	−	−	+	−	
703	*K. sacchari*	−	−	−	−	−	−	−	+	−	+	+	+	+	+	+	+	+	+	+	+	+	−	+	+	+	+	+	+	−	−	−	−	+	+	+	+
704	*K. schimae*	−	−	−	−	−	−	−	+	−	+	+	−	+	+	+	+	+	−	+	+	−	−	+	+	+	+	+	+	−	−	−	−	+	+	+	+

Symbols: +, positive or weak; −, negative; v, variable (+/−, w/−); n, no data.

	Growth reactions and other characteristics																																							
	myo-Inositol	DL-Lactate	Succinate	Citrate	D-Gluconate	D-Glucosamine	*N*-Acetyl-D-glucosamine	Hexadecane	Nitrate	Nitrite	Vitamin-free	2-Keto-D-gluconate	5-Keto-D-gluconate	Saccharate	Xylitol	L-Arabinitol	Arbutin	Propane 1,2 diol	Butane 2,3 diol	Cadaverine	Creatinine	L-Lysine	Ethylamine	50% Glucose	10% NaCl/5% glucose	Starch formation	Urease	Gelatin liquefaction	Cycloheximide 0.01%	Cycloheximide 0.1%	Growth at 19°C	Growth at 25°C	Growth at 30°C	Growth at 35°C	Growth at 37°C	Growth at 40°C	Growth at 45°C	CoQ (Main component)	Mol% G + C (Ave.)	DBB
Itersonilia																																								
651	v	−	+	v	v	+	n	n	v	v	−	+	n	n	v	−	+	−	−	−	−	v	−	−	n	−	+	n	n	n	+	+	−	−	−	−	−	9	62.0	+
Kazachstania																																								
653	−	−	+	−	−	−	−	−	−	n	−	n	n	n	n	n	n	n	n	−	n	+	−	n	n	−	−	n	+	n	+	+	+	+	+	+	n	6	n	−
654	−	+	−	−	+	−	−	−	−	n	−	−	n	n	n	n	n	n	n	−	n	−	−	−	n	−	n	n	−	−	+	+	+	n	v	−	−	6	38.5	−
655	−	−	−	−	−	−	−	−	−	n	−	n	n	n	n	n	n	n	n	+	n	+	+	n	n	−	−	n	n	+	n	+	+	+	+	−	−	6	n	−
656	−	+	v	−	+	−	−	−	−	n	−	n	n	n	n	n	n	n	n	−	n	−	−	n	+	−	n	n	−	+	n	+	v	n	−	−	−	n	n	−
657	−	v	v	−	−	−	−	−	−	n	−	−	−	n	n	n	n	n	n	n	n	n	n	n	−	−	n	n	n	n	n	+	+	+	+	+	−	n	n	−
658	−	v	−	−	v	−	v	−	−	n	−	n	n	n	n	n	n	n	n	−	−	v	v	−	+	−	−	n	+	v	+	+	+	+	+	+	−	n	33.5	−
659	−	v	+	v	−	−	−	−	−	n	−	n	n	n	n	n	n	n	n	−	n	−	−	n	v	n	n	n	v	v	+	+	+	n	−	−	−	6	33.9	−
660	−	+	−	−	−	−	n	n	−	n	−	n	n	n	n	n	n	n	n	−	n	−	+	n	+	−	−	n	n	n	+	+	+	n	−	−	−	6	27.9	−
661	−	−	−	−	−	−	−	−	−	n	−	−	n	n	n	n	n	n	n	n	n	n	n	+	−	−	n	n	n	n	+	+	n	n	−	−	−	n	n	−
662	−	−	−	−	−	−	−	−	−	n	−	−	−	n	n	n	n	n	n	n	n	n	n	n	−	−	n	n	−	−	n	+	+	+	+	v	n	n	n	−
663	−	−	−	−	−	−	−	−	−	n	−	n	n	n	n	n	n	n	n	+	n	−	+	−	−	−	−	n	n	−	+	+	+	n	−	−	−	6	34.0	−
664	−	−	−	−	−	−	−	−	−	n	n	n	n	n	n	n	n	n	n	−	n	−	−	n	−	n	n	n	−	−	+	+	+	+	n	−	−	n	n	−
665	−	−	−	−	−	−	−	−	−	n	−	n	n	n	n	n	n	n	n	−	n	−	−	n	−	n	n	n	−	−	+	+	+	n	−	−	−	n	n	−
666	−	+	+	−	v	−	−	−	−	n	−	−	n	n	n	n	n	n	n	+	n	+	+	n	+	n	n	n	+	−	+	+	+	n	−	−	−	n	35.5	−
667	−	v	v	−	+	−	−	−	−	n	−	n	n	n	n	n	n	n	n	−	n	−	−	n	v	−	n	n	−	−	+	+	+	n	−	−	−	n	n	−
668	−	−	−	v	+	−	−	−	−	n	−	+	+	n	n	n	n	n	n	v	n	+	+	−	+	−	−	n	−	−	+	+	+	n	v	n	n	6	44.5	−
669	−	+	+	−	+	−	−	−	−	n	−	−	−	n	−	n	−	n	n	+	n	+	+	n	n	−	n	n	+	+	+	+	+	+	v	n	−	6	34.2	−
670	−	v	−	−	−	−	−	−	−	n	−	−	−	n	n	n	n	n	n	n	n	n	n	n	−	−	n	n	n	n	n	+	+	+	+	+	n	n	n	−
671	−	−	−	−	−	−	−	−	−	n	−	n	n	n	n	n	n	n	n	−	n	−	−	n	−	n	n	n	−	−	+	+	−	−	−	−	−	n	n	−
672	−	−	v	−	−	−	−	−	−	n	−	n	n	n	n	n	n	n	n	−	n	−	−	n	+	−	n	n	+	+	+	+	+	n	v	n	−	n	35.3	−
673	−	−	−	−	−	−	−	−	−	n	−	n	n	n	n	n	n	n	n	−	n	−	−	n	−	−	−	−	+	+	+	+	+	+	+	+	n	6	n	−
674	−	−	+	−	−	−	−	−	−	n	−	n	n	n	n	n	n	n	n	−	n	−	−	n	+	−	−	−	−	−	+	+	+	n	v	n	−	n	n	−
675	−	−	−	−	−	−	−	−	−	n	−	−	−	−	−	n	n	n	n	n	n	n	n	n	−	n	n	n	n	n	n	+	+	+	+	n	n	n	n	−
676	−	−	−	−	−	v	−	−	−	n	−	n	n	n	n	n	n	n	n	−	n	+	−	n	n	−	−	n	−	−	+	+	+	+	+	−	−	n	n	−
677	−	v	+	−	−	n	−	−	−	n	−	n	n	n	n	n	n	n	n	+	n	+	+	n	−	−	n	n	−	+	n	+	+	+	+	−	−	n	n	−
678	−	−	+	−	−	−	−	−	−	n	−	−	−	−	n	n	n	n	n	n	n	n	n	n	n	−	n	v	n	n	n	+	+	+	+	+	−	6	33.2	−
679	−	−	−	−	−	−	−	−	−	n	−	n	n	n	n	n	n	n	n	−	n	−	−	n	n	−	n	n	−	−	+	+	+	+	+	n	−	6	33.5	−
680	−	−	−	−	−	−	+	−	−	n	−	−	−	n	−	−	−	n	n	−	n	−	−	−	n	−	n	n	−	−	+	+	+	n	v	v	n	n	n	−
681	−	−	v	−	−	−	−	−	−	n	−	n	n	n	n	n	n	n	n	v	n	v	v	n	n	−	n	n	+	n	+	+	+	+	+	n	−	6	34.0	−
682	−	−	−	−	−	−	−	−	−	n	−	n	n	n	n	n	n	n	n	−	n	−	−	n	n	−	n	n	−	−	+	+	+	+	+	n	−	n	n	−
683	−	−	−	−	−	−	−	−	−	n	−	−	−	n	n	n	n	n	n	−	n	+	+	−	−	−	−	n	+	+	+	+	+	n	−	−	−	6	31.5	−
684	−	+	−	−	−	−	n	n	−	n	−	n	n	n	n	n	n	n	n	−	n	−	+	n	−	−	−	n	n	n	+	+	+	n	−	−	−	6	27.4	−
Kloeckera																																								
686	−	−	−	−	−	−	n	n	−	n	−	−	n	n	n	n	n	n	n	n	n	n	n	n	n	−	n	n	+	n	+	+	+	n	n	n	n	n	34.8	−
Kluyveromyces																																								
688	−	+	+	−	−	−	−	−	−	−	−	−	n	n	−	n	n	n	n	+	n	+	+	v	n	−	n	−	−	−	+	+	+	n	−	−	−	6	39.8	−
689	−	+	+	+	−	−	−	−	−	−	−	−	n	n	−	n	n	n	n	+	n	+	+	−	n	−	n	−	+	n	+	+	+	n	−	−	−	6	42.6	−
690	−	v	+	−	−	−	−	−	−	−	−	−	n	n	v	n	n	n	n	+	n	+	+	v	n	−	n	−	+	n	+	+	+	n	v	n	n	6	40.3	−
691	−	v	+	−	−	−	−	−	−	−	−	−	n	n	v	n	n	n	n	+	n	+	+	v	n	−	n	−	+	n	+	+	+	+	+	n	n	n	n	−
692	−	+	+	v	−	−	−	−	−	−	−	−	n	n	v	n	n	n	n	+	n	+	+	v	n	−	n	−	+	n	+	+	+	+	+	n	n	6	41.3	−
693	−	−	−	−	−	−	−	−	−	−	−	−	n	n	−	n	n	n	n	+	n	+	+	−	n	−	n	−	−	−	+	+	+	n	v	n	n	6	36.6	−
694	−	+	v	−	−	−	−	−	−	−	−	−	n	n	+	n	n	n	n	+	n	+	+	−	n	−	n	−	+	n	+	+	+	+	+	n	n	6	42.2	−
Kockovaella																																								
696	+	−	+	+	+	+	+	−	−	−	−	+	+	+	+	+	n	−	−	−	n	+	−	−	n	−	n	−	n	n	+	+	−	−	−	−	−	10	48.5	+
697	−	−	+	+	+	+	+	−	−	−	−	−	+	−	+	+	n	−	−	−	n	+	−	n	n	−	n	−	n	n	+	+	+	n	−	−	−	10	53.5	+
698	−	−	+	+	v	+	+	−	−	−	−	+	+	−	+	+	n	−	−	−	n	+	−	n	n	−	n	−	n	n	+	+	−	−	−	−	−	10	53.7	+
699	+	−	+	−	+	+	+	−	−	−	−	+	+	−	+	+	n	−	−	−	n	+	−	n	n	−	n	+	n	n	+	+	−	−	−	−	−	10	50.7	+
700	+	+	+	+	+	+	+	−	−	−	−	−	+	−	+	+	n	−	−	−	n	+	−	n	n	−	n	−	n	n	+	+	−	−	−	−	−	10	53.2	+
701	−	−	−	+	+	+	+	−	−	−	−	+	+	−	+	+	n	−	−	−	n	+	−	n	n	−	n	−	n	n	+	+	−	−	−	−	−	10	52.0	+
702	−	−	+	+	−	+	+	−	−	−	−	+	+	−	v	v	n	−	−	−	n	+	−	n	n	−	n	−	n	n	+	+	−	−	−	−	−	10	51.0	+
703	+	−	+	+	v	+	+	−	−	−	−	−	−	−	+	+	n	−	−	−	n	+	−	−	n	−	n	−	n	n	+	+	+	n	−	−	−	10	48.0	+
704	−	−	+	+	−	+	+	−	−	−	−	−	−	−	−	+	n	−	−	−	n	+	−	n	n	−	n	−	n	n	+	+	−	−	−	−	−	10	53.0	+

Symbols: +, positive or weak; −, negative; v, variable (+/−, w/−); n, no data.

Ln. no.	Species	Fermentation							Growth reactions and other characteristics																																	
		Glucose	Galactose	Sucrose	Maltose	Lactose	Raffinose	Trehalose	Glucose	Inulin	Sucrose	Raffinose	Melibiose	Galactose	Lactose	Trehalose	Maltose	Melezitose	Methyl-α-D-glucoside	Soluble Starch	Cellobiose	Salicin	L-Sorbose	L-Rhamnose	D-Xylose	L-Arabinose	D-Arabinose	D-Ribose	Methanol	Ethanol	Glycerol	Erythritol	Ribitol	Galactitol	D-Mannitol	D-Glucitol					
	Kockovaella *(cont'd)*																																									
705	*K. thailandica*	−	−	−	−	−	−	−	+	−	+	+	+	+	+	+	+	+	v	+	+	v	+	+	+	+	+	+	−	−	v	−	v	−	+	+						
706	*K. vietnamensis*	−	−	−	−	−	−	−	+	−	+	+	+	+	+	+	+	+	−	+	+	+	+	+	+	+	+	+	−	−	+	+	−	+	+	+						
707	***Kodamaea***																																									
708	*K. anthophila*	+	n	n	n	n	n	n	+	v	+	+	−	+	−	+	+	−	+	−	+	+	+	−	+	−	−	−	−	+	+	−	+	−	+	+						
709	*K. kakaduensis*	+	n	n	n	n	n	n	+	v	+	+	−	v	−	+	+	+	+	−	+	+	+	−	−	−	−	−	−	−	+	+	−	+	−	+	+					
710	*K. laetipori*	+	−	−	+	−	−	+	+	−	+	−	−	−	−	+	+	+	+	+	+	+	+	−	+	−	+	−	−	−	+	+	−	+	−	+	+					
711	*K. nitidulidarum*	+	n	n	n	n	n	n	+	−	+	+	−	+	−	−	+	+	+	−	+	+	+	−	−	−	+	−	−	−	+	+	−	+	−	+	+					
712	*K. ohmeri*	+	+	+	v	−	+	v	+	v	+	+	−	+	−	+	+	v	+	−	+	v	+	−	v	−	−	v	−	−	+	+	−	v	−	+	v					
713	***Komagataella***																																									
714	*K. pastoris*	+	−	−	−	−	−	−	+	−	−	−	−	−	−	+	−	−	−	−	−	−	−	+	v	−	−	−	+	+	+	−	−	−	+	+						
715	*K. phaffii*	+	−	−	−	−	−	−	+	−	−	−	−	−	−	+	−	−	−	−	−	−	−	+	−	−	−	−	+	+	+	−	−	−	+	+						
716	*K. pseudopastoris*	+	−	−	−	−	−	−	+	−	−	−	−	−	−	+	−	−	−	−	−	−	−	+	+	−	v	−	+	+	+	−	−	−	+	+						
717	***Kondoa***																																									
718	*K. aeria*	−	−	−	−	−	−	−	+	−	+	+	−	+	−	+	+	−	−	+	+	+	v	−	+	v	v	−	−	−	+	−	+	v	+	+						
719	*K. malvinella*	−	−	−	−	−	−	−	+	−	+	+	−	−	−	+	+	−	−	+	+	+	+	+	+	v	+	−	−	v	+	−	v	−	+	+						
720	***Kregervanrija***																																									
721	*K. delftensis*	v	−	−	−	−	−	−	+	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	+	−	−	+	−	+	+					
722	*K. fluxuum*	−	−	−	−	−	−	−	+	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	+	v	−	v	−	+	+					
723	*K. pseudodelftensis*	−	−	−	−	−	−	−	+	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	+	−	−	+	−	+	+					
724	***Kriegeria***																																									
725	*K. eriophori*	−	−	−	−	−	−	−	+	−	+	−	−	+	−	+	+	+	+	−	+	+	+	+	+	+	v	+	−	+	+	−	+	+	+	+						
726	***Kuraishia***																																									
727	*K. capsulata*	+	−	−	−	−	−	v	+	−	−	−	−	−	−	+	+	+	v	+	+	+	−	+	+	+	+	+	+	+	+	+	+	+	−	+	+					
728	*K. molischiana*	+	−	−	−	−	−	+	+	−	−	−	−	−	v	+	+	v	v	+	+	+	−	v	+	+	+	+	v	+	+	+	+	+	−	+	+					
729	***Kurtzmaniella***																																									
730	*K. cleridarum*	+	−	+	−	−	−	−	+	−	+	−	−	+	−	+	+	+	+	−	−	+	+	−	+	−	−	+	−	+	+	+	−	+	−	+	+					
731	***Kurtzmanomyces***																																									
732	*K. insolitus*	−	−	−	−	−	−	−	+	−	+	+	−	−	+	+	−	+	−	−	+	+	−	−	−	+	+	+	+	−	+	+	+	+	−	+	−					
733	*K. nectairei*	−	−	−	−	−	−	−	+	−	−	−	−	−	−	+	−	−	−	−	−	−	−	−	−	−	−	−	−	−	+	−	−	+	−	+	+					
734	*K. tardus*	−	−	−	−	−	−	−	+	−	+	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	+	−	−	−	−	+	+					
735	*K.* sp. = *Mycogloea nipponica*	−	−	−	−	−	−	−	+	−	+	+	−	+	−	+	+	+	−	−	+	+	−	−	−	+	−	−	+	−	+	+	+	+	−	+	−					
736	***Kwoniella***																																									
737	*K. mangroviensis*	−	−	−	−	−	−	−	+	−	+	v	−	+	+	+	+	+	+	v	+	+	+	+	+	+	+	+	+	−	+	+	v	+	+	+	+					
738	***Lachancea***																																									
739	*L. cidri*	+	+	+	+	−	+	+	+	−	+	+	+	+	−	+	v	v	v	−	−	−	+	−	v	−	−	−	−	−	+	+	−	v	−	+	+					
740	*L. fermentati*	+	+	+	+	−	v	+	+	v	v	v	−	v	−	+	+	v	+	−	+	+	v	−	v	−	−	−	−	−	+	v	−	v	−	+	+					
741	*L. kluyveri*	+	+	+	−	−	+	−	+	−	+	v	+	+	−	v	+	−	+	−	v	v	v	−	v	−	−	v	−	−	+	v	−	−	−	v	v					
742	*L. meyersii*	+	−	+	v	−	v	+	+	v	+	+	−	+	−	+	+	+	+	−	−	−	v	−	−	−	−	−	−	−	+	+	−	v	−	+	+					
743	*L. thermotolerans*	+	v	+	v	−	+	+	+	v	+	+	−	v	−	+	+	+	+	−	−	−	+	−	−	−	−	−	−	−	v	+	−	v	−	v	v					
744	*L. waltii*	+	−	+	−	−	+	−	+	−	+	+	−	−	−	−	−	−	−	−	−	−	+	−	+	−	+	−	−	−	+	−	−	+	−	+	+					
745	***Lalaria***																																									
746	*L. arrabidae*	−	−	−	−	−	−	−	+	−	+	−	−	−	−	−	−	+	−	−	+	+	−	−	+	−	−	−	−	−	−	+	−	−	−	+	−					
747	*L. carpini*	−	−	−	−	−	−	−	+	−	+	−	−	−	−	+	+	+	−	+	+	+	−	−	+	v	v	v	−	+	+	−	v	−	+	+						
748	*L. inositophila*	−	−	−	−	−	−	−	+	−	+	+	−	v	−	+	+	+	v	v	+	+	v	−	v	v	v	v	−	v	+	−	v	−	+	+						
749	*L. kurtzmanii*	−	−	−	−	−	−	−	+	−	−	−	−	−	−	+	−	−	−	−	+	−	−	−	+	−	−	−	−	+	+	−	−	−	+	+						
750	*L. veronaerambellii*	−	−	−	−	−	−	−	+	−	+	+	−	v	−	+	+	+	−	v	+	+	−	−	+	v	s	v	−	−	+	−	−	−	v	v						
751	***Leucosporidiella***																																									
752	*L. creatinivora*	−	−	−	−	−	−	−	+	−	+	+	−	−	v	+	+	+	+	−	+	+	+	+	+	−	+	−	−	−	+	+	−	+	−	+	+					
753	*L. fragaria*	−	−	−	−	−	−	−	+	−	+	+	−	+	+	+	+	+	+	−	+	+	+	−	+	+	+	+	−	−	+	+	−	+	−	+	+					
754	*L. muscorum*	−	−	−	−	−	−	−	+	−	+	+	−	+	+	+	+	+	+	−	+	+	+	−	+	v	+	+	−	−	+	+	−	+	+	+	+					
755	*L. yakutica*	−	−	−	−	−	−	−	+	−	+	+	−	+	+	+	+	+	+	−	+	+	+	+	+	−	+	+	−	−	+	+	−	+	−	+	+					
756	***Leucosporidium***																																									
757	*L. antarcticum*	−	−	−	−	−	−	−	+	−	v	−	−	−	−	−	v	−	−	v	v	−	−	−	−	−	−	−	v	−	v	v	−	−	−	v	v					
758	*L. fasciculatum*	−	−	−	−	−	−	−	+	−	+	−	−	−	−	+	+	+	−	−	+	+	+	−	+	+	−	−	−	−	+	−	−	+	−	+	+					

Symbols: +, positive or weak; −, negative; v, variable (+/−, w/−); n, no data.

	Growth reactions and other characteristics																																								
	myo-Inositol	DL-Lactate	Succinate	Citrate	D-Gluconate	D-Glucosamine	*N*-Acetyl-D-glucosamine	Hexadecane	Nitrate	Nitrite	Vitamin-free	2-Keto-D-gluconate	5-Keto-D-gluconate	Saccharate	Xylitol	L-Arabinitol	Arbutin	Propane 1,2 diol	Butane 2,3 diol	Cadaverine	Creatinine	L-Lysine	Ethylamine	50% Glucose	10% NaCl/5% glucose	Starch formation	Urease	Gelatin liquefaction	Cycloheximide 0.01%	Cycloheximide 0.1%	Growth at 19°C	Growth at 25°C	Growth at 30°C	Growth at 35°C	Growth at 37°C	Growth at 40°C	Growth at 45°C	CoQ (Main component)	Mol% G + C (Ave.)	DBB
Kockovaella (*cont'd*)																																									
705	v	−	+	v	−	+	+	−	−	−	−	+	+	−	+	+	n	−	−	v	n	+	−	−	n	−	n	+	n	n	+	+	+	n	−	−	−	10	48.6	+
706	+	−	+	+	+	+	+	−	−	−	−	+	+	−	−	−	n	−	−	−	n	+	−	n	n	−	n	−	n	n	+	+	+	n	−	−	−	10	54.1	+
Kodamaea																																									
708	−	−	−	+	−	−	+	−	−	−	−	+	n	n	+	n	n	n	n	+	n	+	+	+	n	−	n	−	−	−	+	+	+	+	+	n	n	n	n	−
709	−	−	+	v	−	+	+	+	−	−	−	+	n	n	v	n	n	n	n	+	n	+	+	+	n	−	n	−	−	−	+	+	+	v	v	n	n	n	n	−
710	−	+	+	+	+	n	n	n	−	n	−	+	n	n	−	n	n	n	n	+	n	+	+	+	n	−	n	n	+	+	+	+	+	+	n	n	n	n	n	−
711	−	−	+	+	−	+	+	+	−	−	−	+	n	n	−	n	n	n	n	+	n	+	+	−	n	−	n	−	−	−	+	+	+	+	+	n	n	n	n	−
712	−	−	v	+	−	+	+	+	−	−	−	+	n	n	−	n	n	n	n	+	n	+	+	+	n	−	n	−	v	−	+	+	+	+	+	n	n	9	43.4	−
Komagataella																																									
714	−	+	+	v	−	−	−	−	−	n	−	−	−	−	n	n	n	n	n	n	n	n	n	n	v	−	n	−	n	n	+	+	+	+	+	n	n	8	41.3	−
715	−	+	+	v	−	−	−	−	−	n	−	−	−	−	n	n	n	n	n	n	n	n	n	n	−	−	n	−	+	n	+	+	+	+	+	n	n	n	n	−
716	−	+	+	−	−	−	−	n	−	n	+	−	n	n	n	n	n	n	n	n	n	n	n	n	−	−	n	n	n	n	+	+	+	n	n	n	n	8	n	−
Kondoa																																									
718	−	+	+	+	v	−	n	n	+	+	−	n	n	n	+	n	+	n	n	+	n	−	−	n	n	−	+	n	−	−	+	+	−	−	−	−	−	n	51.4	+
719	−	+	+	v	v	−	n	n	+	n	−	n	n	n	+	n	n	n	n	v	n	−	−	n	n	−	+	n	−	−	+	−	−	−	−	−	−	9	50.5	+
Kregervanrija																																									
721	−	−	+	−	−	−	+	−	−	n	−	−	−	−	n	n	n	n	n	n	n	n	n	n	+	−	n	−	n	n	+	+	+	n	−	−	−	7	33.2	−
722	−	v	+	−	−	−	−	−	−	n	−	−	−	−	n	n	n	n	n	n	n	n	n	n	−	−	n	−	n	n	+	+	n	n	−	−	−	7	33.0	−
723	−	−	−	−	−	−	−	−	−	n	−	−	−	−	n	n	n	n	n	n	n	n	n	n	+	−	n	−	−	−	+	+	n	n	−	−	−	n	n	−
Kriegeria																																									
725	−	+	+	+	+	−	n	n	+	+	+	n	n	n	v	n	n	n	n	n	n	n	n	n	n	+	n	n	−	−	+	+	−	−	−	−	−	n	n	+
Kuraishia																																									
727	−	−	v	−	v	+	+	−	+	+	−	+	−	−	+	n	n	n	n	+	−	+	+	−	v	−	n	v	n	n	+	+	+	n	v	−	−	8	46.8	−
728	−	−	v	−	v	+	+	−	+	+	−	+	−	−	+	n	n	n	n	+	−	+	+	−	v	−	n	v	n	n	+	+	+	n	v	v	n	8	50.1	−
Kurtzmaniella																																									
730	−	+	+	+	+	+	+	+	−	−	−	+	n	n	+	n	n	n	n	+	n	+	+	+	n	−	n	+	−	−	+	+	+	+	+	n	n	n	n	−
Kurtzmanomyces																																									
732	−	+	+	−	+	−	n	n	+	+	−	n	n	−	+	n	n	n	n	n	n	n	n	n	n	−	n	n	+	+	+	+	+	−	−	−	−	n	49.1	+
733	−	−	+	−	−	−	n	n	+	+	−	n	n	−	−	n	n	n	n	n	n	n	n	n	n	−	n	n	−	−	+	+	−	−	−	−	−	10	52.5	+
734	−	−	−	−	−	−	n	n	+	+	−	n	n	−	−	n	n	n	n	n	n	n	n	n	n	−	n	n	−	−	+	+	+	−	−	−	−	10	58.2	+
735	−	+	+	+	−	−	n	n	+	+	−	n	n	−	−	n	n	n	n	n	n	n	n	n	n	−	n	n	−	−	+	+	+	−	−	−	−	n	n	+
Kwoniella																																									
737	+	−	+	+	+	−	v	−	−	+	v	+	+	+	n	n	n	n	n	−	n	n	n	−	+	+	+	−	n	n	+	+	+	n	−	−	−	n	n	+
Lachancea																																									
739	−	v	+	−	−	−	−	−	−	−	−	v	n	n	+	n	n	n	n	v	n	+	+	v	n	−	n	−	+	+	+	+	+	n	−	−	−	n	43.3	−
740	−	+	v	−	v	−	−	−	−	−	−	v	n	n	v	n	n	n	n	+	n	+	+	+	n	−	n	−	+	+	+	+	+	+	+	n	n	6	43.4	−
741	−	v	v	−	v	−	−	−	−	−	v	v	n	n	v	n	n	n	n	+	n	+	+	v	n	−	n	−	−	−	+	+	+	+	+	n	n	n	41.9	−
742	−	−	−	−	v	−	−	−	−	−	−	+	n	n	+	n	n	n	n	+	n	+	+	v	n	−	n	−	−	−	+	+	+	n	−	−	−	n	n	−
743	−	−	v	−	v	−	−	−	−	−	−	v	n	n	+	n	n	n	n	+	n	+	+	+	n	−	n	v	−	−	+	+	+	n	v	n	n	6	46.2	−
744	−	−	−	−	−	−	−	−	−	−	−	−	n	n	+	n	n	n	n	+	n	+	+	+	n	−	n	−	+	n	+	+	+	n	−	−	−	n	45.7	−
Lalaria																																									
746	−	−	+	+	−	−	n	n	+	+	−	n	n	−	+	n	+	n	n	+	−	+	−	n	n	+	+	n	−	−	+	+	−	−	−	−	−	n	n	−
747	v	−	+	+	+	v	n	n	+	+	−	n	n	−	+	n	+	n	n	+	−	+	−	n	n	+	+	n	−	−	+	+	−	−	−	−	−	n	49.4	−
748	v	v	+	+	v	v	n	n	+	+	v	n	n	−	v	n	+	n	n	+	−	v	v	n	n	+	+	n	−	−	+	+	−	−	−	−	−	n	50.4	−
749	−	−	+	+	−	−	n	n	+	+	−	n	n	−	−	n	+	n	n	−	−	−	−	n	n	+	+	n	−	−	+	+	−	−	−	−	−	n	n	−
750	−	−	+	+	−	v	n	n	+	+	−	n	n	−	+	n	+	n	n	+	−	v	v	n	n	+	+	n	−	−	+	+	−	−	−	−	−	n	n	−
Leucosporidiella																																									
752	−	v	+	+	+	+	n	n	+	+	+	n	n	−	+	n	n	n	n	n	n	n	n	n	n	−	n	n	+	−	+	+	−	−	−	−	−	n	60.2	+
753	−	+	+	+	+	+	n	n	+	+	+	n	n	−	+	n	n	n	n	n	n	n	n	n	n	−	n	n	−	−	+	+	−	−	−	−	−	n	56.6	+
754	−	−	+	+	+	+	n	n	+	+	+	n	n	+	+	n	n	n	n	n	n	n	n	n	n	−	n	n	+	−	+	+	−	−	−	−	−	10	n	+
755	−	+	+	+	+	+	n	n	+	+	+	n	n	−	+	n	n	n	n	n	n	n	n	n	n	+	n	n	+	−	+	+	−	−	−	−	−	n	58.0	+
Leucosporidium																																									
757	−	−	v	−	v	−	n	n	+	+	−	n	n	−	v	n	n	n	n	n	n	n	n	n	n	−	n	n	−	−	−	−	−	−	−	−	−	10	50.5	+
758	−	−	+	+	−	−	n	n	−	−	+	n	n	−	+	n	n	n	n	n	n	n	n	n	n	−	n	n	−	−	+	−	−	−	−	−	−	n	54.2	+

Symbols: +, positive or weak; −, negative; v, variable (+/−, w/−); n, no data.

Ln. no.	Species	Fermentation: Glucose	Galactose	Sucrose	Maltose	Lactose	Raffinose	Trehalose	Growth reactions and other characteristics: Glucose	Inulin	Sucrose	Raffinose	Melibiose	Galactose	Lactose	Trehalose	Maltose	Melezitose	Methyl-α-D-glucoside	Soluble Starch	Cellobiose	Salicin	L-Sorbose	L-Rhamnose	D-Xylose	L-Arabinose	D-Arabinose	D-Ribose	Methanol	Ethanol	Glycerol	Erythritol	Ribitol	Galactitol	D-Mannitol	D-Glucitol
	Leucosporidium *(cont'd)*																																			
759	*L. fellii*	−	−	−	−	−	−	−	+	−	−	−	−	−	−	+	−	−	−	−	+	+	+	+	+	−	+	−	−	−	+	−	+	−	+	+
760	*L. golubevii*	−	−	−	−	−	−	−	+	−	+	+	−	+	+	+	+	+	+	−	+	v	+	−	+	+	+	+	−	+	+	−	+	v	+	+
761	*L. scottii*	−	−	−	−	−	−	−	+	−	+	+	−	+	v	+	+	+	+	−	+	+	+	+	+	+	+	+	−	+	+	−	+	+	+	+
762	***Lindnera***																																			
763	*L. americana*	+	−	−	−	−	−	−	+	−	+	−	−	−	−	+	+	+	+	−	+	+	−	+	+	−	−	−	−	−	+	+	−	−	−	+	+
764	*L. amylophila*	+	−	−	−	−	−	−	+	−	+	−	−	−	−	+	+	+	+	+	+	−	−	−	+	+	−	−	−	−	+	+	−	−	−	+	+
765	*L. bimundalis*	+	−	−	−	−	−	−	+	−	+	−	−	−	−	+	+	+	v	−	+	+	−	+	+	v	+	−	−	−	+	+	−	−	−	+	+
766	*L. euphorbiae*	+	−	+	−	−	−	−	+	−	+	−	−	−	−	+	+	+	+	−	+	+	−	+	+	+	−	−	−	−	+	+	−	−	−	+	+
767	*L. euphorbiiphila*	+	−	−	−	−	−	−	+	−	+	−	−	−	−	+	+	+	+	−	+	+	−	−	+	−	−	−	−	−	+	+	−	−	−	+	+
768	*L. fabianii*	+	−	+	+	−	+	−	+	−	+	+	−	−	−	+	+	+	+	+	+	+	−	−	+	−	−	−	−	−	+	+	−	−	−	+	+
769	*L. jadinii*	+	−	+	−	−	+	−	+	+	+	+	−	−	−	+	+	+	+	−	+	+	−	−	+	−	−	−	−	−	+	+	−	−	−	+	+
770	*L. japonica*	+	−	−	−	−	−	−	+	−	+	−	−	−	−	+	+	+	+	−	+	+	−	+	+	−	−	−	−	−	+	+	−	v	−	+	+
771	*L. lachancei*	+	−	+	−	−	+	−	+	−	+	+	−	−	−	−	−	−	−	−	+	+	−	+	+	−	−	−	−	−	+	+	−	−	−	+	+
772	*L. maclurae*	+	−	+	−	−	+	−	+	v	+	+	−	−	−	+	+	+	+	−	+	+	−	−	−	−	−	−	−	−	+	+	−	−	−	+	+
773	*L. meyerae*	+	−	−	−	−	−	−	+	−	+	−	−	−	−	+	+	−	v	−	+	+	−	+	+	−	−	−	−	−	+	+	−	−	−	v	v
774	*L. mississippiensis*	+	−	−	−	−	−	−	+	−	+	−	−	−	−	+	+	+	+	−	+	v	−	v	+	+	v	−	−	−	+	+	−	−	−	+	+
775	*L. misumaiensis*	+	−	−	−	−	−	−	+	−	−	−	−	−	−	−	−	−	−	−	+	+	−	−	+	−	−	−	−	−	+	+	−	−	−	+	+
776	*L. mrakii*	+	−	−	−	−	+	−	+	v	−	+	−	−	−	v	v	v	v	−	+	v	−	v	+	−	−	−	−	−	+	+	−	−	−	v	v
777	*L. petersonii*	+	−	+	−	−	+	−	+	−	+	+	−	−	−	+	+	+	+	−	+	+	−	+	+	−	−	−	−	−	+	+	−	−	−	+	+
778	*L. rhodanensis*	+	−	v	−	−	−	−	+	−	+	−	−	−	−	+	+	+	v	−	+	v	−	+	+	−	−	−	−	−	+	+	−	−	−	+	+
779	*L. sargentensis*	+	−	−	−	−	−	−	+	−	−	−	−	−	−	−	−	−	−	−	+	+	−	+	+	−	−	−	−	−	+	+	−	−	−	+	+
780	*L. saturnus*	+	−	+	−	−	+	−	+	v	+	+	−	−	−	v	v	v	v	−	+	v	−	v	+	−	−	−	−	−	+	+	−	−	−	v	v
781	*L. suaveolens*	+	−	+	−	−	+	−	+	v	+	+	−	−	−	v	−	v	v	−	+	v	−	−	+	−	−	−	−	−	+	+	−	−	−	v	v
782	*L. subsufficiens*	+	−	+	−	−	+	−	+	v	+	+	−	−	−	v	v	v	v	−	+	v	−	v	+	−	−	−	−	−	+	+	−	−	−	v	v
783	*L. veronae*	+	−	+	−	−	−	−	+	−	+	+	−	−	−	+	+	+	+	−	+	+	−	+	+	+	−	−	−	−	+	+	−	−	−	+	+
784	***Lipomyces***																																			
785	*L. arxii*	−	−	−	−	−	−	−	+	−	−	−	−	−	+	−	+	−	−	−	−	+	+	+	−	+	+	−	−	−	−	+	−	−	−	−	−
786	*L. doorenjongii*	−	−	−	−	−	−	−	+	+	+	+	+	+	+	+	+	+	+	+	+	v	+	−	+	+	+	−	−	−	v	−	+	−	+	+	+
787	*L. japonicus*	−	−	−	−	−	−	−	+	−	+	−	−	+	+	−	−	−	−	−	+	+	+	−	+	+	+	−	−	−	+	+	−	+	−	+	+
788	*L. kockii*	−	−	−	−	−	−	−	+	+	+	+	+	+	−	v	+	+	+	+	+	+	+	−	v	v	−	−	−	−	+	−	v	−	+	+	v
789	*L. kononenkoae*	−	−	−	−	−	−	−	+	+	+	+	+	+	−	+	+	+	+	+	v	v	+	−	v	−	v	−	−	−	+	v	−	−	v	+	+
790	*L. lipofer*	−	−	−	−	−	−	−	+	+	+	+	+	+	v	+	+	+	+	+	+	v	+	−	v	v	v	−	−	−	+	v	+	v	v	+	+
791	*L. mesembrius*	−	−	−	−	−	−	−	+	v	v	v	+	v	v	v	v	v	v	v	v	v	v	−	v	v	−	−	−	−	v	v	−	v	v	v	v
792	*L. oligophaga*	−	−	−	−	−	−	−	+	−	−	−	−	+	−	−	−	−	−	−	−	−	v	−	v	−	−	−	−	−	+	+	−	−	+	−	+
793	*L. orientalis*	−	−	−	−	−	−	−	+	+	+	+	+	+	v	+	+	+	+	+	+	+	+	v	+	v	+	−	−	−	+	−	+	+	+	+	+
794	*L. smithiae*	−	−	−	−	−	−	−	+	−	+	−	−	−	−	−	−	−	−	−	−	+	−	−	+	−	−	−	−	−	+	+	−	−	−	−	−
795	*L. spencer-martinsiae*	−	−	−	−	−	−	−	+	+	+	+	+	+	−	v	+	+	+	+	v	v	+	−	−	−	v	−	−	−	+	+	−	−	−	+	+
796	*L. starkeyi*	−	−	−	−	−	−	−	+	+	+	+	+	+	v	+	+	+	+	v	+	v	+	v	+	v	v	v	−	+	v	v	v	v	+	+
797	*L. suomiensis*	−	−	−	−	−	−	−	+	−	−	−	−	+	+	−	−	−	−	−	+	+	+	−	+	+	+	−	−	−	+	+	−	+	−	+	+
798	*L. tetrasporus*	−	−	−	−	−	−	−	+	+	+	+	v	+	v	+	+	+	+	+	v	v	+	v	+	+	+	v	−	+	v	+	+	+	+	+	+
799	*L. yamadae*	−	−	−	−	−	−	−	+	+	+	+	+	+	−	+	+	+	+	+	+	+	+	−	−	−	−	−	−	−	+	−	−	−	−	+	+
800	*L. yarrowii*	−	−	−	−	−	−	−	+	+	+	+	+	+	−	+	+	+	+	+	+	+	+	−	−	−	−	−	−	−	+	−	−	−	+	+	+
801	***Lodderomyces***																																			
802	*L. elongisporus*	+	−	−	−	−	−	+	+	−	+	−	−	+	−	+	+	+	−	−	−	+	−	+	−	−	−	−	−	+	+	−	+	−	+	+
803	***Magnusiomyces***																																			
804	*M. capitatus*	−	−	−	−	−	−	−	+	−	−	−	−	+	−	−	−	−	−	−	−	−	v	−	−	−	−		−	−	+	+	−	−	−	+	+
805	*M. ingens*	−	−	−	−	−	−	−	+	−	−	−	−	+	−	−	−	−	−	−	−	−	+	−	−	−	−	−	−	−	+	+	−	−	−	−	−
806	*M. magnusii*	+	+	+	−	−	+	n	+	−	+	+	−	+	−	−	−	−	−	−	−	−	+	−	−	−	−	−	−	−	−	+	−	−	−	+	+
807	*M. ovetensis*	−	−	−	−	−	−	−	+	−	−	−	−	+	−	v	−	−	−	−	−	−	v	−	−	−	−	−	−	−	+	+	−	−	−	v	v
808	*M. spicifer*	−	−	−	−	−	−	−	+	−	−	−	−	+	−	−	−	−	−	+	+	−	+	−	+	−	−	−	−	−	+	+	−	−	−	−	−
809	*M. starmeri*	−	−	−	−	−	−	−	+	−	−	−	−	+	−	−	−	−	−	−	−	−	+	−	−	−	−	−	−	−	+	+	−	−	−	−	−
810	*M. tetrasperma*	+	−	−	−	−	−	−	+	−	−	−	−	+	−	−	−	−	−	−	−	−	+	−	−	−	−	−	−	−	+	+	−	−	−	−	+
811	***Mastigobasidium***																																			
812	*M. intermedium*	−	−	−	−	−	−	−	+	−	+	v	−	+	−	v	v	−	−	−	+	−	v	−	−	−	−	v	−		+	+	−	−	−	+	+

Symbols: +, positive or weak; −, negative; v, variable (+/−, w/−); n, no data.

Growth reactions and other characteristics

	myo-Inositol	DL-Lactate	Succinate	Citrate	D-Gluconate	D-Glucosamine	*N*-Acetyl-D-glucosamine	Hexadecane	Nitrate	Nitrite	Vitamin-free	2-Keto-D-gluconate	5-Keto-D-gluconate	Saccharate	Xylitol	L-Arabinitol	Arbutin	Propane 1,2 diol	Butane 2,3 diol	Cadaverine	Creatinine	L-Lysine	Ethylamine	50% Glucose	10% NaCl/5% glucose	Starch formation	Urease	Gelatin liquefaction	Cycloheximide 0.01%	Cycloheximide 0.1%	Growth at 19°C	Growth at 25°C	Growth at 30°C	Growth at 35°C	Growth at 37°C	Growth at 40°C	Growth at 45°C	CoQ (Main component)	Mol% G + C (Ave.)	DBB
Leucosporidium (*cont'd*)																																								
759	−	−	+	+	+	+	n	n	+	+	+	n	n	−	−	n	n	n	n	n	n	n	n	n	n	−	n	n	+	+	+	+	−	−	−	−	−	9	57.7	+
760	−	+	+	+	+	+	n	n	+	+	+	n	n	+	+	n	n	n	n	n	n	n	n	n	n	−	n	n	+	−	+	+	−	−	−	−	−	n	n	+
761	−	+	+	+	+	+	n	n	+	+	v	n	n	−	+	n	n	n	n	n	n	n	n	n	n	−	n	n	+	−	+	+	v	−	−	−	−	9	61.0	+
Lindnera																																								
763	−	+	+	+	+	−	−	−	+	n	−	v	−	−	n	n	n	n	n	n	n	n	n	n	−	−	n	−	n	n	+	+	+	n	−	−	−	7	43.4	−
764	−	+	+	+	+	−	−	−	−	n	−	−	−	−	n	n	n	n	n	n	n	n	n	n	−	−	n	−	n	n	+	+	+	+	+	n	n	7	45.4	−
765	−	+	+	+	+	−	−	−	+	n	−	v	−	−	n	n	n	n	n	n	n	n	n	n	−	−	n	−	n	n	+	+	+	+	+	n	n	7	41.5	−
766	−	+	+	+	+	−	−	−	−	n	−	−	−	−	n	n	n	n	n	n	n	n	n	n	−	−	n	−	n	n	+	+	+	n	v	n	n	n	n	−
767	−	+	+	+	+	−	−	−	+	n	−	−	−	−	n	n	n	n	n	n	n	n	n	n	v	−	n	−	n	n	+	+	+	+	+	n	n	n	47.3	−
768	−	+	+	+	+	−	−	−	+	n	−	−	−	−	n	n	n	n	n	n	n	n	n	n	+	−	n	−	n	n	+	+	+	+	+	n	n	7	46.7	−
769	−	+	+	+	+	−	−	−	+	n	+	v	−	−	n	n	n	n	n	n	n	n	n	n	−	−	n	−	n	n	+	+	+	+	+	n	n	7	44.7	−
770	−	+	+	+	+	−	−	−	−	n	−	−	−	−	n	n	n	n	n	n	n	n	n	n	−	−	n	+	n	n	+	+	+	+	+	+	n	n	46.5	−
771	−	+	+	+	n	−	−	−	−	n	−	−	−	n	n	n	n	n	n	n	n	n	n	n	−	−	n	−	n	n	+	+	+	n	−	−	−	n	40.3	−
772	−	v	+	+	+	−	−	−	−	n	−	−	−	−	n	n	n	n	n	n	n	n	n	n	−	−	n	−	n	n	+	+	+	n	−	−	−	n	n	−
773	−	+	+	+	+	−	−	−	−	n	−	−	−	−	n	n	n	n	n	n	n	n	n	n	−	−	n	−	n	n	+	+	+	+	+	n	n	7	48.7	−
774	−	+	+	v	+	−	−	−	−	n	−	−	−	−	n	n	n	n	n	n	n	n	n	n	−	−	n	−	n	n	+	+	+	+	+	n	n	7	47.6	−
775	−	+	+	+	+	−	−	−	+	n	−	−	−	−	n	n	n	n	n	n	n	n	n	n	−	−	n	−	n	n	+	+	+	n	−	−	−	n	n	−
776	−	+	+	v	+	−	−	−	+	n	+	−	−	−	n	n	n	n	n	n	n	n	n	n	−	−	n	v	n	n	+	+	+	n	v	n	n	7	44.3	−
777	−	+	+	+	+	−	−	−	+	n	−	−	−	−	n	n	n	n	n	n	n	n	n	n	−	−	n	−	n	n	+	+	+	+	+	n	n	7	44.3	−
778	−	+	+	+	+	−	−	−	−	n	−	−	−	−	n	n	n	n	n	n	n	n	n	n	−	−	n	−	n	n	+	+	+	+	+	n	n	7	51.1	−
779	−	+	+	−	−	−	−	−	−	n	−	−	−	−	n	n	n	n	n	n	n	n	n	n	−	−	n	−	n	n	+	+	+	+	+	n	n	n	44.1	−
780	−	+	+	v	+	−	−	−	+	n	+	−	−	−	n	n	n	n	n	n	n	n	n	n	−	−	n	v	n	n	+	+	+	n	v	n	n	7	44.5	−
781	−	+	+	v	+	−	−	−	+	n	+	−	−	−	n	n	n	n	n	n	n	n	n	n	−	−	n	v	n	n	+	+	+	n	v	n	n	n	44.5	−
782	−	+	+	v	+	−	−	−	+	n	−	−	−	−	n	n	n	n	n	n	n	n	n	n	−	−	n	v	n	n	+	+	+	n	v	n	n	7	43.6	−
783	−	+	+	+	+	−	−	−	−	n	−	−	−	−	n	n	n	n	n	n	n	n	n	n	−	−	n	−	n	n	+	+	+	n	−	−	−	7	48.1	−
Lipomyces																																								
785	−	−	+	−	−	−	n	n	−	n	−	n	n	n	n	n	n	+	+	n	n	n	n	−	n	n	n	n	+	+	+	+	+	−	n	−	−	9	47.4	−
786	−	−	v	v	−	−	n	n	−	n	v	n	n	n	n	n	n	v	v	n	n	n	n	−	n	n	n	n	+	+	+	+	+	−	n	−	−	9	48.0	−
787	−	−	−	+	−	−	n	n	−	n	−	n	n	n	n	n	n	−	+	n	n	n	n	−	n	n	n	n	+	+	+	+	+	−	n	−	−	9	41.9	−
788	−	−	v	−	−	−	n	n	−	n	+	n	n	n	n	n	n	−	v	n	n	n	n	−	n	n	n	n	+	+	+	+	+	−	n	−	−	9	46.5	−
789	−	−	v	v	+	−	n	n	−	n	+	n	n	n	n	n	n	−	−	n	n	n	n	−	n	n	n	n	+	+	+	+	+	v	−	−	−	9	47.7	−
790	−	−	+	+	+	−	n	n	−	n	+	n	n	n	n	n	n	−	+	n	n	n	n	−	n	n	n	n	n	−	+	+	+	−	n	−	−	10	48.2	−
791	−	−	+	+	v	−	n	n	−	n	v	n	n	n	n	n	n	−	v	n	n	n	n	−	n	n	n	n	+	+	+	+	v	−	n	−	−	9	47.5	−
792	v	−	+	−	+	−	n	n	−	n	−	n	n	n	n	n	n	+	+	n	n	n	n	−	n	n	n	n	+	+	+	+	+	−	n	−	−	8	41.7	−
793	−	−	+	+	+	−	n	n	−	n	+	n	n	n	n	n	n	−	−	n	n	n	n	n	n	n	n	n	+	+	+	+	+	−	n	−	−	9	n	−
794	−	−	+	−	−	−	n	n	−	n	−	n	n	n	n	n	n	v	−	n	n	n	n	−	n	n	n	n	+	+	+	+	+	−	n	−	−	9	55.5	−
795	−	−	−	v	v	−	n	n	−	n	+	n	n	n	n	n	n	−	−	n	n	n	n	−	n	n	n	n	+	+	+	+	+	+	+	+	n	9	47.1	−
796	v	−	+	+	v	−	n	n	−	n	v	n	n	n	n	n	n	v	+	n	n	n	n	−	n	v	n	n	+	+	+	+	+	v	n	−	−	9	47.5	−
797	−	−	+	+	+	−	n	n	−	n	−	n	n	n	n	n	n	+	+	n	n	n	n	−	n	n	n	n	+	+	+	+	+	−	n	−	−	8	45.1	−
798	v	−	v	+	+	−	n	n	−	n	+	n	n	n	n	n	n	+	+	n	n	n	n	−	n	n	n	n	+	+	+	+	+	v	−	−	−	9	48.5	−
799	−	−	−	+	+	−	n	n	−	n	+	n	n	n	n	n	n	−	−	n	n	n	n	−	n	n	n	n	+	+	+	+	n	+	−	−	−	9	47.4	−
800	−	−	−	v	+	−	n	n	−	n	+	n	n	n	n	n	n	−	−	n	n	n	n	−	n	n	n	n	+	+	+	+	+	−	n	−	−	9	47.7	−
Lodderomyces																																								
802	−	−	+	+	+	−	+	+	−	n	−	+	+	−	n	n	n	n	n	n	n	n	n	n	+	−	n	−	n	n	+	+	+	+	+	n	n	9	39.7	−
Magnusiomyces																																								
804	−	+	+	v	−	−	n	n	−	n	−	−	n	n	−	n	−	n	n	n	n	n	n	n	n	n	n	n	n	n	+	+	+	+	+	+	n	9	35.3	−
805	−	+	+	−	−	−	n	n	−	n	+	−	n	n	−	n	−	n	n	n	n	n	n	n	n	n	n	n	n	n	+	+	+	+	+	−	−	n	43.5	−
806	−	v	+	−	−	−	n	n	−	n	−	−	n	n	−	n	−	n	n	n	n	n	n	n	n	n	n	n	n	n	+	+	+	−	−	−	−	9	38.6	−
807	−	+	+	−	−	−	n	n	−	n	−	−	n	n	−	n	−	n	n	n	n	n	n	n	n	n	n	n	n	n	+	+	+	v	−	−	−	9	48.5	−
808	−	+	+	+	−	−	n	n	−	n	−	−	n	n	−	n	+	n	n	n	n	n	n	n	n	n	n	n	n	n	+	+	+	+	+	+	n	n	34.3	−
809	−	−	+	−	−	−	−	−	−	n	−	−	n	n	−	n	−	n	n	n	n	n	n	n	n	n	n	n	n	n	+	+	+	+	+	+	+	9	39.3	−
810	−	+	+	+	−	−	n	n	−	n	−	−	n	n	−	n	−	n	n	n	n	n	n	n	n	n	n	n	n	n	+	+	+	+	+	+	n	n	40.0	−
Mastigobasidium																																								
812	−	+	+	+	+	−	+	−	−	−	+	+	+	−	−	−	+	n	−	+	−	+	+	−	−	−	+	−	−	−	+	−	−	−	−	−	−	9	59.9	+

Symbols: +, positive or weak; −, negative; v, variable (+/−, w/−); n, no data.

Ln. no.	Species	Fermentation							Growth reactions and other characteristics																																	
		Glucose	Galactose	Sucrose	Maltose	Lactose	Raffinose	Trehalose	Glucose	Inulin	Sucrose	Raffinose	Melibiose	Galactose	Lactose	Trehalose	Maltose	Melezitose	Methyl-α-D-glucoside	Soluble Starch	Cellobiose	Salicin	L-Sorbose	L-Rhamnose	D-Xylose	L-Arabinose	D-Arabinose	D-Ribose	Methanol	Ethanol	Glycerol	Erythritol	Ribitol	Galactitol	D-Mannitol	D-Glucitol					
813	***Meira***																																									
814	*M. argovae*	−	−	−	−	−	−	−	+	+	+	+	v	+	v	+	+	+	−	+	+	+	−	−	+	+	+	+	−	+	+	+	+	+	+	+					
815	*M. geulakonigii*	−	−	−	−	−	−	−	+	+	+	+	+	+	+	+	+	+	−	+	+	+	−	−	+	+	+	+	−	+	+	+	+	+	+	+					
816	***Metschnikowia***																																								
817	*M. aberdeeniae*	+	−	−	−	−	−	v	+	−	+	−	−	+	−	+	+	+	−	−	+	+	+	−	+	−	−	−	−	−	+	+	−	+	−	+	+					
818	*M. agaves*	+	−	−	−	−	−	+	+	−	+	−	−	+	−	+	+	+	−	−	+	+	+	−	+	−	−	−	−	−	+	−	−	+	−	+	+					
819	*M. andauensis*	+	−	−	−	−	−	−	+	−	+	−	−	+	n	+	+	+	+	−	+	+	+	−	+	−	−	−	−	−	+	+	−	+	−	+	+					
820	*M. arizonensis*	+	−	−	−	−	−	−	+	−	v	−	−	v	−	v	+	+	−	−	+	+	v	−	−	−	−	−	−	−	v	−	−	−	−	−	v					
821	*M. australis*	−	−	−	−	−	−	−	+	−	+	−	−	+	−	+	+	v	−	−	+	+	v	−	v	−	−	−	−	−	+	+	−	+	−	+	+					
822	*M. bicuspidata* var. *bicuspidata*	+	−	−	−	−	−	−	+	−	+	−	−	+	−	+	+	v	−	−	+	v	+	−	v	−	−	−	−	−	v	v	−	−	−	+	+					
823	*M. bicuspidata* var. *californica*	+	−	−	−	−	−	−	+	−	+	−	−	+	−	+	+	v	+	−	+	v	+	−	v	−	−	−	−	−	v	v	−	−	−	+	+					
824	*M. bicuspidata* var. *chathamia*	+	−	−	−	−	−	−	+	−	+	−	−	+	−	+	+	v	+	−	+	v	+	−	v	−	−	−	−	−	v	v	−	−	−	+	+					
825	*M. borealis*	+	−	−	−	−	−	+	+	−	+	−	−	+	−	+	+	+	+	−	+	+	+	−	+	−	−	−	−	−	+	+	−	−	−	+	+					
826	*M. cerradonensis*	+	−	−	−	−	−	−	+	−	+	−	−	+	−	+	+	+	−	−	+	+	+	−	+	−	−	−	−	−	+	+	−	−	−	+	+					
827	*M. chrysoperlae*	+	v	−	−	−	−	−	+	−	+	−	−	+	−	+	+	+	+	−	−	−	−	−	−	−	−	−	+	−	−	+	−	+	−	+	+					
828	*M. colocasiae*	+	−	−	−	−	−	+	+	−	+	−	−	+	−	+	+	+	−	−	+	+	+	−	+	−	−	−	−	−	−	+	−	+	−	+	+					
829	*M. continentalis*	+	−	−	−	−	−	+	+	−	+	−	−	+	−	+	+	+	+	−	+	+	+	−	+	−	−	−	−	−	+	+	−	−	−	+	+					
830	*M. corniflorae*	+	−	−	−	−	−	−	+	−	+	+	−	+	+	+	+	+	+	−	+	+	+	−	+	+	+	+	+	−	+	+	−	+	−	+	+					
831	*M. dekortorum*	+	−	−	−	−	−	+	+	−	+	−	−	+	−	+	+	+	−	−	+	+	+	−	+	−	−	−	−	−	+	−	−	+	−	+	+					
832	*M. drosophilae*	+	−	−	−	−	−	+	+	−	−	−	−	+	−	+	−	−	−	−	+	+	+	−	+	−	−	−	−	−	+	+	−	+	−	+	+					
833	*M. fructicola*	+	+	−	−	−	−	−	+	−	+	−	−	+	−	+	+	+	+	−	+	+	+	−	+	−	−	−	−	−	+	+	−	+	−	+	+					
834	*M. gruessii*	+	−	−	−	−	−	−	+	−	+	−	−	v	−	−	+	+	−	−	+	+	+	−	v	−	−	v	−	−	+	+	−	−	−	v	v					
835	*M. hamakuensis*	+	−	−	−	−	−	v	+	−	+	−	−	+	−	+	+	+	−	−	+	+	+	−	+	−	−	+	−	−	+	+	−	+	−	+	+					
836	*M. hawaiiensis*	+	−	−	−	−	−	+	+	−	+	−	−	+	−	+	+	+	−	−	+	+	+	−	+	−	−	−	−	−	+	+	−	+	−	+	+					
837	*M. hibisci*	+	−	−	−	−	−	+	+	−	+	−	−	+	−	+	+	+	−	−	+	+	+	−	+	−	−	+	−	−	−	+	−	+	−	+	+					
838	*M. kamakouana*	+	−	−	−	−	−	v	+	−	+	−	−	+	−	+	+	+	+	−	+	+	+	−	+	−	−	−	−	−	+	+	−	+	−	+	+					
839	*M. koreensis*	+	−	−	−	−	−	−	+	−	+	−	−	v	−	+	+	+	+	−	+	+	+	−	+	−	−	−	−	−	+	+	−	+	−	+	+					
840	*M. krissii*	−	−	−	−	−	−	−	+	−	+	−	−	−	−	+	+	+	+	−	+	+	−	−	−	−	−	−	−	−	+	+	−	−	−	+	−					
841	*M. kunwiensis*	+	−	−	−	−	−	−	+	−	+	−	−	+	−	+	+	+	+	−	+	+	+	−	+	−	−	−	−	−	+	+	−	+	−	+	+					
842	*M. lachancei*	+	−	−	−	−	−	−	+	−	+	−	−	v	−	−	+	+	−	−	+	+	v	−	+	−	−	−	−	−	−	+	−	+	−	−	−					
843	*M. lochheadii*	+	−	−	−	−	−	+	+	−	+	−	−	+	−	+	+	+	v	−	+	+	+	−	+	−	−	−	−	−	v	v	−	v	−	+	+					
844	*M. lunata*	+	−	−	−	−	−	−	+	−	+	−	−	+	−	+	+	+	v	−	+	+	v	−	+	−	−	−	−	−	v	+	−	v	−	+	+					
845	*M. mauinuiana*	+	−	−	−	−	−	+	+	−	+	−	−	+	−	+	+	+	−	−	+	+	+	−	+	−	−	+	−	−	+	+	−	+	−	+	+					
846	*M. noctiluminum*	+	−	−	−	−	−	−	+	−	+	−	−	+	−	+	+	+	+	−	+	+	+	−	−	−	−	−	−	−	−	+	−	+	−	+	+					
847	*M. orientalis*	+	−	−	−	−	−	+	+	−	+	−	−	+	−	+	+	+	−	−	+	+	+	−	+	−	−	v	−	−	+	+	−	+	−	+	+					
848	*M. pulcherrima*	+	v	−	−	−	−	−	+	−	+	−	−	+	−	+	+	+	+	−	+	+	v	−	v	−	−	v	−	−	+	+	−	v	−	+	+					
849	*M. reukaufii*	+	v	−	−	−	−	−	+	−	+	−	−	v	−	v	+	+	v	−	+	+	+	−	v	−	v	v	−	−	v	+	−	v	−	+	+					
850	*M. santaceciliae*	+	−	−	−	−	−	+	+	−	+	−	−	+	−	+	+	+	+	−	+	+	+	−	+	−	−	−	−	−	+	+	−	+	−	+	+					
851	*M. shanxiensis*	+	+	−	−	−	−	n	+	−	+	−	−	+	−	+	+	+	+	−	+	+	+	−	+	−	−	−	−	−	+	+	−	+	−	+	n					
852	*M. similis*	+	−	−	−	−	−	+	+	−	+	−	−	+	−	+	+	+	+	−	+	v	+	−	+	−	−	−	−	−	+	−	−	+	−	+	+					
853	*M. sinensis*	+	+	−	−	−	−	n	+	−	+	−	−	+	−	+	+	+	+	−	+	+	+	−	+	−	−	−	−	−	+	+	−	+	−	+	n					
854	*M. vanudenii*	+	n	n	n	n	n	n	+	−	+	−	−	−	−	−	+	+	−	−	v	−	v	−	v	−	−	−	−	−	v	v	−	−	−	v	−					
855	*M. viticola*	+	−	−	−	−	−	−	+	−	+	−	−	+	−	+	+	+	+	−	+	+	+	−	+	−	−	−	−	−	+	+	−	+	−	+	+					
856	*M. zizyphicola*	+	−	−	−	−	−	n	+	−	+	−	−	+	−	+	+	+	+	−	+	+	+	−	+	−	−	−	−	−	+	+	−	+	−	+	n					
857	*M. zobellii*	+	+	−	−	−	−	−	+	−	+	−	−	+	−	+	+	+	+	−	+	+	+	−	+	−	−	−	+	−	v	+	−	+	−	+	+					
858	***Meyerozyma***																																								
859	*M. caribbica*	+	+	+	v	−	+	+	+	+	+	+	v	+	−	+	+	+	+	−	+	+	v	v	+	v	+	v	−	+	v	−	+	+	+	+					
860	*M. guilliermondii*	+	v	+	−	−	+	+	+	+	+	+	+	+	−	+	+	+	+	−	+	+	v	v	+	+	+	+	−	+	+	−	+	v	+	+					
861	***Millerozyma***																																								
862	*M. acaciae*	+	v	−	+	−	−	+	+	−	−	−	−	+	v	+	+	−	+	−	+	+	v	−	+	+	−	+	−		+	+	+	+	−	+	+					
863	*M. farinosa*	+	v	−	−	−	−	v	+	−	−	−	−	+	v	v	v	−	v	v	v	v	v	−	v	v	−	+	−		+	+	+	+	−	+	+					
864	***Mixia***																																								
865	*M. osmundae*	−	−	−	−	−	−	−	+	−	−	−	−	v	−	−	−	−	−	+	−	−	−	−	−	−	v	−	−		−	−	−	−	−	−	v					
866	***Moniliella***																																								
867	*M. acetoabutens*	+	−	+	+	−	−	n	+	−	+	−	−	−	+	−	+	−	−	−	+	−	−	−	−	−	v	n			n	+	+	v	−	+	+					

Symbols: +, positive or weak; −, negative; v, variable (+/−, w/−); n, no data.

Growth reactions and other characteristics

	myo-Inositol	DL-Lactate	Succinate	Citrate	D-Gluconate	D-Glucosamine	*N*-Acetyl-D-glucosamine	Hexadecane	Nitrate	Nitrite	Vitamin-free	2-Keto-D-gluconate	5-Keto-D-gluconate	Saccharate	Xylitol	L-Arabinitol	Arbutin	Propane 1,2 diol	Butane 2,3 diol	Cadaverine	Creatinine	L-Lysine	Ethylamine	50% Glucose	10% NaCl/5% glucose	Starch formation	Urease	Gelatin liquefaction	Cycloheximide 0.01%	Cycloheximide 0.1%	Growth at 19°C	Growth at 25°C	Growth at 30°C	Growth at 35°C	Growth at 37°C	Growth at 40°C	Growth at 45°C	CoQ (Main component)	Mol% G + C (Ave.)	DBB
Meira																																								
814	−	+	+	+	−	−	n	n	+	+	v	−	n	n	n	n	n	n	n	n	n	n	n	−	n	−	+	n	n	n	+	+	+	−	−	−	−	n	n	+
815	−	+	+	+	+	−	n	n	−	−	+	−	n	n	n	n	n	n	n	n	n	n	n	−	n	−	+	n	n	n	+	+	+	+	+	−	−	n	n	+
Metschnikowia																																								
817	−	−	+	−	+	+	+	−	−	−	−	+	n	n	+	n	n	n	n	+	n	+	+	+	n	−	n	−	−	−	+	+	+	n	−	−	−	n	n	−
818	−	−	+	+	−	−	+	+	−	−	−	+	n	n	−	n	n	n	n	+	n	+	+	+	n	−	n	−	−	−	+	+	+	+	+	n	n	9	n	−
819	−	−	+	−	+	+	+	n	−	−	−	+	n	n	+	n	n	n	n	+	n	+	−	+	n	−	n	n	−	−	+	+	+	+	−	−	−	n	n	−
820	−	−	−	−	−	−	−	−	−	−	−	−	n	n	−	n	n	n	n	v	n	−	+	−	n	−	n	−	−	−	+	+	+	n	−	−	−	n	n	−
821	−	−	v	−	−	−	+	−	−	−	−	−	n	n	v	n	n	n	n	v	n	+	v	−	n	−	n	−	−	−	+	+	−	−	−	−	−	9	47.0	−
822	−	−	v	−	+	v	+	−	−	−	−	+	n	n	+	n	n	n	n	+	n	+	+	v	n	−	n	−	−	−	+	+	v	n	−	−	−	9	48.0	−
823	−	−	v	−	+	v	+	−	−	−	−	+	n	n	+	n	n	n	n	+	n	+	+	v	n	−	n	−	+	+	+	+	v	n	−	−	−	9	47.6	−
824	−	−	v	−	−	v	+	−	−	−	−	−	n	n	+	n	n	n	n	+	n	+	+	v	n	−	n	−	+	−	+	+	+	−	−	−	−	9	47.5	−
825	−	−	v	+	v	−	+	+	−	−	−	v	n	n	+	n	n	n	n	+	n	+	+	+	n	−	n	−	−	−	+	+	+	+	n	n	n	n	n	−
826	−	−	+	+	−	−	+	+	−	−	−	+	n	n	+	n	n	n	n	+	n	+	+	+	n	−	n	−	−	−	+	+	+	−	−	−	−	n	n	−
827	−	−	−	−	+	−	+	−	−	−	−	−	n	n	+	n	n	n	n	+	n	−	+	−	n	−	n	−	−	−	+	+	+	n	−	−	−	n	n	−
828	−	−	+	+	+	−	+	−	−	−	−	+	n	n	+	n	n	n	n	+	n	−	+	+	n	−	n	−	−	−	+	+	+	n	−	−	−	n	n	−
829	−	−	+	+	v	−	+	+	−	−	−	v	n	n	+	n	n	n	n	+	n	+	+	+	n	−	n	−	−	−	+	+	+	n	−	−	−	n	n	−
830	−	+	+	+	+	+	n	n	−	−	−	+	n	n	+	n	n	n	n	n	n	n	n	−	n	−	n	n	−	−	+	+	−	−	−	−	−	n	n	−
831	−	−	v	+	−	+	+	+	−	−	−	+	n	n	+	n	n	n	n	+	n	−	+	+	n	−	n	−	−	−	+	+	+	n	−	−	−	n	n	−
832	−	+	+	+	+	−	+	+	−	−	−	−	n	n	+	n	n	n	n	+	n	+	+	+	n	−	n	−	−	−	+	+	+	+	+	n	n	n	n	−
833	−	+	+	+	+	+	+	+	−	−	−	+	n	n	+	n	n	n	n	+	n	+	+	+	n	−	n	−	−	−	+	+	+	n	−	−	−	n	n	−
834	−	−	+	−	v	v	+	−	−	−	−	+	n	n	n	n	n	n	n	+	n	+	+	+	n	−	n	−	−	−	+	+	+	n	−	−	−	9	39.2	−
835	−	−	+	+	+	+	+	+	−	−	−	+	n	n	+	n	n	n	n	+	n	+	+	+	n	−	n	−	−	−	+	+	−	−	−	−	−	n	n	−
836	−	−	+	+	+	−	+	+	−	−	−	+	n	n	+	n	n	n	n	+	n	+	+	+	n	−	n	−	−	−	+	+	+	−	−	−	−	9	46.7	−
837	−	−	+	+	+	v	+	+	−	−	−	+	n	n	+	n	n	n	n	+	n	+	+	+	n	−	n	−	−	−	+	+	+	n	−	−	−	n	n	−
838	−	−	+	+	+	+	+	+	−	−	−	+	n	n	+	n	n	n	n	+	n	+	+	−	n	−	n	−	−	−	+	+	−	−	−	−	−	n	n	−
839	−	−	+	−	+	+	+	v	−	−	−	+	n	n	+	n	n	n	n	+	n	+	+	+	n	−	n	−	−	−	+	+	+	n	−	−	−	9	41.3	−
840	−	−	+	−	−	−	−	−	−	−	−	−	n	n	−	n	n	n	n	−	n	+	+	−	n	−	n	−	−	−	+	+	+	n	−	−	−	9	45.4	−
841	−	+	+	v	+	+	+	+	−	−	−	+	n	n	+	n	n	n	n	+	n	+	+	+	n	−	n	−	−	−	+	+	+	n	−	−	−	9	41.1	−
842	−	−	−	−	+	−	+	−	−	−	−	+	n	n	+	n	n	n	n	+	n	+	+	+	n	−	n	−	−	−	+	+	+	n	−	−	−	n	46.9	−
843	−	−	+	+	−	−	+	+	−	−	−	+	n	n	v	n	n	n	n	+	n	v	+	v	n	−	n	−	−	−	+	+	+	n	−	−	−	n	n	−
844	−	−	+	+	+	v	+	+	−	−	−	+	n	n	+	n	n	n	n	+	n	+	+	+	n	−	n	−	−	−	+	+	+	+	+	n	n	9	44.2	−
845	−	−	+	+	+	+	+	+	−	−	−	+	n	n	+	n	n	n	n	+	n	+	+	+	n	−	n	−	−	−	+	+	−	−	−	−	−	n	n	−
846	−	+	+	+	+	−	n	n	−	−	−	+	n	n	+	n	n	n	n	n	n	n	n	−	n	−	n	n	−	−	+	+	+	n	−	−	−	n	n	−
847	−	−	+	v	+	+	+	−	−	−	−	+	n	n	+	n	n	n	n	+	n	+	+	+	n	−	n	−	−	−	+	+	+	−	−	−	−	n	n	−
848	−	v	+	+	+	v	+	+	−	−	−	+	n	n	+	n	n	n	n	+	n	+	+	v	n	−	n	−	−	−	+	+	v	n	−	−	−	9	45.6	−
849	−	−	+	v	+	v	+	+	−	−	−	+	n	n	+	n	n	n	n	+	n	+	+	v	n	−	n	v	−	−	+	+	+	n	v	n	n	9	41.3	−
850	−	−	+	+	+	+	+	+	−	−	−	+	n	n	+	n	n	n	n	+	n	+	+	+	n	−	n	+	−	−	+	+	n	+	−	−	−	n	n	−
851	−	−	+	−	n	−	n	−	−	−	−	n	n	n	n	n	n	n	n	+	n	+	+	+	n	−	n	n	n	n	+	+	n	+	−	−	−	n	n	−
852	−	−	v	−	−	+	+	+	−	−	−	+	n	n	+	n	n	n	n	+	n	−	+	+	n	−	n	−	−	−	+	+	+	−	−	−	−	n	n	−
853	−	−	+	−	n	−	n	−	−	−	−	n	n	n	n	n	n	n	n	+	n	+	+	+	n	−	n	n	n	n	+	+	+	+	−	−	−	n	n	−
854	−	−	−	−	v	−	−	−	−	−	−	v	n	n	+	n	n	n	n	+	n	+	+	+	n	−	n	v	−	−	+	+	+	n	−	−	−	n	43.5	−
855	−	−	+	+	+	+	+	+	−	−	−	+	n	n	+	n	n	n	n	+	n	+	+	+	n	−	n	n	−	−	+	+	+	−	−	−	−	n	n	−
856	−	−	+	−	n	−	n	−	−	−	−	n	n	n	n	n	n	n	n	+	n	+	+	+	n	−	n	n	n	n	+	+	+	n	−	−	−	n	n	−
857	−	−	+	−	−	+	−	−	−	−	−	−	n	n	−	n	n	n	n	+	n	+	+	+	n	−	n	−	+	−	+	+	+	n	−	−	−	9	47.5	−
Meyerozyma																																								
859	−	−	v	+	−	v	+	n	−	n	v	+	−	−	n	n	n	n	n	n	n	n	n	n	+	−	n	n	+	v	+	+	+	+	+	+	−	n	49.6	−
860	−	v	+	v	v	+	+	+	−	n	−	+	−	−	n	n	n	n	n	n	n	n	n	n	+	−	n	−	n	n	+	+	+	+	+	n	n	9	44.5	−
Millerozyma																																								
862	−	−	+	+	v	−	+	+	−	n	−	−	−	−	n	n	n	n	n	n	n	n	n	n	+	−	n	v	n	n	+	+	+	+	+	n	n	9	46.0	−
863	−	−	v	+	+	−	+	+	−	n	v	−	−	−	n	n	n	n	n	n	n	n	n	n	+	−	n	v	n	n	+	+	+	+	+	n	n	9	39.3	−
Mixia																																								
865	−	−	−	−	−	−	−	−	−	−	−	−	−	−	v	n	n	n	n	−	n	−	−	−	−	−	+	−	n	n	+	v	−	−	−	−	−	10	53.9	−
Moniliella																																								
867	−	−	v	v	n	n	n	n	+	n	+	n	n	n	n	n	n	n	n	n	n	n	n	n	n	n	n	n	n	n	+	+	+	+	+	n	n	9	61.2	+

Symbols: +, positive or weak; −, negative; v, variable (+/−, w/−); n, no data.

Ln. no.	Species	Fermentation: Glucose	Galactose	Sucrose	Maltose	Lactose	Raffinose	Trehalose	Growth reactions and other characteristics: Glucose	Inulin	Sucrose	Raffinose	Melibiose	Galactose	Lactose	Trehalose	Maltose	Melezitose	Methyl-α-D-glucoside	Soluble Starch	Cellobiose	Salicin	L-Sorbose	L-Rhamnose	D-Xylose	L-Arabinose	D-Arabinose	D-Ribose	Methanol	Ethanol	Glycerol	Erythritol	Ribitol	Galactitol	D-Mannitol	D-Glucitol
	Moniliella (*cont'd*)																																			
868	*M. fonsecae*	−	−	−	−	−	−	−	+	v	+	−	−	−	−	−	−	−	−	−	+	−	−	−	−	−	−	−	−	+	+	+	−	−	−	−
869	*M. madida*	+	v	+	+	−	−	n	+	−	+	−	−	−	−	−	+	−	−	v	+	−	−	−	v	v	−	+	n	n	+	+	−	−	+	+
870	*M. megachiliensis*	+	−	+	+	−	−	n	+	−	+	−	−	−	−	−	+	−	−	v	+	−	−	−	−	−	−	v	n	n	+	+	−	−	+	v
871	*M. mellis*	+	+	−	+	−	−	n	+	−	−	−	−	+	−	−	+	−	−	−	+	−	−	−	−	−	−	+	n	n	+	+	−	−	+	+
872	*M. nigrescens*	+	+	−	+	−	−	n	+	−	−	−	−	+	−	−	+	−	−	−	+	−	−	−	−	−	−	−	n	n	+	+	−	−	+	+
873	*M. oedocephalis*	+	+	+	+	−	−	n	+	−	+	−	−	+	−	−	+	−	−	−	+	−	−	−	−	v	−	+	n	n	+	+	−	−	+	+
874	*M. spathulata*	+	+	+	+	v	−	n	+	−	+	+	−	v	v	−	+	+	−	−	+	+	−	−	v	−	−	+	n	n	+	+	−	−	+	+
875	*M. suaveolens*	+	v	+	+	v	−	n	+	−	+	v	−	v	v	−	+	v	−	v	+	v	−	−	v	v	−	+	n	n	+	+	v	−	+	v
876	***Mrakia***																																			
877	*M. curviuscula*	−	−	−	−	−	−	−	+	−	−	−	−	+	+	+	+	+	−	v	+	+	v	+	+	+	v	+	−	v	−	−	+	n	+	+
878	*M. frigida*	+	v	+	−	−	v	−	+	−	+	+	v	+	v	+	−	−	−	−	+	+	+	v	+	+	+	−	−	+	v	−	+	−	+	+
879	*M. gelida*	+	+	+	v	−	v	n	+	−	+	+	v	+	−	+	+	+	v	+	+	+	+	+	+	+	v	v	−	+	−	−	+	−	+	+
880	***Mrakiella***																																			
881	*M. aquatica*	v	−	v	v	−	v	n	+	−	+	+	+	+	+	+	+	+	−	+	+	+	+	−	+	+	−	−	−	+	v	−	+	−	+	+
882	*M. cryoconiti*	−	−	−	−	−	−	−	+	v	+	+	+	v	+	+	+	+	−	+	+	+	+	v	+	+	+	+	−	+	+	−	+	−	+	+
883	***Myxozyma***																																			
884	*M. geophila*	−	−	−	−	−	−	−	+	−	+	−	−	+	v	−	−	−	−	−	−	−	+	−	+	+	+	+	−	+	+	−	+	+	+	+
885	*M. kluyveri*	−	−	−	−	−	−	−	+	v	+	+	+	+	+	+	−	−	+	−	+	+	+	+	+	+	+	+	−	+	+	−	+	−	+	+
886	*M. lipomycoides*	−	−	−	−	−	−	−	+	−	−	−	−	+	+	+	−	−	−	−	+	−	+	+	+	+	+	+	−	+	+	−	+	−	−	+
887	*M. melibiosi*	−	−	−	−	−	−	−	+	−	−	−	+	+	v	−	−	−	−	−	+	+	v	−	+	+	+	+	−	+	+	−	+	−	v	+
888	*M. monticola*	−	−	−	−	−	−	−	+	−	+	v	+	+	+	+	+	+	+	−	−	+	+	+	+	+	+	+	−	+	+	+	+	−	+	+
889	*M. mucilagina*	−	−	−	−	−	−	−	+	−	+	−	−	+	−	v	+	+	+	−	+	+	+	+	+	+	v	v	−	+	+	−	+	−	+	+
890	*M. neglecta*	−	−	−	−	−	−	−	+	−	−	−	−	+	−	−	−	−	−	−	+	+	+	−	+	+	+	−	−	+	+	−	+	−	−	−
891	*M. neotropica*	−	−	−	−	−	−	−	+	−	+	−	+	+	+	+	+	+	+	−	+	+	+	+	+	+	+	+	−	+	+	−	+	−	−	−
892	*M. nipponensis*	−	−	−	−	−	−	−	+	−	−	−	−	+	−	+	−	−	−	−	+	+	+	+	+	+	+	+	−	−	+	+	+	−	+	+
893	*M. sirexii*	−	−	−	−	−	−	−	+	−	−	−	−	+	−	−	−	−	−	−	−	−	+	−	+	+	+	+	−	+	+	+	+	−	+	+
894	*M. udenii*	−	−	−	−	−	−	−	+	−	+	−	−	+	+	+	+	+	+	−	+	+	+	−	+	+	−	−	−	+	+	−	+	−	+	+
895	*M. vanderwaltii*	−	−	−	−	−	−	−	+	−	+	−	−	+	v	+	+	+	+	−	+	+	+	−	+	+	+	v	−	+	+	−	+	−	−	+
896	***Nadsonia***																																			
897	*N. commutata*	−	−	−	−	−	−	−	+	−	−	−	−	−	−	−	v	−	−	−	−	−	−	−	−	−	−	−	−	+	+	−	−	−	−	v
898	*N. fulvescens* var. *fulvescens*	+	+	+	+	−	−	−	+	−	+	−	−	+	−	−	+	−	+	−	−	−	+	−	−	−	−	−	−	+	+	−	v	−	+	+
899	*N. fulvescens* var. *elongata*	+	−	−	−	−	−	−	+	−	−	−	−	−	−	−	−	−	−	−	−	−	+	−	−	−	−	−	−	+	+	−	v	−	−	+
900	***Nakaseomyces***																																			
901	*N. bacillisporus*	+	−	−	−	−	−	−	+	−	n	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	+	−	−	−	−	−
902	*N. delphensis*	+	−	−	−	−	−	−	+	−	−	−	−	−	−	+	−	−	−	−	−	−	−	−	−	−	−	−	−	+	+	−	−	−	−	−
903	***Nakazawaea***																																			
904	*N. holstii*	+	v	−	−	−	−	+	+	−	+	−	−	+	−	+	+	+	+	+	+	+	+	+	+	+	+	+	−	+	+	v	+	v	+	+
905	***Naohidea***																																			
906	*N. sebacea*	−	−	−	−	−	−	−	+	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	+	−	+	−	+	−
907	***Naumovozyma***																																			
908	*N. castellii*	+	+	−	−	−	−	−	+	−	v	−	−	+	−	v	−	−	−	−	−	−	−	−	−	−	−	v	−	v	v	−	−	−	−	−
909	*N. dairenensis*	+	+	−	−	−	−	−	+	−	−	−	−	+	−	v	−	−	−	−	−	−	−	−	−	−	−	v	−	v	−	−	−	−	−	−
910	***Occultifur***																																			
911	*O. externus*	−	−	−	−	−	−	−	+	−	+	−	−	+	+	+	+	+	−	−	+	+	+	−	+	+	+	v	−	+	+	−	v	−	+	+
912	***Ogataea***																																			
913	*O. allantospora*	−	−	−	−	−	−	−	+	−	−	−	−	−	−	+	−	−	−	−	+	+	+	−	+	−	+	+	+	+	+	+	+	−	+	+
914	*O. chonburiensis*	−	−	−	−	−	−	−	+	−	−	−	−	−	−	+	−	−	−	−	+	+	+	−	+	+	−	−	+	+	+	+	−	−	+	+
915	*O. corticis*	+	−	−	−	−	−	−	+	−	−	−	−	−	−	+	−	−	−	−	+	+	−	+	+	−	−	−	+	+	+	+	+	−	+	+
916	*O. dorogensis*	+	−	−	−	−	−	v	+	−	−	−	−	−	−	+	−	−	−	−	+	+	+	−	+	+	+	+	+	+	+	+	+	−	+	+
917	*O. falcaomoraisii*	v	−	v	n	−	−	n	+	−	+	−	−	−	−	+	+	+	v	−	+	+	v	v	+	−	−	+	v	+	v	+	+	−	+	+
918	*O. ganodermae*	+	−	−	−	−	−	n	+	−	+	+	+	−	−	+	+	−	−	−	+	+	+	+	+	−	−	+	+	+	+	+	+	−	+	+
919	*O. glucozyma*	+	−	−	−	−	−	+	+	−	−	−	−	−	−	+	−	−	−	−	+	v	−	+	+	−	−	+	+	+	+	+	+	−	+	+
920	*O. henricii*	−	−	−	−	−	−	−	+	−	−	−	−	−	−	v	−	−	−	−	+	+	−	+	+	−	−	+	+	+	+	+	+	−	+	+
921	*O. kodamae*	+	−	−	−	−	−	−	+	−	−	−	−	−	−	−	−	−	−	−	+	+	v	−	+	v	−	+	+	+	+	+	+	−	+	+

Symbols: +, positive or weak; −, negative; v, variable (+/−, w/−); n, no data.

Growth reactions and other characteristics

	myo-Inositol	DL-Lactate	Succinate	Citrate	D-Gluconate	D-Glucosamine	*N*-Acetyl-D-glucosamine	Hexadecane	Nitrate	Nitrite	Vitamin-free	2-Keto-D-gluconate	5-Keto-D-gluconate	Saccharate	Xylitol	L-Arabinitol	Arbutin	Propane 1,2 diol	Butane 2,3 diol	Cadaverine	Creatinine	L-Lysine	Ethylamine	50% Glucose	10% NaCl/5% glucose	Starch formation	Urease	Gelatin liquefaction	Cycloheximide 0.01%	Cycloheximide 0.1%	Growth at 19°C	Growth at 25°C	Growth at 30°C	Growth at 35°C	Growth at 37°C	Growth at 40°C	Growth at 45°C	CoQ (Main component)	Mol% G + C (Ave.)	DBB
Moniliella (*cont'd*)																																								
868	−	−	+	−	+	−	−	+	+	n	+	n	n	n	n	n	n	n	n	n	n	n	n	n	n	n	+	n	n	n	+	+	+	n	v	n	n	n	n	+
869	−	−	+	+	n	n	n	n	+	n	v	n	n	n	n	n	n	n	n	n	n	n	n	n	n	n	+	n	n	n	+	+	+	+	+	n	n	9	50.3	+
870	−	−	v	+	n	n	n	n	v	n	n	n	n	n	n	n	n	n	n	+	n	+	v	+	n	n	n	n	n	n	+	+	+	+	+	n	n	9	n	+
871	−	−	+	+	n	n	n	n	+	n	−	n	n	n	n	n	n	n	n	n	n	n	n	n	n	n	+	n	n	n	+	+	+	n	−	−	−	9	58.7	+
872	−	−	−	−	n	n	n	n	+	n	+	n	n	n	n	n	n	n	n	n	n	n	n	n	n	n	n	n	n	n	+	+	+	+	+	n	n	9	57.0	+
873	−	−	v	v	n	n	n	n	+	n	−	n	n	n	n	n	n	n	n	n	n	n	n	n	n	n	+	n	n	n	+	+	+	+	+	n	n	9	45.8	+
874	−	+	+	+	n	n	n	n	+	n	+	n	n	n	n	n	n	n	n	n	n	n	n	n	n	n	+	n	n	n	+	+	+	+	+	n	n	n	62.0	+
875	−	−	+	v	n	n	n	n	+	n	+	n	n	n	n	n	n	n	n	n	n	n	n	n	n	n	+	n	n	n	+	+	+	n	−	−	−	9	59.9	+
Mrakia																																								
877	−	+	+	+	+	+	+	−	+	n	−	+	+	−	n	n	n	n	n	n	−	n	n	v	n	+	n	−	n	n	+	+	−	−	−	−	−	n	51.2	+
878	v	−	+	v	+	−	+	−	+	+	−	+	+	n	+	n	n	n	n	n	−	+	n	−	n	+	n	n	n	n	v	−	−	−	−	−	−	8	54.1	+
879	v	−	v	v	+	+	+	−	+	+	−	+	n	n	+	n	+	n	n	n	−	+	n	−	n	+	n	+	n	n	+	−	−	−	−	−	−	8	56.1	+
Mrakiella																																								
881	−	−	+	+	+	−	−	−	+	+	−	+	n	+	+	n	+	n	n	−	−	+	−	−	−	+	+	−	n	n	+	−	−	−	−	−	−	8	58.4	+
882	+	−	+	−	+	v	+	−	+	n	−	+	+	n	+	n	+	n	n	−	n	+	n	+	−	+	+	−	n	n	+	−	−	−	−	−	−	n	n	+
Myxozyma																																								
884	+	+	+	−	+	−	−	−	−	n	−	+	+	−	n	n	n	n	n	n	n	n	n	n	−	+	n	+	n	n	+	+	+	n	−	−	−	8	46.4	−
885	v	−	+	v	+	−	−	−	−	n	−	+	+	−	n	n	n	n	n	n	n	n	n	n	−	+	n	−	n	n	+	+	+	n	−	−	−	8	39.5	−
886	−	−	+	+	−	−	−	−	−	n	−	+	−	−	n	n	n	n	n	n	n	n	n	n	−	+	n	−	n	n	+	+	+	n	−	−	−	9	40.9	−
887	+	−	+	−	+	−	−	−	−	n	−	+	+	−	n	n	n	n	n	n	n	n	n	n	−	+	n	−	n	n	+	+	+	n	−	−	−	8	50.3	−
888	+	+	+	−	v	−	−	−	−	n	−	+	+	−	n	n	n	n	n	n	n	n	n	n	−	+	n	−	n	n	+	+	+	n	−	−	−	8	45.2	−
889	−	v	+	+	+	−	−	−	−	n	−	+	+	−	n	n	n	n	n	n	n	n	n	n	−	+	n	−	n	n	+	+	+	+	+	n	n	8	43.6	−
890	−	−	+	+	−	−	n	n	−	n	−	+	−	n	n	n	n	n	n	n	n	n	n	n	n	+	n	n	n	n	+	+	+	n	−	−	−	8	42.8	−
891	+	+	+	+	+	+	n	n	−	n	−	+	+	n	n	n	n	n	n	n	n	n	n	n	n	+	n	n	n	n	+	+	+	n	−	−	−	8	45.2	−
892	+	−	+	−	−	−	n	n	−	n	−	−	−	n	n	n	n	n	n	n	n	n	n	n	n	+	n	n	n	n	+	+	+	n	−	−	−	9	48.9	−
893	+	−	+	−	−	−	n	n	−	n	−	−	−	n	n	n	n	n	n	n	n	n	n	n	n	+	n	n	n	n	+	+	+	+	+	n	n	8	48.4	−
894	+	+	+	+	+	−	−	−	−	n	−	+	+	−	n	n	n	n	n	n	n	n	n	n	−	+	n	−	n	n	+	+	+	+	+	n	n	8	49.2	−
895	−	+	v	−	+	−	−	−	−	n	−	+	+	−	n	n	n	n	n	n	n	n	n	n	−	+	n	−	n	n	+	+	+	n	−	−	−	8	44.8	−
Nadsonia																																								
897	−	−	+	−	−	−	n	−	−	n	−	−	−	−	−	n	n	n	n	−	n	−	−	−	n	−	n	n	−	−	+	−	−	−	−	−	−	6	40.0	−
898	−	v	+	−	−	−	n	−	−	n	v	−	−	−	−	n	n	n	n	+	n	+	v	−	n	−	n	n	+	−	+	+	−	−	−	−	−	6	41.5	−
899	−	v	+	−	−	−	n	−	−	n	v	−	−	−	−	n	n	n	n	+	n	+	v	−	n	−	n	n	+	−	+	+	−	−	−	−	−	n	41.0	−
Nakaseomyces																																								
901	−	−	−	−	+	−	−	−	−	−	−	+	n	n	−	n	n	n	n	−	n	−	−	+	n	−	n	−	−	−	+	+	+	+	+	n	n	6	38.0	−
902	−	−	−	−	−	−	−	−	−	−	−	−	n	n	−	n	n	n	n	−	n	−	−	+	n	−	n	−	−	−	+	+	+	+	+	n	n	6	40.2	−
Nakazawaea																																								
904	−	−	+	+	v	+	+	−	+	n	−	v	−	−	n	n	n	n	n	n	n	n	n	n	+	−	n	v	n	n	+	+	+	n	v	n	n	8	37.0	−
Naohidea																																								
906	−	+	−	−	−	−	n	n	−	−	−	n	n	n	−	n	n	n	n	n	n	n	n	n	n	−	n	n	−	−	+	+	+	−	−	−	−	n	n	+
Naumovozyma																																								
908	−	−	v	−	v	−	−	−	−	n	−	n	n	n	n	n	n	n	n	−	n	−	−	n	n	n	n	n	v	−	+	+	+	n	v	n	n	n	38.2	−
909	−	−	v	−	v	−	−	−	−	n	−	n	n	n	n	n	n	n	n	−	n	−	−	n	n	n	n	n	v	−	+	+	+	+	+	−	−	n	37.1	−
Occultifur																																								
911	−	+	+	+	+	−	−	−	−	−	−	n	n	n	v	n	n	n	n	n	n	n	n	n	n	−	+	n	+	+	+	+	+	−	−	−	−	n	50.0	+
Ogataea																																								
913	−	−	+	+	v	−	−	−	+	+	−	−	n	n	n	n	n	n	n	n	n	n	n	n	−	−	n	n	+	+	+	+	+	+	+	−	−	n	n	−
914	−	−	+	+	−	n	n	n	+	+	−	−	−	n	n	n	n	n	n	n	n	n	n	n	−	n	n	n	+	+	+	+	+	+	+	+	−	7	n	−
915	−	+	−	+	+	−	−	−	−	−	−	n	n	−	n	n	n	n	n	n	n	n	n	n	+	n	n	n	+	+	+	+	+	+	+	−	−	7	48.3	−
916	−	−	+	+	−	−	−	−	−	−	−	−	n	n	n	n	n	n	n	n	n	n	n	n	−	−	n	n	+	+	+	+	+	+	+	+	−	7	n	−
917	−	−	+	+	−	−	−	−	−	−	−	−	n	n	n	n	n	n	n	n	n	n	n	n	−	−	n	n	+	+	+	+	+	n	v	v	n	n	n	−
918	+	−	+	−	n	−	n	−	v	−	n	n	n	n	n	n	n	n	n	n	n	n	n	n	n	n	n	n	+	+	+	+	+	+	+	n	n	n	n	−
919	−	−	−	+	v	−	−	−	+	+	−	−	−	−	n	n	n	n	n	n	n	n	n	n	+	−	n	v	n	n	+	+	+	+	+	n	n	7	45.1	−
920	−	−	v	−	v	−	−	−	+	+	−	−	−	−	n	n	n	n	n	n	n	n	n	n	v	−	n	+	n	n	+	+	+	+	+	n	n	7	49.6	−
921	−	−	+	−	v	−	−	−	−	n	−	−	−	−	n	n	n	n	n	n	n	n	n	n	−	−	n	−	n	n	+	+	+	+	+	n	n	7	n	−

Symbols: +, positive or weak; −, negative; v, variable (+/−, w/−); n, no data.

Ln. no.	Species	Fermentation: Glucose	Galactose	Sucrose	Maltose	Lactose	Raffinose	Trehalose	Growth reactions and other characteristics: Glucose	Inulin	Sucrose	Raffinose	Melibiose	Galactose	Lactose	Trehalose	Maltose	Melezitose	Methyl-α-D-glucoside	Soluble Starch	Cellobiose	Salicin	L-Sorbose	L-Rhamnose	D-Xylose	L-Arabinose	D-Arabinose	D-Ribose	Methanol	Ethanol	Glycerol	Erythritol	Ribitol	Galactitol	D-Mannitol	D-Glucitol
	Ogataea (*cont'd*)																																			
922	*O. methanolica*	+	−	−	−	−	−	+	+	−	v	−	−	+	−	+	−	−	−	−	+	+	v	−	+	+	+	+	+	+	+	+	+	+	+	+
923	*O. methylivora*	−	−	−	−	−	−	−	+	−	+	+	−	−	−	+	−	−	−	−	−	+	+	+	+	+	+	+	+	+	+	+	+	−	+	+
924	*O. minuta*	+	−	−	−	−	−	+	+	−	−	−	−	−	−	+	−	−	−	−	+	+	−	−	+	−	−	+	+	+	+	−	+	−	+	+
925	*O. naganishii*	+	−	−	−	−	−	+	+	−	+	−	−	+	−	+	+	+	+	−	+	+	−	+	+	+	−	+	+	+	+	+	+	−	+	+
926	*O. nakhonphanomensis*	−	−	−	−	−	−	−	+	−	−	−	−	−	−	+	+	+	+	−	+	+	+	+	+	+	+	+	+	+	+	+	+	−	+	+
927	*O. neopini*	v	−	−	−	−	−	n	+	−	−	−	−	−	−	+	−	−	−	−	+	+	−	+	+	+	−	+	+	v	+	+	+	−	+	+
928	*O. nitratoaversa*	+	−	−	−	−	−	+	+	−	−	−	−	−	−	+	−	−	−	−	+	+	−	−	+	+	−	+	+	+	+	+	+	−	+	+
929	*O. nonfermentans*	−	−	−	−	−	−	−	+	−	−	−	−	−	−	+	−	−	−	−	+	+	−	−	+	−	−	+	+	+	+	−	+	−	+	+
930	*O. paradorogensis*	−	−	−	−	−	−	−	+	−	−	−	−	−	−	+	−	−	−	−	+	+	+	−	+	v	v	+	+	+	+	+	+	−	+	+
931	*O. philodendri*	−	−	−	−	−	−	−	+	−	−	−	−	−	−	+	−	−	−	−	−	−	+	−	+	v	−	+	+	+	+	+	+	−	+	+
932	*O. pilisensis*	+	−	−	−	−	−	−	+	−	−	−	−	−	−	+	−	−	−	−	+	+	−	−	+	+	−	+	+	+	+	+	+	−	+	+
933	*O. pini*	v	−	−	−	−	−	v	+	−	−	−	−	−	−	+	−	−	−	−	+	+	v	v	v	v	v	v	+	v	v	+	+	−	+	+
934	*O. polymorpha*	+	−	−	−	−	−	v	+	−	v	−	−	v	−	+	v	v	v	−	v	v	v	v	v	v	v	+	+	+	+	+	+	v	+	+
935	*O. populialbae*	−	−	−	−	−	−	−	+	−	−	−	−	−	−	−	−	−	−	−	v	+	v	+	v	−	−	v	+	+	v	−	v	−	+	+
936	*O. ramenticola*	+	+	−	−	−	−	+	+	−	−	−	−	+	−	+	−	−	−	−	−	v	−	+	+	+	+	+	+	+	+	−	+	−	+	+
937	*O. salicorniae*	+	−	−	−	−	−	−	+	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	+	+	+	+	−	+	+	+	+	−	+	+
938	*O. siamensis*	+	−	−	−	−	−	−	+	−	+	−	−	+	−	+	+	−	−	+	+	+	+	−	+	−	−	+	+	+	+	+	+	+	+	+
939	*O. thermomethanolica*	+	−	−	−	−	−	n	+	−	+	−	−	−	−	+	+	+	+	−	+	+	+	+	+	−	+	+	+	+	+	+	+	−	+	+
940	*O. trehaloabstinens*	−	−	−	−	−	−	−	+	−	−	−	−	−	−	−	−	−	−	−	+	+	+	+	+	−	+	+	+	+	+	+	+	−	+	+
941	*O. trehalophila*	+	−	−	−	−	−	v	+	−	−	−	−	−	−	+	−	−	−	−	−	−	+	−	+	+	v	+	+	+	+	+	+	−	+	+
942	*O. wickerhamii*	−	−	−	−	−	−	−	+	−	−	−	−	−	−	+	−	−	−	−	−	−	+	+	+	v	+	+	+	+	+	+	+	−	+	+
943	*O. zsoltii*	+	−	−	−	−	−	−	+	−	−	−	−	−	−	+	−	−	−	−	+	+	−	+	+	v	−	+	+	+	+	+	+	−	+	+
944	***Pachysolen***																																			
945	*P. tannophilus*	+	−	−	−	−	−	−	+	−	−	−	−	+	−	−	−	−	−	−	+	+	−	−	+	+	−	v	−	+	+	−	+	−	+	+
946	***Papiliotrema***																																			
947	*P. bandonii*	−	−	−	−	−	−	−	+	−	+	+	+	+	+	+	+	+	+	+	+	+	−	+	+	+	+	+	−	+	−	−	+	+	+	+
948	***Peterozyma***																																			
949	*P. toletana*	+	−	−	−	−	−	−	+	−	+	−	−	−	−	+	+	v	v	−	+	+	−	v	+	−	−	−	−	+	+	−	−	−	+	+
950	*P. xylosa*	v	−	−	−	−	−	−	+	−	+	−	−	−	−	v	+	v	v	−	+	+	−	+	+	−	−	−	−	+	+	−	−	−	+	+
951	***Phaffomyces***																																			
952	*P. antillensis*	−	−	−	−	−	−	−	+	−	−	−	−	−	−	−	−	−	−	−	−	v	−	+	−	−	−	−	−	+	+	−	−	−	v	−
953	*P. opuntiae*	−	−	−	−	−	−	−	+	−	−	−	−	−	−	−	−	−	−	−	v	+	−	+	−	−	−	−	−	+	+	−	−	−	+	−
954	*P. thermotolerans*	−	−	−	−	−	−	−	+	−	−	−	−	−	−	−	−	−	−	−	+	+	−	v	−	−	−	−	−	+	+	−	−	−	+	v
955	***Pichia***																																			
956	*P. barkeri*	+	−	−	−	−	−	−	+	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	v	−	−	−	−	+	+	−	−	−	−	−
957	*P. cactophila*	v	−	−	−	−	−	−	+	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	+	−	−	−	−	+	+	−	−	−	−	−
958	*P. cecembensis*	+	−	−	−	−	−	n	+	n	−	−	n	−	−	−	−	−	n	n	−	−	−	−	−	−	+	n	n	n	+	−	+	+	−	−
959	*P. cephalocereana*	+	−	−	−	−	−	−	+	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	v	−	−	−	−	+	+	−	−	−	−	−
960	*P. deserticola*	−	−	−	−	−	−	−	+	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	+	+	−	−	−	−	−
961	*P. eremophila*	v	−	−	−	−	−	−	+	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	v	−	−	−	−	+	+	−	−	−	−	−
962	*P. exigua*	+	−	−	−	−	−	−	+	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	+	−	−	−	−	−	−
963	*P. fermentans*	+	−	−	−	−	−	−	+	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	+	−	−	−	−	+	+	−	−	−	−	−
964	*P. heedii*	−	−	−	−	−	−	−	+	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	+	−	−	−	−	+	+	−	−	−	−	−
965	*P. kluyveri*	+	−	−	−	−	−	−	+	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	v	−	−	−	−	+	+	−	−	−	−	−
966	*P. kudriavzevii*	+	−	−	−	−	−	−	+	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	+	+	−	−	−	−	−
967	*P. manshurica*	v	−	−	−	−	−	−	+	−	−	−	−	−	−	−	−	−	−	−	−	−	v	−	−	−	−	−	−	+	v	−	−	−	−	−
968	*P. membranifaciens*	v	−	−	−	−	−	−	+	−	−	−	−	−	−	−	−	−	−	−	−	−	v	−	v	−	−	−	−	+	v	−	−	−	−	−
969	*P. nakasei*	+	−	−	−	−	−	−	+	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	+	+	−	−	−	−	−
970	*P. norvegensis*	+	−	−	−	−	−	−	+	−	−	−	−	−	−	−	−	−	−	−	+	+	−	−	−	−	−	−	−	+	+	−	−	−	−	−
971	*P. occidentalis*	+	−	−	−	−	−	−	+	−	−	−	−	−	−	−	−	−	−	−	−	−	v	−	−	−	−	−	−	+	+	−	−	−	−	−
972	*P. pseudocactophila*	−	−	−	−	−	−	−	+	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	+	+	−	−	−	−	−
973	*P. scutulata*	+	−	−	−	−	−	−	+	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	+	+	−	−	−	−	−
974	*P. sporocuriosa*	v	−	−	−	−	−	−	+	−	−	−	−	−	−	−	−	−	−	−	−	−	+	−	+	−	−	−	−	+	+	−	−	−	−	−
975	*P. terricola*	+	−	−	−	−	−	−	+	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	+	+	−	−	−	−	−

Symbols: +, positive or weak; −, negative; v, variable (+/−, w/−); n, no data.

	Growth reactions and other characteristics																																							
	myo-Inositol	DL-Lactate	Succinate	Citrate	D-Gluconate	D-Glucosamine	*N*-Acetyl-D-glucosamine	Hexadecane	Nitrate	Nitrite	Vitamin-free	2-Keto-D-gluconate	5-Keto-D-gluconate	Saccharate	Xylitol	L-Arabinitol	Arbutin	Propane 1,2 diol	Butane 2,3 diol	Cadaverine	Creatinine	L-Lysine	Ethylamine	50% Glucose	10% NaCl/5% glucose	Starch formation	Urease	Gelatin liquefaction	Cycloheximide 0.01%	Cycloheximide 0.1%	Growth at 19°C	Growth at 25°C	Growth at 30°C	Growth at 35°C	Growth at 37°C	Growth at 40°C	Growth at 45°C	CoQ (Main component)	Mol% G + C (Ave.)	DBB
Ogataea (*cont'd*)																																								
922	−	v	+	−	v	−	−	−	−	n	−	−	−	−	n	n	n	n	n	n	n	n	n	n	−	−	n	v	n	n	+	+	+	n	−	−	−	7/8	36.7	−
923	−	+	−	+	+	+	+	−	+	n	−	−	−	−	n	n	n	n	n	n	n	n	n	n	−	−	n	−	n	n	+	+	+	+	+	n	n	7	35.8	−
924	−	−	v	v	v	−	−	−	v	n	−	−	−	−	n	n	n	n	n	n	n	n	n	n	v	−	n	v	n	n	+	+	+	n	−	−	−	7	47.4	−
925	−	+	+	−	−	+	+	−	−	n	−	−	−	−	n	n	n	n	n	n	n	n	n	n	+	−	n	+	n	n	+	+	+	+	+	n	n	7	46.1	−
926	−	n	+	+	−	n	−	n	+	n	−	−	−	n	n	n	n	n	n	n	n	n	n	n	+	n	n	+	+	+	+	+	+	+	+	+	−	7	n	−
927	−	−	v	+	v	−	−	−	−	n	v	+	−	−	n	n	n	n	n	n	n	n	n	n	v	−	n	+	n	n	+	+	+	+	+	+	−	7	43.3	−
928	−	−	+	−	−	−	−	−	−	n	−	−	n	−	n	n	n	n	n	n	n	n	n	n	−	−	n	n	+	+	+	+	+	−	−	−	−	n	n	−
929	−	−	v	v	−	−	−	−	+	n	−	−	−	−	n	n	n	n	n	n	n	n	n	n	−	−	n	v	n	−	+	+	+	+	+	n	n	7	45.2	−
930	−	−	−	+	+	−	−	−	−	n	−	−	−	n	n	n	n	n	n	n	n	n	n	n	−	−	n	−	+	+	+	+	+	+	−	−	−	7	41.6	−
931	−	−	+	+	−	−	−	−	+	n	−	−	−	−	n	n	n	n	n	n	n	n	n	n	+	−	n	−	n	n	+	+	+	+	+	n	n	7	46.9	−
932	−	−	+	−	−	−	−	−	−	n	v	−	n	n	n	n	n	n	n	n	n	n	n	n	−	−	n	n	+	+	+	+	+	n	−	−	−	7	n	−
933	−	−	v	v	v	−	−	−	−	v	v	v	−	−	n	n	n	n	n	n	n	n	n	n	v	−	n	v	n	n	+	+	+	n	v	n	n	7	43.7	−
934	−	−	v	v	v	−	−	−	+	n	−	−	−	−	n	n	n	n	n	n	n	n	n	n	+	−	n	v	n	n	+	+	+	+	+	+	+	n	48.0	−
935	−	v	+	+	v	−	−	−	−	n	−	−	n	−	n	n	n	n	n	n	n	n	n	n	−	−	n	n	+	+	+	+	+	+	+	−	−	n	n	−
936	−	v	v	−	v	+	+	−	+	n	v	−	−	−	n	n	n	n	n	n	n	n	n	n	−	−	n	−	+	+	+	+	+	+	+	n	n	n	n	−
937	−	−	−	−	−	−	+	n	−	n	−	−	−	−	n	n	n	n	n	n	n	n	n	n	−	−	n	−	n	n	+	+	+	n	−	−	−	n	36.7	−
938	−	−	+	+	−	n	−	n	+	n	−	−	−	n	n	n	n	n	n	n	n	n	n	n	+	−	n	+	+	+	+	+	+	+	+	+	+	7	n	−
939	−	−	+	+	+	n	−	n	+	n	−	−	−	−	n	n	n	n	n	n	n	n	n	n	+	−	n	+	+	+	+	+	+	+	+	n	−	7	n	−
940	−	+	+	−	+	−	−	−	+	n	+	−	n	n	n	n	n	n	n	n	n	n	n	n	−	−	n	n	+	+	+	+	+	+	+	−	−	7	n	−
941	−	−	+	−	−	−	−	−	−	n	−	−	−	−	n	n	n	n	n	n	n	n	n	n	v	−	n	−	n	n	+	+	+	n	−	−	−	7	37.6	−
942	−	−	v	−	v	−	−	−	+	n	−	−	−	−	n	n	n	n	n	n	n	n	n	n	−	−	n	v	n	n	+	+	+	n	−	−	−	7	45.4	−
943	−	−	+	+	−	−	−	−	−	n	v	−	n	n	n	n	n	n	n	n	n	n	n	n	+	−	n	n	+	+	+	+	+	+	+	+	+	n	n	−
Pachysolen																																								
945	−	−	+	−	−	−	−	−	+	n	−	−	−	−	n	n	n	n	n	n	n	n	n	n	+	−	n	−	n	n	+	+	+	+	+	n	n	8	37.8	−
Papiliotrema																																								
947	+	−	+	+	+	+	n	n	−	−	−	n	n	+	+	n	n	n	n	−	−	−	+	n	n	+	n	n	+	−	+	+	+	−	−	−	−	n	n	+
Peterozyma																																								
949	−	+	+	+	v	−	+	−	−	n	−	−	−	−	n	n	n	n	n	n	n	n	n	n	−	−	n	−	n	n	+	+	+	n	−	−	−	7	39.5	−
950	−	+	+	v	v	v	+	−	−	n	−	−	−	−	n	n	n	n	n	n	n	n	n	n	−	−	n	−	n	n	+	+	+	n	−	−	−	7	40.1	−
Phaffomyces																																								
952	−	+	+	+	−	−	−	−	−	n	−	−	−	−	n	n	n	n	n	n	n	n	n	n	−	−	n	−	n	n	+	+	+	n	v	n	n	7	33.6	−
953	−	+	+	+	−	−	−	−	−	n	−	−	−	−	n	n	n	n	n	n	n	n	n	n	−	−	n	−	n	n	+	+	+	n	−	−	−	7	33.2	−
954	−	+	+	−	−	−	−	−	−	n	−	−	−	−	n	n	n	n	n	n	n	n	n	n	−	−	n	−	n	n	+	+	+	+	+	n	n	n	32.9	−
Pichia																																								
956	−	+	+	−	−	+	+	−	−	n	−	−	−	−	n	n	n	n	n	n	n	n	n	n	+	−	n	−	n	n	+	+	+	+	+	n	n	7	36.2	−
957	−	+	+	v	−	+	−	−	−	n	−	−	−	−	n	n	n	n	n	n	n	n	n	n	−	−	n	−	n	n	+	+	+	+	+	n	n	7	36.3	−
958	n	−	+	+	n	n	n	n	−	n	+	n	n	n	n	n	n	n	n	n	n	n	n	n	n	n	n	n	n	n	+	+	+	+	+	+	n	7	42.5	−
959	−	+	+	+	−	+	+	−	−	n	−	−	−	−	n	n	n	n	n	n	n	n	n	n	+	−	n	v	n	n	+	+	+	n	v	n	n	n	30.2	−
960	−	+	+	−	−	−	−	−	−	n	−	−	−	−	n	n	n	n	n	n	n	n	n	n	−	−	n	−	n	n	+	+	+	+	+	n	n	n	27.9	−
961	−	+	+	+	−	+	+	−	−	n	−	−	−	−	n	n	n	n	n	n	n	n	n	n	+	−	n	v	n	n	+	+	+	n	v	n	n	n	30.3	−
962	−	+	+	−	−	−	+	−	−	n	+	−	−	−	n	n	n	n	n	n	n	n	n	n	−	−	n	−	n	n	+	+	+	n	−	−	−	7	32.5	−
963	−	+	+	+	−	+	+	−	−	n	−	−	−	−	n	n	n	n	n	n	n	n	n	n	v	−	n	−	n	n	+	+	+	+	+	n	n	7	43.1	−
964	−	v	+	v	−	−	−	−	−	n	−	−	−	−	n	n	n	n	n	n	n	n	n	n	−	−	n	−	n	n	+	+	+	+	+	n	n	7	32.5	−
965	−	+	+	v	−	+	+	−	−	n	−	−	−	−	n	n	n	n	n	n	n	n	n	n	+	−	n	v	n	n	+	+	+	n	v	n	n	7	30.4	−
966	−	+	+	+	−	+	+	−	−	n	+	−	−	−	n	n	n	n	n	n	n	n	n	n	+	−	n	v	n	n	+	+	+	+	+	+	n	7	40.0	−
967	−	v	+	v	−	+	+	−	−	n	v	−	−	−	n	n	n	n	n	n	n	n	n	n	+	−	n	−	n	n	+	+	+	+	+	n	n	7	35.6	−
968	−	v	v	v	−	v	+	−	−	n	v	−	−	−	n	n	n	n	n	n	n	n	n	n	+	−	n	v	n	n	+	+	+	n	−	−	−	7	42.7	−
969	−	−	+	−	v	−	−	−	−	n	−	−	−	−	n	n	n	n	n	n	n	n	n	n	+	−	n	v	n	n	+	+	+	n	−	−	−	n	33.1	−
970	−	+	+	+	−	+	−	−	−	n	−	−	−	−	n	n	n	n	n	n	n	n	n	n	+	−	n	−	n	n	+	+	+	+	+	n	n	7	37.5	−
971	−	+	+	−	−	+	+	−	−	n	+	−	−	−	n	n	n	n	n	n	n	n	n	n	+	−	n	−	n	n	+	+	+	+	+	−	−	7	41.0	−
972	−	+	+	v	−	+	−	−	−	n	−	−	−	−	n	n	n	n	n	n	n	n	n	n	−	−	n	v	n	n	+	+	+	+	+	n	n	n	36.6	−
973	−	+	+	−	−	−	−	−	−	n	+	−	−	−	n	n	n	n	n	n	n	n	n	n	+	−	n	−	n	n	+	+	+	n	−	−	−	7	32.8	−
974	−	−	v	v	−	+	−	−	−	n	−	−	−	−	n	n	n	n	n	n	n	n	n	n	−	−	n	−	n	n	+	+	+	+	−	−	−	7	31.3	−
975	−	−	+	v	−	−	−	−	−	n	−	−	−	−	n	n	n	n	n	n	n	n	n	n	v	−	n	−	n	n	+	+	+	n	v	−	−	7	38.1	−

Symbols: +, positive or weak; −, negative; v, variable (+/−, w/−); n, no data.

Ln. no.	Species	Fermentation: Glucose	Fermentation: Galactose	Fermentation: Sucrose	Fermentation: Maltose	Fermentation: Lactose	Fermentation: Raffinose	Fermentation: Trehalose	Growth: Glucose	Inulin	Sucrose	Raffinose	Melibiose	Galactose	Lactose	Trehalose	Maltose	Melezitose	Methyl-α-D-glucoside	Soluble Starch	Cellobiose	Salicin	L-Sorbose	L-Rhamnose	D-Xylose	L-Arabinose	D-Arabinose	D-Ribose	Methanol	Ethanol	Glycerol	Erythritol	Ribitol	Galactitol	D-Mannitol	D-Glucitol
976	***Priceomyces***																																			
977	*P. carsonii*	−	−	−	−	−	−	−	+	−	+	v	v	+	−	+	+	+	+	+	v	+	+	−	+	v	−	v	−	+	+	−	+	v	+	+
978	*P. castillae*	−	−	−	−	−	−	−	+	−	−	+	+	+	−	+	+	−	−	−	+	+	+	−	+	+	+	+	−	+	+	+	+	+	+	+
979	*P. haplophilus*	−	−	−	−	−	−	−	+	−	−	−	−	+	−	−	−	−	−	−	−	−	v	−	+	+	v	+	−	+	+	+	+	+	+	+
980	*P. medius*	−	−	−	−	−	−	−	+	−	−	−	−	+	−	+	+	−	−	v	+	v	+	−	+	+	+	+	−	+	+	+	+	v	+	+
981	*P. melissophilus*	−	−	−	−	−	−	−	+	+	+	−	−	+	−	−	+	+	+	v	v	v	v	−	−	−	−	−	−	+	+	+	+	−	+	+
982	***Protomyces***																																			
983	*P. gravidus*	−	−	−	−	−	−	−	+	+	+	+	−	−	−	+	+	+	−	−	+	+	−	−	+	−	+	−	−	−	+	−	−	−	+	+
984	*P. inouyei*	−	−	−	−	−	−	−	+	+	+	+	−	v	−	+	+	+	+	+	+	+	−	−	+	+	+	−	−	−	+	−	+	v	+	+
985	*P. inundatus*	−	−	−	−	−	−	−	+	+	+	+	−	−	−	+	+	+	v	+	−	−	−	−	+	−	+	−	−	−	+	−	+	−	+	+
986	*P. lactucaedebilis*	−	−	−	−	−	−	−	+	+	+	+	−	+	−	+	+	+	+	+	+	−	+	−	+	+	+	+	−	+	+	−	+	+	+	+
987	*P. macrosporus*	−	−	−	−	−	−	−	+	+	+	+	−	−	−	+	+	+	−	+	−	−	−	−	+	−	−	−	−	−	+	−	−	−	+	−
988	*P. pachydermus*	−	−	−	−	−	−	−	+	+	+	+	−	−	−	+	+	+	v	v	v	−	v	−	v	−	v	−	−	−	+	−	v	v	+	+
989	***Prototheca***																																			
990	*P. stagnora*	−	−	−	−	−	−	−	+	n	−	−	−	+	v	−	+	−	n	−	n	n	n	−	−	−	n	n	n	n	v	n	n	n	−	n
991	*P. ulmea*	−	−	−	−	−	−	−	+	n	−	−	−	−	−	−	−	−	n	−	n	n	n	−	−	−	n	n	n	n	v	n	n	n	−	n
992	*P. wickerhamii*	−	−	−	−	−	−	−	+	−	−	−	−	+	v	+	−	−	−	−	−	−	−	−	−	−	−	−	−	+	+	−	n	n	−	n
993	*P. zopfii* var. *zopfii*	−	−	−	−	−	−	−	+	−	−	v	−	−	v	−	+	−	−	−	−	−	−	−	−	−	−	−	−	+	v	−	n	n	−	n
994	*P. zopfii* var. 1	−	−	−	−	−	−	−	+	n	−	−	−	−	−	−	+	−	n	−	n	n	n	−	−	−	n	n	n	n	−	n	n	n	−	−
995	*P. zopfii* var. 2	−	−	−	−	−	−	−	+	−	−	v	−	−	v	−	+	−	−	−	−	−	−	−	−	−	−	−	−	+	v	−	n	n	−	n
996	*P. zopfii* var. 3	−	−	−	−	−	−	−	+	−	−	v	−	−	v	−	+	−	−	−	−	−	−	−	−	−	−	−	−	+	v	−	n	n	−	n
997	*P. zopfii* var. *portoricensis*	−	−	−	−	−	−	−	+	−	−	v	−	−	v	−	+	−	−	−	−	−	−	−	−	−	−	−	−	+	v	−	n	n	−	n
998	***Pseudozyma***																																			
999	*P. antarctica*	−	−	−	−	−	−	−	+	−	+	+	−	+	+	+	+	+	+	+	+	+	+	v	+	+	+	+	−	+	+	+	+	−	+	+
1000	*P. aphidis*	−	−	−	−	−	−	−	+	−	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	−	−	+	+	+	−	+	+
1001	*P. flocculosa*	−	−	−	−	−	−	−	+	−	+	+	+	+	−	+	+	+	+	+	+	+	+	−	+	+	+	+	+	−	−	+	+	−	+	+
1002	*P. fusiformata*	−	−	−	−	−	−	−	+	−	+	+	v	−	−	+	+	+	+	−	+	v	+	−	+	+	+	+	−	+	+	+	+	−	+	+
1003	*P. parantarctica*	−	−	−	−	−	−	−	+	−	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	−	+	+	+	+	−	+	+
1004	*P. prolifica*	−	−	−	−	−	−	−	+	−	+	+	−	−	+	+	+	+	+	+	+	−	+	+	+	+	+	+	−	+	+	+	+	−	+	+
1005	*P. rugulosa*	−	−	−	−	−	−	−	+	−	+	+	+	+	−	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	−	+	+
1006	*P. thailandica*	−	−	−	−	−	−	−	+	−	+	+	+	+	−	+	+	+	+	+	+	+	+	−	+	+	+	+	−	+	+	+	+	−	+	+
1007	*P. tsukubaensis*	−	−	−	−	−	−	−	+	−	+	+	−	+	+	+	+	+	+	+	+	−	+	−	+	+	+	+	−	+	+	+	−	−	−	−
1008	***Reniforma***																																			
1009	*R. strues*	−	−	−	−	−	−	−	+	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	+	−
1010	***Rhodosporidium***																																			
1011	*R. azoricum*	−	−	−	−	−	−	−	+	−	+	+	−	+	−	+	+	−	−	−	+	+	+	−	+	+	+	+	−	+	+	−	+	+	+	+
1012	*R. babjevae*	−	−	−	−	−	−	−	+	v	+	+	−	+	−	+	+	+	+	−	+	+	+	+	+	−	+	+	−	+	+	−	+	−	+	+
1013	*R. diobovatum*	−	−	−	−	−	−	−	+	+	+	+	−	+	−	+	+	+	+	−	+	+	+	v	+	v	+	+	−	+	+	−	+	−	+	+
1014	*R. fluviale*	−	−	−	−	−	−	−	+	−	+	+	−	+	−	+	+	+	+	−	+	+	+	−	+	+	+	+	−	+	+	−	+	+	+	+
1015	*R. kratochvilovae*	−	−	−	−	−	−	−	+	−	+	+	−	+	−	+	+	+	+	−	+	+	+	−	+	+	+	+	−	+	+	−	+	−	+	+
1016	*R. lusitaniae*	−	−	−	−	−	−	−	+	−	−	−	−	+	−	+	−	−	−	−	v	+	+	−	+	−	−	−	−	+	+	−	+	+	+	+
1017	*R. paludigenum*	−	−	−	−	−	−	−	+	−	+	+	−	+	−	+	+	−	v	−	+	+	+	v	+	+	+	+	−	+	+	−	+	+	+	+
1018	*R. sphaerocarpum*	−	−	−	−	−	−	−	+	−	+	+	−	+	−	+	+	+	+	−	+	+	+	−	+	+	+	+	−	+	+	−	+	+	v	v
1019	*R. toruloides*	−	−	−	−	−	−	−	+	−	+	+	−	+	−	+	+	+	+	−	+	+	−	−	+	+	+	+	−	+	+	−	+	−	+	+
1020	***Rhodotorula***																																			
1021	*R. acheniorum*	−	−	−	−	−	−	−	+	−	+	+	+	v	+	+	+	+	+	−	+	−	v	−	+	+	v	+	−	−	v	+	+	v	+	+
1022	*R. araucariae*	−	−	−	−	−	−	−	+	−	v	v	−	v	−	+	−	−	−	−	−	−	v	−	v	−	v	−	−	+	+	−	v	−	+	+
1023	*R. armeniaca*	−	−	−	−	−	−	−	+	−	−	−	−	+	−	−	−	−	−	−	−	−	+	+	+	+	+	+	−	−	+	−	+	+	+	+
1024	*R. aurantiaca*	−	−	−	−	−	−	−	+	−	+	−	−	v	−	v	+	+	−	−	+	−	v	−	+	+	+	−	−	+	+	−	+	−	+	+
1025	*R. auriculariae*	−	−	−	−	−	−	−	+	−	+	−	−	−	−	+	+	+	−	−	−	−	−	−	−	−	−	−	−	+	+	−	−	−	+	+
1026	*R. bacarum*	−	−	−	−	−	−	−	+	−	+	+	−	−	−	+	+	+	+	+	+	v	v	−	+	+	v	+	−	+	+	+	v	−	+	+
1027	*R. benthica*	−	−	−	−	−	−	−	+	+	+	+	+	+	+	+	+	+	+	+	+	−	+	+	+	+	+	+	−	+	+	+	+	+	−	−
1028	*R. bogoriensis*	−	−	−	−	−	−	−	+	v	−	−	−	+	−	+	+	+	−	+	+	+	+	−	+	+	+	+	−	+	+	−	+	v	+	+
1029	*R. buffonii*	−	−	−	−	−	−	−	+	−	−	−	−	−	−	v	+	+	−	+	+	v	v	−	v	v	+	−	−	+	+	−	+	−	+	+
1030	*R. calyptogenae*	−	−	−	−	−	−	−	+	+	−	+	+	+	+	+	+	+	+	+	+	+	−	+	+	+	+	+	−	+	+	+	+	+	−	−

Symbols: +, positive or weak; −, negative; v, variable (+/−, w/−); n, no data.

Growth reactions and other characteristics

	myo-Inositol	DL-Lactate	Succinate	Citrate	D-Gluconate	D-Glucosamine	*N*-Acetyl-D-glucosamine	Hexadecane	Nitrate	Nitrite	Vitamin-free	2-Keto-D-gluconate	5-Keto-D-gluconate	Saccharate	Xylitol	L-Arabinitol	Arbutin	Propane 1,2 diol	Butane 2,3 diol	Cadaverine	Creatinine	L-Lysine	Ethylamine	50% Glucose	10% NaCl/5% glucose	Starch formation	Urease	Gelatin liquefaction	Cycloheximide 0.01%	Cycloheximide 0.1%	Growth at 19°C	Growth at 25°C	Growth at 30°C	Growth at 35°C	Growth at 37°C	Growth at 40°C	Growth at 45°C	CoQ (Main component)	Mol% G + C (Ave.)	DBB
Priceomyces																																								
977	−	v	+	+	−	−	+	+	−	n	−	+	−	−	n	n	n	n	n	n	n	n	n	n	+	−	n	v	n	n	+	+	+	n	v	n	n	9	38.5	−
978	−	−	+	+	+	−	+	+	−	n	−	−	−	−	n	n	n	n	n	n	n	n	n	n	+	−	n	−	n	n	+	+	+	+	+	n	n	9	39.5	−
979	−	−	−	−	v	−	+	+	−	n	−	+	−	−	n	n	n	n	n	n	n	n	n	n	+	−	n	v	n	n	+	+	+	n	−	−	−	9	40.0	−
980	−	−	+	+	+	v	+	+	−	n	−	−	−	−	n	n	n	n	n	n	n	n	n	n	+	−	n	−	n	n	+	+	+	n	−	−	−	9	36.1	−
981	−	−	−	+	+	−	v	+	−	n	−	v	−	−	n	n	n	n	n	n	n	n	n	n	+	−	n	n	n	n	+	+	+	n	−	−	−	9	39.8	−
Protomyces																																								
983	−	+	+	+	−	−	−	−	+	n	−	−	−	−	n	n	n	n	n	n	n	n	n	n	−	+	n	−	−	−	+	+	n	n	−	−	−	n	n	−
984	−	+	+	v	−	−	−	v	v	n	−	−	−	−	n	n	n	n	n	n	n	n	n	n	−	+	n	−	n	n	+	+	n	n	−	−	−	10	52.0	−
985	−	v	+	+	−	−	−	−	+	n	−	−	−	−	n	n	n	n	n	n	n	n	n	n	−	v	n	v	−	n	+	−	−	−	−	−	−	n	n	−
986	−	+	+	+	−	−	+	−	+	n	−	−	−	−	n	n	n	n	n	n	n	n	n	n	−	n	v	+	−	n	+	+	n	n	−	−	−	10	52.0	−
987	−	−	+	+	−	−	−	−	+	n	−	−	−	−	n	n	n	n	n	n	n	n	n	n	−	+	n	−	−	n	+	n	n	n	−	−	−	n	n	−
988	−	v	v	+	−	−	−	−	v	n	−	−	−	−	n	n	n	n	n	n	n	n	n	n	−	+	n	+	−	n	+	−	−	−	−	−	−	10	52.4	−
Prototheca																																								
990	−	n	+	n	n	n	n	−	−	n	−	n	n	n	n	n	n	n	n	n	n	n	n	n	n	n	n	n	n	n	+	+	n	n	−	−	−	n	65.8	n
991	−	n	n	n	n	n	n	−	−	n	−	n	n	n	n	n	n	n	n	n	n	n	n	n	n	n	n	n	n	n	+	+	n	n	−	−	−	n	75.9	n
992	−	+	n	n	−	n	−	−	−	n	−	n	n	n	n	n	n	n	n	n	n	n	n	n	n	n	n	n	n	n	+	+	+	v	v	n	n	n	60.5	n
993	−	+	−	−	−	n	−	v	−	n	−	n	n	n	n	n	n	n	n	n	n	n	n	n	n	n	n	n	n	n	+	+	+	v	v	n	n	n	69.5	n
994	−	n	n	n	n	n	n	n	−	n	−	n	n	n	n	n	n	n	n	n	n	n	n	n	n	n	n	n	n	n	+	+	+	+	+	n	n	n	n	n
995	−	+	−	−	−	n	−	v	−	n	−	n	n	n	n	n	n	n	n	n	n	n	n	n	n	n	n	n	n	n	+	+	n	n	−	−	−	n	n	n
996	−	+	−	−	−	n	−	v	−	n	−	n	n	n	n	n	n	n	n	n	n	n	n	n	n	n	n	n	n	n	+	+	n	n	v	n	n	n	n	n
997	−	+	−	−	−	n	−	v	−	n	−	n	n	n	n	n	n	n	n	n	n	n	n	n	n	n	n	n	n	n	+	+	n	n	n	n	n	n	n	n
Pseudozyma																																								
999	+	+	+	+	+	+	n	n	+	+	−	+	n	−	n	n	n	n	n	n	n	n	n	−	n	−	+	n	n	n	+	+	+	n	v	n	n	10	61.4	+
1000	+	+	+	+	+	+	n	n	+	+	−	+	n	+	n	n	n	n	n	n	n	n	n	−	n	−	+	n	n	n	+	+	+	+	+	n	n	10	61.5	+
1001	+	+	+	+	+	+	n	n	+	+	+	+	n	−	n	n	n	n	n	n	n	n	n	−	n	−	+	n	n	n	+	+	+	n	−	−	−	n	n	+
1002	+	+	+	+	+	v	n	n	+	+	+	+	n	−	n	n	n	n	n	n	n	n	n	−	n	−	+	n	n	n	+	+	+	n	−	−	−	n	58.1	+
1003	+	+	+	+	+	+	n	n	+	+	−	+	+	n	n	n	n	n	n	n	n	n	n	−	n	−	+	n	n	n	+	+	+	+	+	n	n	10	n	+
1004	+	+	+	−	+	+	n	n	+	+	+	+	n	−	n	n	n	n	n	n	n	n	n	−	n	−	+	n	n	n	+	+	+	n	−	−	−	n	n	+
1005	+	+	+	+	+	+	n	n	+	+	+	+	n	+	n	n	n	n	n	n	n	n	n	−	n	−	+	n	n	n	+	+	+	+	+	n	n	n	n	+
1006	+	+	+	+	+	+	n	n	+	+	−	+	n	n	n	n	n	n	n	n	n	n	n	−	n	−	+	n	n	n	+	+	+	+	+	n	n	10	n	+
1007	+	+	+	+	−	+	n	n	+	+	+	+	n	−	n	n	n	n	n	n	n	n	n	−	n	−	+	n	n	n	+	+	+	n	−	−	−	n	53.3	+
Reniforma																																								
1009	−	−	−	+	−	−	−	+	−	−	+	n	n	n	n	n	n	n	n	n	−	n	n	n	n	−	+	n	n	n	+	+	+	+	−	−	−	7	n	+
Rhodosporidium																																								
1011	−	−	+	+	+	−	n	n	+	+	−	n	n	+	+	n	n	n	n	n	n	n	n	n	n	−	+	n	+	+	+	+	+	−	−	−	−	10	61.1	+
1012	−	+	+	+	+	−	n	n	+	+	+	+	−	+	+	n	n	n	n	n	n	n	n	n	n	−	+	n	+	+	+	+	+	−	−	−	−	10	66.2	+
1013	−	−	+	+	+	−	n	n	+	+	+	n	n	v	+	n	n	n	n	n	n	n	n	n	n	−	+	n	+	+	+	+	+	v	−	−	−	10	66.1	+
1014	−	+	+	+	+	−	n	n	+	+	+	−	n	−	+	n	n	n	n	n	n	n	n	n	n	−	+	n	+	−	+	+	+	+	+	−	−	n	61.4	+
1015	−	v	+	+	+	−	n	n	+	+	+	n	n	−	−	n	n	n	n	n	n	n	n	n	n	−	+	n	−	−	+	+	+	−	−	−	−	10	67.8	+
1016	−	−	+	+	+	v	n	n	+	+	+	n	n	v	+	n	n	n	n	n	n	n	n	n	n	−	+	n	−	−	+	+	+	−	−	−	−	9	62.0	+
1017	−	−	+	+	+	−	n	n	+	+	+	n	n	+	+	n	n	n	n	n	n	n	n	n	n	−	+	n	+	+	+	+	+	−	−	−	−	10	63.9	+
1018	−	+	+	+	+	−	n	n	+	+	−	n	n	−	+	n	n	n	n	n	n	n	n	n	n	−	+	n	−	−	+	+	+	−	−	−	−	10	63.8	+
1019	−	v	+	+	+	−	n	n	+	+	+	n	n	−	+	n	n	n	n	n	n	n	n	n	n	−	+	n	+	−	+	+	+	+	+	−	−	9	60.2	+
Rhodotorula																																								
1021	−	+	+	+	−	+	n	n	+	+	−	n	n	−	+	n	n	n	n	n	n	n	n	n	n	−	n	n	−	−	+	+	−	−	−	−	−	10	53.9	+
1022	−	v	+	v	+	−	n	n	+	+	+	n	n	−	−	n	n	n	n	n	n	n	n	n	n	−	n	n	−	−	+	+	+	v	−	−	−	10	64.6	+
1023	−	+	+	−	−	−	n	n	−	−	−	n	n	−	+	n	n	n	n	n	n	n	n	n	n	−	n	n	−	−	+	+	−	−	−	−	−	n	n	+
1024	−	v	+	+	+	−	n	n	v	+	−	n	n	−	+	n	n	n	n	n	n	n	n	n	n	−	n	n	−	−	+	+	−	−	−	−	−	10	55.4	+
1025	−	−	+	−	+	−	n	n	−	−	−	n	n	−	−	n	n	n	n	n	n	n	n	n	n	−	n	n	+	−	+	+	−	−	−	−	−	n	54.4	+
1026	v	−	+	+	−	−	n	n	v	+	v	n	n	−	+	n	n	n	n	n	n	n	n	n	n	−	n	n	−	−	+	+	−	−	−	−	−	n	52.4	+
1027	+	−	+	−	+	−	n	n	−	−	−	n	n	+	+	n	n	n	n	n	n	n	n	n	n	−	n	n	+	−	+	+	+	+	+	−	−	10	47.2	+
1028	−	v	+	+	+	+	n	n	−	−	−	n	n	+	+	n	n	n	n	n	n	n	n	n	+	−	n	n	+	−	+	+	−	−	−	−	−	10	57.3	+
1029	−	−	+	+	+	−	n	n	+	+	−	n	n	n	+	n	n	n	n	n	n	n	n	n	n	−	n	n	+	−	+	v	−	−	−	−	−	n	50.8	+
1030	+	−	+	−	−	−	n	n	−	−	−	n	n	+	+	n	n	n	n	n	n	n	n	n	n	−	n	n	+	+	+	+	+	+	+	−	−	9	48.0	+

Symbols: +, positive or weak; −, negative; v, variable (+/−, w/−); n, no data.

Ln. no.	Species	Fermentation: Glucose	Galactose	Sucrose	Maltose	Lactose	Raffinose	Trehalose	Growth reactions and other characteristics: Glucose	Inulin	Sucrose	Raffinose	Melibiose	Galactose	Lactose	Trehalose	Maltose	Melezitose	Methyl-α-D-glucoside	Soluble Starch	Cellobiose	Salicin	L-Sorbose	L-Rhamnose	D-Xylose	L-Arabinose	D-Arabinose	D-Ribose	Methanol	Ethanol	Glycerol	Erythritol	Ribitol	Galactitol	D-Mannitol	D-Glucitol
	Rhodotorula *(cont'd)*																																		
1031	*R. colostri*	−	−	−	−	−	−	−	+	−	+	−	−	+	−	+	+	v	v	−	+	+	−	−	v	−	−	−	−	+	+	−	+	−	+	+
1032	*R. cresolica*	−	−	−	−	−	−	−	+	−	+	−	−	+	−	+	+	+	+	−	+	−	−	−	+	−	+	+	−	+	+	−	+	−	+	+
1033	*R. crocea*	−	−	−	−	−	−	−	+	−	+	−	−	+	−	+	+	+	−	−	+	−	+	−	+	v	v	+	−	v	+	−	+	−	+	+
1034	*R. cycloclastica*	−	−	−	−	−	−	−	+	−	−	−	−	−	−	+	−	−	−	−	−	−	−	−	v	−	−	−	−	+	v	−	+	−	+	+
1035	*R. dairenensis*	−	−	−	−	−	−	−	+	−	+	+	−	+	−	+	+	+	+	−	+	+	−	−	+	+	+	+	−	+	+	−	+	+	+	+
1036	*R. diffluens*	−	−	−	−	−	−	−	+	−	+	+	−	+	−	+	+	+	−	−	−	+	−	+	−	+	+	+	−	+	+	+	+	+	+	+
1037	*R. ferulica*	−	−	−	−	−	−	−	+	−	+	−	−	+	+	+	+	+	+	−	+	v	−	+	−	v	−	+	v	−	+	+	+	v	−	+	v
1038	*R. foliorum*	−	−	−	−	−	−	−	+	−	−	−	−	−	−	+	−	−	−	−	+	−	−	−	+	+	+	+	−	−	+	+	−	+	−	+	+
1039	*R. glutinis*	−	−	−	−	−	−	−	+	−	+	+	−	+	−	+	+	+	+	−	+	+	−	+	−	+	+	+	+	−	+	+	−	+	−	+	+
1040	*R. graminis*	−	−	−	−	−	−	−	+	−	+	+	−	+	−	+	−	−	−	−	−	+	−	+	+	+	+	+	+	−	+	+	−	+	−	+	+
1041	*R. hordea*	−	−	−	−	−	−	−	+	−	+	−	−	+	+	+	+	+	+	+	+	+	−	+	−	−	−	−	+	−	−	+	+	−	+	+	+
1042	*R. hylophila*	−	−	−	−	−	−	−	+	−	−	−	−	−	−	−	−	−	−	−	−	−	−	+	−	−	−	−	−	−	+	+	−	−	−	+	+
1043	*R. ingeniosa*	−	−	−	−	−	−	−	+	−	+	+	−	+	+	+	+	+	+	+	+	+	+	+	−	+	−	−	+	−	v	+	−	+	−	+	+
1044	*R. javanica*	−	−	−	−	−	−	−	+	−	−	+	+	+	−	+	+	−	−	+	+	+	+	+	−	+	+	+	+	−	+	+	−	+	+	+	+
1045	*R. lactosa*	−	−	−	−	−	−	−	+	−	+	+	+	+	+	+	+	+	−	+	+	+	+	−	v	+	+	+	−	−	+	+	−	+	−	+	+
1046	*R. lamellibrachii*	−	−	−	−	−	−	−	+	−	+	−	−	+	−	+	+	+	−	+	−	−	−	+	−	+	+	+	−	n	n	+	+	−	−	−	−
1047	*R. laryngis*	−	−	−	−	−	−	−	+	−	+	−	−	v	−	+	−	+	−	−	+	+	+	v	−	+	+	+	−	−	+	+	−	+	−	+	+
1048	*R. lignophila*	−	−	−	−	−	−	−	+	−	−	−	−	−	+	+	−	−	−	−	+	−	−	−	−	+	−	−	−	−	+	+	−	−	−	+	+
1049	*R. lysiniphila*	−	−	−	−	−	−	−	+	−	+	+	−	+	+	+	+	+	−	+	+	−	+	−	+	+	+	+	+	−	+	+	+	+	−	−	−
1050	*R. marina*	−	−	−	−	−	−	−	+	−	+	+	−	+	+	−	+	+	+	−	+	+	+	+	+	+	+	+	+	−	−	+	−	+	+	+	+
1051	*R. minuta*	−	−	−	−	−	−	−	+	−	+	−	−	v	+	+	−	+	−	−	+	+	+	+	−	+	+	+	+	−	+	+	−	+	−	v	v
1052	*R. mucilaginosa*	−	−	−	−	−	−	−	+	−	+	+	−	+	−	+	+	+	v	−	+	+	+	v	−	+	+	+	+	−	+	+	−	+	−	v	v
1053	*R. nothofagi*	−	−	−	−	−	−	−	+	−	−	−	−	+	−	−	−	−	−	−	+	−	+	+	−	+	+	+	+	−	+	+	−	+	+	+	+
1054	*R. oryzae*	−	−	−	−	−	−	−	+	−	+	−	−	+	−	+	−	+	−	n	+	−	+	−	−	−	−	−	−	−	−	+	−	+	−	+	+
1055	*R. pacifica*	−	−	−	−	−	−	−	+	−	+	+	−	+	−	+	+	+	+	−	+	+	+	+	+	+	+	+	+	−	+	+	−	+	+	+	+
1056	*R. pallida*	−	−	−	−	−	−	−	+	−	−	−	−	−	−	−	−	−	−	−	−	−	−	+	−	+	−	−	+	−	+	+	−	+	−	+	+
1057	*R. philyla*	−	−	−	−	−	−	−	+	−	−	−	−	−	−	+	−	−	−	−	−	−	−	−	−	+	−	+	−	−	+	v	−	+	−	+	+
1058	*R. phylloplana*	−	−	−	−	−	−	−	+	−	−	+	+	−	−	−	v	+	+	+	−	+	−	−	−	+	+	−	v	−	v	+	+	−	−	+	+
1059	*R. pilati*	−	−	−	−	−	−	−	+	−	−	+	−	−	−	+	+	+	+	+	−	+	−	+	−	+	−	+	−	−	+	+	−	+	−	+	+
1060	*R. pinicola*	−	−	−	−	−	−	−	+	+	−	+	−	−	+	+	+	+	−	−	+	+	−	+	+	+	+	+	+	−	+	+	−	+	−	+	−
1061	*R. pustula*	−	−	−	−	−	−	−	+	−	−	−	−	v	−	+	−	−	−	−	+	+	−	+	−	+	+	+	+	−	+	+	−	+	−	+	+
1062	*R. retinophila*	−	−	−	−	−	−	−	+	−	−	−	−	−	−	+	−	−	−	−	−	−	−	−	−	+	−	+	−	−	+	v	−	+	−	+	+
1063	*R. slooffiae*	−	−	−	−	−	−	−	+	−	+	−	−	−	+	v	−	+	−	−	+	v	−	+	−	+	+	+	+	−	+	+	−	+	−	+	+
1064	*R. sonckii*	−	−	−	−	−	−	−	+	−	−	−	−	+	−	+	−	−	−	−	−	−	−	+	−	+	−	−	−	−	−	+	−	+	−	+	+
1065	*R. terpenoidalis*	−	−	−	−	−	−	−	+	−	+	−	−	−	−	+	+	+	+	−	−	−	−	−	−	+	−	+	−	−	+	+	−	+	−	+	+
1066	*R. vanillica*	−	−	−	−	−	−	−	+	−	+	+	−	−	+	+	+	+	v	+	+	+	+	−	v	−	v	v	−	−	+	−	+	−	v	−	+	+
1067	*R. yarrowii*	−	−	−	−	−	−	−	+	−	+	+	+	+	−	+	+	+	+	v	+	v	+	−	v	−	v	−	−	+	+	−	v	−	+	+
1068	***Saccharomyces***																																			
1069	*S. arboricolus*	+	+	+	−	−	+	n	+	−	+	+	+	+	−	+	v	+	+	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	v	n
1070	*S. bayanus* var. *bayanus*	+	v	+	+	−	+	−	+	−	+	+	v	v	−	+	+	−	−	−	−	−	−	−	−	−	−	−	−	−	+	+	−	−	−	v	−
1071	*S. bayanus* var. *uvarum*	+	v	+	+	−	+	−	+	−	+	+	v	v	−	+	+	−	−	−	−	−	−	−	−	−	−	−	−	−	+	+	−	−	−	v	−
1072	*S. cariocanus*	+	+	+	−	−	+	−	+	−	+	+	−	+	−	−	−	+	−	−	−	−	−	−	−	−	−	−	−	−	+	−	−	−	−	+	−
1073	*S. cerevisiae*	+	v	+	+	−	+	−	+	−	+	+	−	v	−	+	+	v	−	−	−	−	−	−	−	−	−	−	−	−	+	v	−	−	−	−	−
1074	*S. kudriavzevii*	+	−	+	+	−	+	−	+	+	v	+	−	+	−	−	+	v	−	−	−	−	−	−	−	−	−	−	−	−	+	v	−	−	−	v	−
1075	*S. mikatae*	+	+	+	+	−	+	−	+	−	+	+	+	+	−	+	+	+	+	−	−	−	−	−	−	−	−	−	−	n	+	−	−	+	+	+	−
1076	*S. paradoxus*	+	+	+	v	−	v	−	+	−	+	+	−	+	−	+	+	+	+	−	−	−	−	−	−	−	−	−	−	−	+	v	−	−	−	+	−
1077	*S. pastorianus*	+	v	v	+	−	+	−	+	−	v	+	−	+	−	v	+	v	v	−	−	−	−	−	−	−	−	−	−	−	+	v	−	−	−	−	−
1078	***Saccharomycodes***																																				
1079	*S. ludwigii*	+	−	+	−	−	+	−	+	−	+	+	−	−	−	−	−	−	−	−	−	+	+	−	−	−	−	−	−	−	+	+	−	−	−	−	−
1080	*S. sinensis*	+	+	−	−	−	−	−	+	−	−	−	−	+	−	−	−	−	−	−	−	−	−	−	−	−	−	−	v	−	−	−	−	−	−	−	−
1081	***Saccharomycopsis***																																				
1082	*S. capsularis*	+	−	−	+	−	−	−	+	−	−	−	−	−	−	v	+	−	v	+	+	v	−	−	−	−	v	v	−	+	+	+	+	−	+	+
1083	*S. crataegensis*	v	−	−	−	−	−	−	+	−	−	−	−	−	−	v	−	−	−	−	−	−	−	+	−	+	v	v	+	−	+	+	−	v	−	+	+
1084	*S. fermentans*	+	−	−	−	−	−	−	+	−	−	−	−	−	−	+	−	−	−	−	−	−	−	v	−	−	−	−	−	−	+	+	−	−	−	−	−

Symbols: +, positive or weak; −, negative; v, variable (+/−, w/−); n, no data.

Growth reactions and other characteristics

	myo-Inositol	DL-Lactate	Succinate	Citrate	D-Gluconate	D-Glucosamine	*N*-Acetyl-D-glucosamine	Hexadecane	Nitrate	Nitrite	Vitamin-free	2-Keto-D-gluconate	5-Keto-D-gluconate	Saccharate	Xylitol	L-Arabinitol	Arbutin	Propane 1,2 diol	Butane 2,3 diol	Cadaverine	Creatinine	L-Lysine	Ethylamine	50% Glucose	10% NaCl/5% glucose	Starch formation	Urease	Gelatin liquefaction	Cycloheximide 0.01%	Cycloheximide 0.1%	Growth at 19°C	Growth at 25°C	Growth at 30°C	Growth at 35°C	Growth at 37°C	Growth at 40°C	Growth at 45°C	CoQ (Main component)	Mol% G + C (Ave.)	DBB
Rhodotorula (*cont'd*)																																								
1031	−	−	+	+	+	−	n	n	+	+	−	n	n	−	+	n	n	n	n	n	n	n	n	n	n	−	n	n	v	−	+	+	v	−	−	−	−	9	57.7	+
1032	−	+	+	+	+	+	n	n	+	+	+	n	n	n	+	n	n	n	n	n	n	n	n	n	n	−	n	n	−	−	+	+	−	−	−	−	−	10	49.2	+
1033	−	−	+	+	+	−	n	n	+	+	−	n	n	n	+	n	n	n	n	n	n	n	n	n	n	−	n	n	−	−	+	+	+	+	−	−	−	10	58.8	+
1034	−	+	+	+	−	v	n	+	−	−	+	n	n	n	v	n	n	n	n	n	n	n	n	n	n	−	n	n	+	−	+	+	+	v	−	−	−	10	n	+
1035	−	+	+	+	+	−	n	n	+	+	−	n	n	−	+	n	n	n	n	n	n	n	n	n	n	−	n	n	+	+	+	+	+	+	−	−	−	10	60.7	+
1036	−	−	+	+	+	+	n	n	+	+	+	n	n	n	−	n	n	n	n	n	n	n	n	n	n	−	n	n	+	−	+	+	−	−	−	−	−	10	60.5	+
1037	−	v	+	+	+	v	−	n	+	+	−	n	n	n	+	n	n	n	n	n	n	n	n	n	n	−	n	n	+	−	+	+	v	−	−	−	−	10	66.1	+
1038	−	+	+	+	+	+	n	n	+	+	+	n	n	n	+	n	n	n	n	n	n	n	n	n	n	−	n	n	+	−	+	+	−	−	−	−	−	10	56.0	+
1039	−	−	+	+	+	−	n	n	+	+	+	n	n	−	+	n	n	n	n	n	n	n	n	n	n	−	n	n	+	+	+	+	+	−	−	−	−	10	66.8	+
1040	−	−	+	+	−	−	n	n	+	+	+	n	n	+	v	n	n	n	n	n	n	n	n	n	n	−	n	n	+	+	+	+	+	−	−	−	−	10	66.9	+
1041	−	+	+	+	−	−	n	n	+	+	−	n	n	−	−	n	n	n	n	n	n	n	n	n	n	−	n	n	−	−	+	+	−	−	−	−	−	n	46.9	+
1042	−	+	+	−	+	−	n	n	−	−	−	n	n	−	−	n	n	n	n	n	n	n	n	n	n	−	n	n	+	−	+	+	−	−	−	−	−	n	48.3	+
1043	−	+	+	+	+	+	n	n	+	+	+	n	n	n	v	n	n	n	n	n	n	n	n	n	n	−	n	n	v	−	+	+	v	−	−	−	−	10	55.6	+
1044	−	−	+	+	+	−	n	n	+	+	−	n	n	−	+	n	n	n	n	n	n	n	n	n	n	−	n	n	+	−	+	+	−	−	−	−	−	9	59.0	+
1045	−	+	+	+	+	−	n	n	+	+	−	n	n	−	+	n	n	n	n	n	n	n	n	n	n	−	n	n	+	−	+	+	+	−	−	−	−	9	57.4	+
1046	−	−	−	−	+	−	n	n	−	−	−	n	n	+	+	n	n	n	n	n	n	n	n	n	n	n	n	n	+	−	+	+	+	−	−	−	−	10	50.7	+
1047	−	+	+	−	+	−	n	n	−	−	−	n	n	+	+	n	n	n	n	n	n	n	n	n	n	−	n	n	+	−	+	+	v	−	−	−	−	10	50.1	+
1048	−	+	+	+	+	−	n	n	−	−	−	n	n	+	+	n	n	n	n	n	n	n	n	n	n	−	n	n	−	−	+	+	−	−	−	−	−	n	n	+
1049	−	−	−	−	−	−	n	n	−	−	−	n	n	−	+	n	n	n	n	n	n	n	n	n	n	−	n	n	−	−	+	+	+	−	−	−	−	10	49.1	+
1050	−	−	+	+	+	−	n	n	−	−	−	n	n	−	+	n	n	n	n	n	n	n	n	n	n	−	n	n	+	−	+	+	+	−	−	−	−	10	53.9	+
1051	−	v	+	−	+	−	n	n	−	−	−	n	n	+	+	n	n	n	n	n	n	n	n	n	n	−	n	n	+	−	+	+	+	v	−	−	−	10	50.3	+
1052	−	v	+	+	+	−	n	n	−	−	−	n	n	−	+	n	n	n	n	n	n	n	n	n	n	−	n	n	v	v	+	+	+	v	−	−	−	10	60.6	+
1053	−	+	+	+	+	−	n	n	−	−	+	n	n	n	+	n	n	n	n	n	n	n	n	n	n	−	n	n	+	−	+	+	+	−	−	−	−	n	n	+
1054	−	−	+	+	n	−	n	n	−	−	−	n	n	n	n	n	n	n	n	n	n	n	n	n	n	−	n	n	n	n	+	+	+	+	−	−	−	10	n	+
1055	−	+	+	+	n	n	n	n	+	+	n	n	n	n	n	n	n	n	n	n	n	n	n	n	n	−	n	n	−	−	+	+	+	+	−	−	−	10	57.6	+
1056	−	+	+	−	+	−	n	n	−	−	−	n	n	n	+	n	n	n	n	n	n	n	n	n	n	−	n	n	−	−	+	+	+	−	−	−	−	10	50.8	+
1057	−	v	+	+	+	+	n	n	−	−	+	n	n	n	+	n	n	n	n	n	n	n	n	n	n	−	n	n	−	−	+	+	+	−	−	−	−	10	62.9	+
1058	+	+	+	v	−	−	n	n	+	+	+	n	n	−	−	n	n	n	n	n	n	n	n	n	n	−	n	n	−	−	+	+	−	−	−	−	−	n	n	+
1059	−	+	+	+	+	−	n	n	+	+	+	n	n	+	+	n	n	n	n	n	n	n	n	n	n	−	n	n	+	−	+	+	−	−	−	−	−	n	n	+
1060	+	−	+	−	+	−	n	−	−	−	−	n	n	+	+	n	n	n	n	n	n	n	n	n	n	−	n	n	−	−	+	+	+	−	−	−	−	10	n	+
1061	−	−	+	+	+	+	n	n	+	+	−	n	n	n	+	n	n	n	n	n	n	n	n	n	n	−	n	n	−	−	+	+	−	−	−	−	−	n	51.0	+
1062	−	+	+	+	+	+	n	+	−	−	+	n	n	n	v	n	n	n	n	n	n	n	n	n	n	−	n	n	+	−	+	+	+	+	+	−	−	10	n	+
1063	−	+	+	−	+	−	n	n	−	−	−	n	n	+	+	n	n	n	n	n	n	n	n	n	n	−	n	n	+	−	+	+	+	−	−	−	−	10	50.7	+
1064	−	+	+	−	+	−	n	n	+	+	−	n	n	−	−	n	n	n	n	n	n	n	n	n	n	−	n	n	−	−	+	+	−	−	−	−	−	n	44.1	+
1065	−	+	+	+	+	+	n	+	−	−	+	n	n	n	+	n	n	n	n	n	n	n	n	n	n	−	n	n	+	−	+	+	+	+	+	−	−	10	n	+
1066	−	+	+	+	+	+	n	n	+	+	+	n	n	−	+	n	n	n	n	n	n	n	n	n	n	−	n	n	v	−	+	+	+	−	−	−	−	n	59.4	+
1067	+	+	+	+	+	+	n	n	+	+	−	n	n	+	−	n	n	n	n	n	n	n	n	n	n	−	n	n	+	−	+	+	−	−	−	−	−	9	60.3	+
Saccharomyces																																								
1069	−	−	−	−	n	−	n	−	−	n	+	n	n	n	n	n	n	n	n	−	n	−	+	n	n	−	−	n	n	n	+	+	+	n	−	−	−	n	n	−
1070	−	v	−	−	v	−	−	−	−	n	+	−	−	n	−	n	n	n	n	−	n	−	−	+	+	−	n	−	n	n	+	+	+	n	−	−	−	6	39.9	−
1071	−	v	−	−	v	−	−	−	−	n	+	−	−	n	−	n	n	n	n	−	n	−	−	+	+	−	n	−	n	n	+	+	+	n	−	−	−	6	39.9	−
1072	−	+	−	−	−	−	n	−	−	n	−	n	n	n	n	n	n	n	n	−	n	−	−	+	+	−	n	n	n	n	+	+	+	n	−	−	−	n	n	−
1073	−	v	−	−	v	−	−	−	−	n	−	−	−	n	−	n	n	n	n	−	n	−	−	+	−	−	n	−	n	n	+	+	+	n	v	v	n	6	39.9	−
1074	−	−	−	−	−	−	−	−	−	n	−	n	n	n	−	n	n	n	n	−	n	−	−	+	+	+	n	n	−	−	+	+	v	−	−	−	−	n	n	−
1075	−	+	−	−	−	−	n	−	−	n	−	n	n	n	−	n	n	n	n	−	n	−	−	+	−	−	n	n	−	−	+	+	+	n	−	−	−	n	n	−
1076	−	+	−	−	v	−	−	−	−	n	−	−	−	n	−	n	n	n	n	−	n	−	−	n	n	−	n	−	n	n	+	+	+	+	+	n	n	n	42.6	−
1077	−	v	v	−	v	−	−	−	−	n	−	−	−	n	−	n	n	n	n	−	n	−	−	n	n	−	n	−	n	n	+	+	+	n	−	−	−	6	40.5	−
Saccharomycodes																																								
1079	−	+	−	−	−	−	−	−	−	−	n	−	−	−	n	n	n	n	n	+	n	+	+	−	n	−	−	+	−	−	+	+	+	n	−	−	−	6	38.3	−
1080	−	−	−	−	−	−	n	n	−	−	n	−	n	−	−	n	n	n	n	−	−	−	n	−	−	n	n	n	−	−	+	+	+	n	−	−	−	6	n	−
Saccharomycopsis																																								
1082	−	−	+	v	+	−	−	−	−	n	−	+	+	−	n	n	n	n	n	n	n	n	n	n	+	−	n	+	n	n	+	+	+	n	−	−	−	8	43.4	−
1083	−	+	+	−	+	+	v	−	−	n	−	−	+	−	n	n	n	n	n	n	n	n	n	n	−	−	n	−	n	n	+	+	+	n	−	−	−	n	39.1	−
1084	−	−	v	−	−	−	−	−	−	n	−	−	−	−	n	n	n	n	n	n	n	n	n	n	−	−	n	−	n	n	+	+	+	n	−	−	−	8	37.0	−

Symbols: +, positive or weak; −, negative; v, variable (+/−, w/−); n, no data.

Ln. no.	Species	Fermentation							Growth reactions and other characteristics																																	
		Glucose	Galactose	Sucrose	Maltose	Lactose	Raffinose	Trehalose	Glucose	Inulin	Sucrose	Raffinose	Melibiose	Galactose	Lactose	Trehalose	Maltose	Melezitose	Methyl-α-D-glucoside	Soluble Starch	Cellobiose	Salicin	L-Sorbose	L-Rhamnose	D-Xylose	L-Arabinose	D-Arabinose	D-Ribose	Methanol	Ethanol	Glycerol	Erythritol	Ribitol	Galactitol	D-Mannitol	D-Glucitol				
	Saccharomycopsis (*cont'd*)																																								
1085	*S. fibuliger*a	+	−	+	+	−	v	−	+	−	+	v	−	−	−	v	+	v	+	+	+	+	−	−	−	−	−	−	−	+	+	v	v	−	v	v				
1086	*S. javanensis*	−	−	−	−	−	−	−	+	−	−	−	−	−	−	+	−	−	−	v	−	−	+	−	v	−	−	−	−	+	+	−	−	−	−	−				
1087	*S. malanga*	+	−	−	+	−	−	−	+	−	−	−	−	−	−	v	+	−	−	+	+	+	−	−	v	−	v	+	−	+	+	v	+	−	+	+				
1088	*S. microspora*	−	−	−	−	−	−	−	+	−	−	−	−	−	−	−	+	−	−	+	−	−	−	+	+	−	v	+	−	+	+	+	+	−	+	+				
1089	*S. schoenii*	−	−	−	−	−	−	−	+	−	v	−	−	−	−	+	−	−	−	v	−	−	v	−	v	−	−	−	−	+	+	−	−	−	−	−				
1090	*S. selenospora*	+	−	−	−	−	−	−	+	−	−	−	−	+	−	−	−	−	−	v	−	−	−	−	+	+	−	−	−	+	v	−	+	−	−	−				
1091	*S. synnaedendra*	−	−	−	−	−	−	−	+	−	−	−	−	−	−	−	+	−	−	+	−	−	−	+	v	−	+	+	−	+	+	+	+	−	+	+				
1092	*S. vini*	+	−	v	−	−	v	−	+	−	v	v	−	−	−	v	v	−	v	−	−	v	+	−	−	−	−	−	−	+	+	−	v	−	v	+				
1093	***Saitoella***																																								
1094	*S. complicata*	−	−	−	−	−	−	−	+	+	+	+	+	+	−	+	+	+	+	−	+	+	+	−	+	−	+	−	v	−	+	+	−	+	−	+	+				
1095	***Sakaguchia***																																								
1096	*S. dacryoidea*	−	−	−	−	−	−	−	+	−	v	−	−	+	−	+	v	v	−	−	v	−	v	v	−	−	−	−	−	v	+	−	−	−	v	+				
1097	***Saprochaete***																																								
1098	*S. chiloensis*	−	−	−	−	−	−	−	+	−	−	−	−	+	−	+	−	−	−	−	−	−	+	−	−	−	−	−	−	+	+	−	−	−	−	−				
1099	*S. clavata*	−	−	−	−	−	−	−	+	−	−	−	−	+	−	−	−	−	−	−	+	+	+	−	−	−	−	−	−	+	+	−	−	−	−	−				
1100	*S. fungicola*	−	−	−	−	−	−	−	+	−	−	−	−	+	−	−	−	−	−	−	−	−	+	−	+	−	−	v	−	+	+	−	+	−	+	+				
1101	*S. gigas*	+	+	−	−	−	−	−	+	−	−	−	−	+	−	−	−	−	−	−	−	−	+	−	−	−	−	−	−	+	+	−	−	−	+	+				
1102	*S. ingens*	−	−	−	−	−	−	−	+	−	−	−	−	+	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	+	+	−	−	−	−	−				
1103	*S. japonica*	−	−	−	−	−	−	−	+	−	−	−	−	+	−	−	−	−	−	−	−	−	+	−	−	−	−	−	−	+	+	−	−	−	+	+				
1104	*S. psychrophila*	−	−	−	−	−	−	−	+	−	−	−	−	+	−	−	−	−	−	−	−	−	+	−	+	−	−	−	−	+	+	−	+	−	+	+				
1105	*S. quercus*	−	−	−	−	−	−	−	+	−	−	−	−	+	−	−	−	−	−	−	−	−	v	−	−	−	−	−	−	+	+	−	−	−	−	−				
1106	*S. saccharophila*	−	−	−	−	−	−	−	+	−	−	−	−	−	−	−	−	−	−	−	−	−	+	−	−	−	−	−	−	+	+	−	−	−	−	−				
1107	*S. suaveolens*	+	v	−	−	−	−	−	+	−	−	−	−	+	−	−	−	−	−	−	−	−	+	−	−	−	−	−	−	+	+	−	−	−	v	v				
1108	***Saturnispora***																																								
1109	*S. ahearnii*	+	−	−	−	−	−	−	+	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	+	−	−	−	−	+	+				
1110	*S. besseyi*	+	−	−	−	−	−	−	+	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	+	−	−	−	−	+	+				
1111	*S. dispora*	+	−	−	−	−	−	v	+	−	−	−	−	−	−	+	−	−	−	−	−	−	−	−	−	−	−	−	−	+	−	−	−	+	−	+				
1112	*S. hagleri*	+	−	−	−	−	−	v	+	−	−	−	−	−	−	+	−	−	−	−	−	−	−	−	−	−	−	−	−	+	+	−	−	+	−	+				
1113	*S. mendoncae*	v	−	−	−	−	−	−	+	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	+	v	−	v	−	+	+				
1114	*S. saitoi*	+	−	−	−	−	−	−	+	−	−	−	−	−	−	+	−	−	−	−	−	−	−	−	−	−	−	−	−	+	−	−	v	−	+	+				
1115	*S. zaruensis*	+	−	−	−	−	−	−	+	−	−	−	−	−	−	+	−	−	−	−	−	−	−	−	−	−	−	−	−	+	−	−	+	−	+	+				
1116	***Scheffersomyces***																																								
1117	*S. segobiensis*	+	+	−	−	−	−	+	+	−	+	−	−	+	−	+	+	−	+	−	+	+	+	−	+	−	+	+	−	+	+	−	+	−	+	+				
1118	*S. spartinae*	+	−	+	v	−	−	−	+	−	+	−	−	−	−	+	+	+	+	−	+	+	+	−	−	−	−	−	−	+	+	−	+	−	+	+				
1119	*S. stipitis*	+	+	−	+	−	−	+	+	−	+	−	−	+	v	+	+	+	+	+	+	+	+	v	+	+	v	+	+	−	+	+	+	+	−	+	+				
1120	***Schizoblastosporion***																																								
1121	*S. starkeyi-henricii*	−	−	−	−	−	−	−	+	−	−	−	−	v	−	v	−	−	−	−	−	−	−	v	−	−	−	v	−	−	v	−	v	−	v	+				
1122	***Schizosaccharomyces***																																								
1123	*S. japonicus*	+	−	+	v	−	+	−	+	v	+	+	−	−	−	−	v	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−				
1124	*S. octosporus*	+	−	−	v	−	−	−	+	−	v	−	−	−	−	−	v	−	−	−	−	−	−	−	−	−	−	−	−	−	−	v	−	−	−	−				
1125	*S. pombe*	+	−	+	v	−	v	−	+	−	+	+	−	−	−	−	v	−	−	−	−	−	−	−	−	−	−	−	−	−	−	v	−	−	−	−				
1126	***Schwanniomyces***																																								
1127	*S. capriottii*	+	−	+	+	−	+	−	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	−	−	−	+	+	−	+	+	+	+				
1128	*S. etchellsii*	+	−	v	v	−	−	−	+	−	+	−	−	+	−	+	+	+	+	−	+	v	+	−	+	+	−	−	−	+	+	−	+	−	+	+				
1129	*S. occidentalis* var. *occidentalis*	+	+	+	v	−	v	−	+	+	+	+	v	+	v	+	+	+	v	+	+	+	v	−	+	v	−	−	−	+	+	−	v	−	+	v				
1130	*S. occidentalis* var. *persoonii*	+	+	+	v	−	v	−	+	+	+	+	v	−	v	+	+	+	v	+	−	−	v	−	−	v	−	−	−	+	+	−	v	−	+	v				
1131	*S. polymorphus* var. *polymorphus*	+	v	+	v	−	+	−	+	+	+	+	v	+	v	+	+	+	+	+	+	+	+	−	+	v	v	v	−	+	+	−	+	+	+	+				
1132	*S. polymorphus* var. *africanus*	+	v	+	v	−	+	−	+	+	+	+	v	+	v	+	+	+	+	+	+	+	+	+	+	v	v	v	−	+	+	−	+	+	+	+				
1133	*S. pseudopolymorphus*	+	+	+	v	−	−	−	+	−	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	−	+	−	+	+	−	+	+	+	+				
1134	*S. vanrijiae* var. *vanrijiae*	v	−	v	−	−	−	−	+	v	+	+	+	+	−	+	+	+	+	+	v	+	+	v	+	v	−	v	−	+	+	−	+	+	+	+				
1135	*S. vanrijiae* var. *yarrowii*	v	−	v	−	−	−	−	+	v	+	+	−	+	−	v	+	+	+	v	v	v	+	v	+	v	−	v	−	+	+	v	+	+	+	+				
1136	*S. yamadae*	+	+	−	−	−	−	−	+	−	+	−	−	+	+	+	+	+	+	v	+	+	+	+	+	+	−	−	−	+	+	−	+	+	+	+				
1137	***Sirobasidium***																																								
1138	*S. intermedium*	−	−	−	−	−	−	−	+	−	+	+	−	v	+	+	+	+	+	+	+	+	+	+	+	+	+	+	−	+	+	+	+	+	+	+				
1139	*S. magnum*	−	−	−	−	−	−	−	+	−	−	−	−	+	+	+	v	+	+	−	+	+	+	+	+	+	+	+	−	+	+	+	+	+	+	+				

Symbols: +, positive or weak; −, negative; v, variable (+/−, w/−); n, no data.

Growth reactions and other characteristics

	myo-Inositol	DL-Lactate	Succinate	Citrate	D-Gluconate	D-Glucosamine	*N*-Acetyl-D-glucosamine	Hexadecane	Nitrate	Nitrite	Vitamin-free	2-Keto-D-gluconate	5-Keto-D-gluconate	Saccharate	Xylitol	L-Arabinitol	Arbutin	Propane 1,2 diol	Butane 2,3 diol	Cadaverine	Creatinine	L-Lysine	Ethylamine	50% Glucose	10% NaCl/5% glucose	Starch formation	Urease	Gelatin liquefaction	Cycloheximide 0.01%	Cycloheximide 0.1%	Growth at 19°C	Growth at 25°C	Growth at 30°C	Growth at 35°C	Growth at 37°C	Growth at 40°C	Growth at 45°C	CoQ (Main component)	Mol% G + C (Ave.)	DBB
Saccharomycopsis (*cont'd*)																																								
1085	+	+	+	v	+	−	−	−	−	n	−	−	v	−	n	n	n	n	n	n	n	n	n	n	v	−	n	+	n	n	+	+	+	+	+	n	n	8	39.3	−
1086	−	−	+	−	−	−	+	−	−	n	−	−	−	−	n	n	n	n	n	n	n	n	n	n	−	−	n	−	n	n	+	+	n	n	−	−	−	8	31.3	−
1087	−	−	+	−	+	−	−	−	−	n	−	+	+	−	n	n	n	n	n	n	n	n	n	n	+	−	n	+	n	n	+	+	+	+	+	n	n	n	n	−
1088	+	v	+	−	+	−	−	−	−	n	−	−	v	−	n	n	n	n	n	−	n	n	n	n	−	−	n	+	n	n	+	+	+	n	−	−	−	n	n	−
1089	−	−	+	−	−	−	−	−	−	n	−	−	−	−	n	n	n	n	n	n	n	n	n	n	−	−	n	−	n	n	+	+	+	n	−	−	−	8	33.7	−
1090	−	+	+	−	v	−	−	−	−	n	−	−	+	−	n	n	n	n	n	n	n	n	n	n	−	−	n	v	n	n	+	+	+	n	−	−	−	8	30.2	−
1091	+	+	+	v	+	−	−	−	−	n	−	−	+	−	n	n	n	n	n	n	n	n	n	n	−	−	n	−	n	n	+	+	+	n	−	−	−	8	42.0	−
1092	−	−	v	−	−	v	−	−	−	n	−	+	−	−	n	n	n	n	n	n	n	n	n	n	v	−	n	v	n	n	+	+	+	n	−	−	−	8	n	−
Saitoella																																								
1094	−	+	+	+	v	−	n	n	+	+	+	−	n	n	+	+	+	n	n	−	−	−	v	−	n	−	+	n	n	n	+	+	+	−	−	−	−	10	51.9	−
Sakaguchia																																								
1096	−	+	+	+	+	−	−	−	−	−	−	+	n	−	v	n	n	n	n	−	−	+	+	−	−	−	+	−	n	n	+	+	+	−	−	−	−	10	58.3	+
Saprochaete																																								
1098	−	+	+	−	−	−	n	n	−	n	+	−	n	n	−	n	−	n	n	n	n	n	n	n	n	−	n	n	n	n	+	+	−	−	−	−	−	n	40.6	−
1099	−	+	+	+	−	−	n	n	−	n	−	−	n	n	−	n	+	n	n	n	n	n	n	n	n	−	n	n	n	n	+	+	+	+	+	+	n	n	35.3	−
1100	−	+	+	+	−	−	n	n	−	n	−	−	n	n	+	n	−	n	n	n	n	n	n	n	n	−	n	n	n	n	+	+	+	+	+	−	−	n	41.3	−
1101	−	+	+	v	−	−	n	n	−	n	−	−	n	n	−	n	−	n	n	n	n	n	n	n	n	−	n	n	n	n	+	+	+	+	−	−	−	n	41.2	−
1102	−	+	+	−	−	−	n	n	−	n	+	−	n	n	−	n	−	n	n	n	n	n	n	n	n	−	n	n	n	n	+	+	+	+	+	−	−	9	38.4	−
1103	−	+	+	+	−	−	n	n	−	n	−	−	n	n	−	n	−	n	n	n	n	n	n	n	n	−	n	n	n	n	+	+	+	−	−	−	−	n	42.2	−
1104	−	+	+	v	−	−	n	n	−	n	−	−	n	n	−	n	−	n	n	n	n	n	n	n	n	−	n	n	n	n	+	+	−	−	−	−	−	n	43.4	−
1105	−	+	+	−	−	−	n	n	−	n	+	−	n	n	−	n	−	n	n	n	n	n	n	n	n	−	n	n	n	n	+	+	+	−	−	−	−	n	49.0	−
1106	−	−	+	−	−	−	n	n	−	n	−	−	n	n	−	n	−	n	n	n	n	n	n	n	n	−	n	n	n	n	+	+	+	−	−	−	−	n	38.7	−
1107	−	+	+	−	−	−	n	n	−	n	−	−	n	n	−	n	−	n	n	n	n	n	n	n	n	−	n	n	n	n	+	+	+	+	−	−	−	n	41.8	−
Saturnispora																																								
1109	−	+	+	−	−	−	−	−	−	n	−	−	−	−	n	n	n	n	n	n	n	n	n	n	−	−	n	+	n	n	+	+	+	n	−	−	−	n	34.9	−
1110	−	+	+	−	−	−	−	−	−	n	−	−	−	−	n	n	n	n	n	n	n	n	n	n	−	−	n	+	n	n	+	+	+	n	−	−	−	7	35.2	−
1111	−	v	+	−	−	−	−	−	−	n	−	−	−	−	n	n	n	n	n	n	n	n	n	n	−	−	n	−	n	n	+	+	+	n	−	−	−	7	37.8	−
1112	−	+	+	−	−	−	−	−	−	n	−	−	−	−	n	n	n	n	n	n	n	n	n	n	−	−	n	+	n	n	+	+	+	n	−	−	−	n	n	−
1113	−	+	+	−	−	−	−	−	−	n	−	−	−	−	n	n	n	n	n	n	n	n	n	n	−	−	n	−	n	n	+	+	+	n	−	−	−	n	n	−
1114	−	+	+	−	−	−	−	−	−	n	−	−	−	−	n	n	n	n	n	n	n	n	n	n	−	−	n	+	n	n	+	+	+	n	−	−	−	7	33.3	−
1115	−	+	+	−	−	−	−	−	−	n	−	−	−	−	n	n	n	n	n	n	n	n	n	n	−	−	n	−	n	n	+	+	+	n	−	−	−	7	39.5	−
Scheffersomyces																																								
1117	−	−	+	+	+	+	+	+	−	n	−	+	−	−	n	n	n	n	n	n	n	n	n	n	−	−	n	v	n	n	+	+	+	n	−	−	−	9	41.5	−
1118	−	v	+	+	v	−	+	+	−	n	−	+	−	−	n	n	n	n	n	n	n	n	n	n	+	−	n	−	n	n	+	+	+	+	+	−	−	9	39.6	−
1119	−	+	+	+	v	+	+	+	−	n	−	+	−	−	n	n	n	n	n	n	n	n	n	n	v	−	n	−	n	n	+	+	+	n	v	n	n	9	43.1	−
Schizoblastosporion																																								
1121	−	−	+	−	v	−	n	n	−	n	−	v	n	−	−	n	n	n	n	n	n	n	n	n	n	−	n	n	n	n	+	+	v	−	−	−	−	6	41.1	−
Schizosaccharomyces																																								
1123	−	−	−	−	−	−	−	−	−	n	−	n	n	n	n	n	n	n	n	−	n	−	−	n	−	n	n	n	−	−	+	+	+	+	+	v	−	n	34.3	−
1124	−	−	−	−	−	−	−	−	−	n	−	n	n	n	n	n	n	n	n	−	n	−	−	n	n	n	n	n	−	−	+	+	+	n	v	n	−	9	39.4	−
1125	−	−	−	−	v	−	−	−	−	n	−	n	n	n	n	n	n	n	n	−	n	−	−	n	n	n	n	n	−	−	+	+	+	n	−	−	−	10	38.2	−
Schwanniomyces																																								
1127	−	−	+	+	+	+	+	+	−	n	−	+	−	−	n	n	n	n	n	n	n	n	n	−	+	−	n	n	n	n	+	+	+	n	−	−	−	9	37.1	−
1128	−	v	+	+	−	+	+	+	−	n	−	+	−	−	n	n	n	n	n	n	n	n	n	−	+	−	n	n	n	n	+	+	+	+	+	n	−	9	39.5	−
1129	−	−	+	+	+	+	+	v	−	n	−	+	−	−	n	n	n	n	n	n	n	n	n	−	−	−	n	n	n	n	+	+	+	n	v	n	−	9	35.2	−
1130	−	−	+	+	+	+	+	v	−	n	−	+	−	−	n	n	n	n	n	n	n	n	n	−	−	−	n	n	n	n	+	+	+	n	v	n	−	n	35.4	−
1131	−	−	+	+	+	v	+	v	−	n	+	+	v	−	n	n	n	n	n	n	n	n	n	−	+	−	n	n	n	n	+	+	+	n	v	n	−	9	35.8	−
1132	−	−	+	+	+	v	+	v	−	n	+	+	v	−	n	n	n	n	n	n	n	n	n	−	+	−	n	n	n	n	+	+	+	n	v	n	−	n	n	−
1133	−	+	+	+	+	v	+	−	−	n	−	+	−	−	n	n	n	n	n	n	n	n	n	−	+	−	n	n	n	n	+	+	+	n	−	−	−	9	35.7	−
1134	−	v	+	+	+	v	+	+	−	n	+	+	−	−	n	n	n	n	n	n	n	n	n	−	+	−	n	n	n	n	+	+	+	+	+	n	n	9	32.6	−
1135	−	v	+	v	+	v	+	+	−	n	+	+	−	−	n	n	n	n	n	n	n	n	n	−	+	−	n	n	n	n	+	+	+	+	−	−	−	n	33.0	−
1136	−	−	+	+	+	+	+	−	−	n	−	+	−	−	n	n	n	n	n	n	n	n	n	−	v	−	n	n	n	n	+	+	+	n	−	−	−	9	35.1	−
Sirobasidium																																								
1138	+	+	+	+	+	+	n	n	−	−	+	+	n	n	n	n	n	n	n	n	n	n	n	−	n	+	+	n	n	n	+	+	+	n	−	−	−	n	n	+
1139	+	+	+	+	+	−	n	n	−	−	−	+	n	n	n	n	n	n	n	n	n	n	n	−	n	+	+	n	n	n	+	+	v	n	−	−	−	n	n	+

Symbols: +, positive or weak; −, negative; v, variable (+/−, w/−); n, no data.

Ln. no.	Species	Fermentation							Growth reactions and other characteristics																												
		Glucose	Galactose	Sucrose	Maltose	Lactose	Raffinose	Trehalose	Glucose	Inulin	Sucrose	Raffinose	Melibiose	Galactose	Lactose	Trehalose	Maltose	Melezitose	Methyl-α-D-glucoside	Soluble Starch	Cellobiose	Salicin	L-Sorbose	L-Rhamnose	D-Xylose	L-Arabinose	D-Arabinose	D-Ribose	Methanol	Ethanol	Glycerol	Erythritol	Ribitol	Galactitol	D-Mannitol	D-Glucitol
1140	***Spathaspora***																																			
1141	*S. passalidarum*	+	+	−	+	−	−	+	+	−	+	−	−	+	−	+	+	+	+	+	+	+	−	−	+	−	+	+	−	+	+	+	+	−	+	+
1142	***Sporidiobolus***																																			
1143	*S. johnsonii*	−	−	−	−	−	−	−	+	−	+	−	−	−	−	+	+	+	+	+	+	+	+	−	+	−	+	+	−	+	+	−	+	−	+	+
1144	*S. longiusculus*	−	−	−	−	−	−	−	+	−	+	+	−	+	−	+	+	+	+	+	+	v	+	−	+	−	+	+	−	+	+	−	v	−	+	+
1145	*S. metaroseus*	−	−	−	−	−	−	−	+	−	+	+	−	+	−	+	+	+	+	+	+	+	+	−	v	−	+	+	−	+	+	−	+	−	+	+
1146	*S. microsporus*	−	−	−	−	−	−	−	+	−	+	+	−	+	−	+	−	−	−	−	+	+	+	−	+	+	+	+	−	+	+	−	+	+	+	+
1147	*S. pararoseus*	−	−	−	−	−	−	−	+	−	+	+	−	+	−	+	+	+	+	+	+	+	+	−	v	+	+	v	−	+	+	−	v	−	+	+
1148	*S. ruineniae*	−	−	−	−	−	−	−	+	−	+	+	−	+	−	+	+	−	v	−	+	+	+	v	+	+	+	+	−	+	+	−	+	+	+	+
1149	*S. salmonicolor*	−	−	−	−	−	−	−	+	−	+	+	−	−	−	+	−	−	−	−	−	−	+	−	+	v	+	v	−	+	+	−	+	−	+	+
1150	***Sporobolomyces***																																			
1151	*S. bannaensis*	−	−	−	−	−	−	−	+	+	+	+	−	v	−	+	+	+	+	+	+	v	+	−	−	−	−	−	−	+	+	−	v	−	+	+
1152	*S. beijingensis*	−	−	−	−	−	−	−	+	−	+	+	−	−	−	+	+	+	−	+	+	v	+	−	−	−	+	−	−	+	v	−	−	−	+	+
1153	*S. bischofiae*	−	−	−	−	−	−	−	+	−	+	+	+	+	−	+	+	+	−	+	+	+	+	−	+	−	−	−	−	−	+	−	+	−	+	+
1154	*S. blumeae*	−	−	−	−	−	−	−	+	−	+	+	−	−	−	+	+	+	−	+	+	+	+	−	−	−	−	−	−	−	−	−	−	−	+	+
1155	*S. carnicolor*	−	−	−	−	−	−	−	+	+	+	+	−	+	−	+	+	+	+	+	+	+	+	−	+	−	+	+	−	+	+	−	+	−	+	+
1156	*S. clavatus*	−	−	−	−	−	−	−	+	−	+	+	+	−	−	+	+	+	−	+	+	−	−	−	+	−	−	+	−	−	−	−	+	−	+	+
1157	*S. coprosmae*	−	−	−	−	−	−	−	+	−	+	+	−	+	−	+	+	+	+	+	+	+	+	+	+	+	+	+	−	−	+	−	+	+	+	+
1158	*S. coprosmicola*	−	−	−	−	−	−	−	+	−	+	+	−	−	−	+	−	−	−	−	−	−	−	−	−	−	−	−	−	−	+	−	−	−	+	+
1159	*S. dimennae*	−	−	−	−	−	−	−	+	−	v	v	−	−	−	+	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	+	v
1160	*S. diospyroris*	−	−	−	−	−	−	−	+	−	+	+	+	−	+	−	−	+	−	+	+	+	−	−	−	+	−	−	−	−	+	−	+	+	+	+
1161	*S. dracophylli*	−	−	−	−	−	−	−	+	−	+	+	+	−	−	−	+	+	−	−	+	+	+	−	−	−	−	−	−	−	+	−	+	+	+	+
1162	*S. elongatus*	−	−	−	−	−	−	−	+	−	+	−	−	−	−	+	+	+	−	−	+	+	+	+	+	+	+	−	−	−	+	−	−	−	+	+
1163	*S. falcatus*	−	−	−	−	−	−	−	+	−	−	−	−	+	−	+	−	−	−	−	+	+	−	−	+	−	−	−	−	+	+	−	−	−	+	+
1164	*S. foliicola*	−	−	−	−	−	−	−	+	−	+	−	−	+	−	+	−	+	−	−	+	−	+	−	+	+	+	+	−	−	+	−	+	−	+	+
1165	*S. fushanensis*	−	−	−	−	−	−	−	+	−	−	−	−	+	−	+	+	+	v	−	+	v	−	−	−	−	−	−	−	+	−	−	+	−	+	+
1166	*S. gracilis*	−	−	−	−	−	−	−	+	−	−	−	−	−	−	+	−	−	−	−	+	−	−	−	+	−	v	+	−	−	+	−	+	−	+	v
1167	*S. griseoflavus*	−	−	−	−	−	−	−	+	−	+	−	−	+	−	+	+	+	−	+	+	+	−	−	+	−	+	−	−	+	+	−	+	−	+	+
1168	*S. inositophilus*	−	−	−	−	−	−	−	+	−	+	−	−	−	−	+	+	+	−	−	+	−	−	−	+	−	−	−	−	+	+	−	+	−	+	+
1169	*S. japonicus*	−	−	−	−	−	−	−	+	−	+	+	−	+	−	+	+	+	+	+	+	+	+	−	−	−	−	−	−	+	+	−	+	−	+	+
1170	*S. jilinensis*	−	−	−	−	−	−	−	+	−	+	+	−	+	−	+	+	+	+	+	−	−	+	−	+	−	−	−	−	+	+	−	−	−	+	+
1171	*S. kluyveri-nielii*	−	−	−	−	−	−	−	+	−	−	−	−	+	−	−	−	−	−	−	−	−	−	−	+	+	+	−	−	+	+	−	+	+	+	+
1172	*S. lactophilus*	−	−	−	−	−	−	−	+	−	+	−	−	−	+	+	+	+	v	+	+	−	v	−	+	−	+	−	−	v	+	v	+	−	+	v
1173	*S. linderae*	−	−	−	−	−	−	−	+	−	+	−	−	−	−	+	−	−	−	−	−	−	−	−	−	−	−	−	−	−	+	−	v	−	v	v
1174	*S. lophatheri*	−	−	−	−	−	−	−	+	−	+	+	+	−	+	+	+	−	+	+	+	+	+	−	+	−	+	+	−	+	+	+	+	−	+	+
1175	*S. magnisporus*	−	−	−	−	−	−	−	+	−	+	+	+	+	−	+	+	+	v	+	−	v	+	v	v	v	−	v	−	−	v	−	+	−	+	+
1176	*S. novazealandicus*	−	−	−	−	−	−	−	+	−	−	−	−	−	−	v	−	−	−	−	−	−	−	−	−	−	−	−	−	−	+	−	−	−	+	+
1177	*S. nylandii*	−	−	−	−	−	−	−	+	−	+	+	−	−	−	+	+	+	+	+	+	−	+	−	−	−	+	+	−	+	+	−	+	−	+	+
1178	*S. odoratus*	−	−	−	−	−	−	−	+	−	+	+	−	v	−	+	−	−	−	−	−	v	+	−	+	v	v	−	−	+	+	−	+	−	+	+
1179	*S. ogasawarensis*	−	−	−	−	−	−	−	+	−	+	+	v	+	v	+	+	+	−	+	v	+	+	v	+	+	v	−	−	−	+	−	v	v	+	+
1180	*S. oryzicola*	−	−	−	−	−	−	−	+	−	+	+	−	+	−	+	+	+	+	−	+	+	+	−	+	+	+	+	−	−	+	−	+	−	+	+
1181	*S. patagonicus*	−	−	−	−	−	−	−	+	−	+	+	−	+	−	v	v	+	v	+	v	−	+	n	−	−	−	+	n	−	+	−	−	−	+	v
1182	*S. phaffii*	−	−	−	−	−	−	−	+	−	+	+	+	v	−	+	+	+	+	+	+	+	−	−	−	−	−	−	n	+	−	−	−	−	+	v
1183	*S. phyllomatis*	−	−	−	−	−	−	−	+	−	+	−	−	+	−	+	+	+	−	−	+	−	v	+	+	+	+	−	−	+	+	−	+	+	+	+
1184	*S. poonsookiae*	−	−	−	−	−	−	−	+	−	−	−	−	+	−	+	−	−	−	+	+	+	+	−	+	+	+	+	−	+	+	−	+	+	+	+
1185	*S. pyrrosiae*	−	−	−	−	−	−	−	+	−	+	+	+	+	+	+	+	+	−	+	+	+	−	−	−	−	−	−	−	−	+	−	+	+	+	+
1186	*S. roseus*	−	−	−	−	−	−	−	+	−	+	+	−	+	−	+	+	+	+	+	+	+	+	−	v	−	+	+	−	+	+	−	+	−	−	+
1187	*S. ruber*	−	−	−	−	−	−	−	+	−	+	+	+	−	−	−	−	+	+	−	−	−	−	−	−	−	−	−	−	−	+	−	+	−	+	+
1188	*S. ruberrimus*	−	−	−	−	−	−	−	+	−	+	+	−	+	−	+	+	+	−	−	+	+	−	−	−	−	−	−	−	+	+	−	−	−	+	−
1189	*S. salicinus*	−	−	−	−	−	−	−	+	−	+	+	−	+	−	+	−	−	−	−	+	+	−	−	+	+	+	−	−	−	+	−	+	+	+	+
1190	*S. salmoneus*	−	−	−	−	−	−	−	+	−	+	+	−	v	−	+	+	+	+	+	+	+	+	−	v	−	+	v	−	+	+	−	−	−	+	+
1191	*S. sasicola*	−	−	−	−	−	−	−	+	−	+	+	−	−	+	+	+	−	−	+	+	+	+	−	+	+	−	−	−	−	−	−	+	−	+	+
1192	*S. singularis*	−	−	−	−	−	−	−	+	−	−	−	−	−	+	+	−	−	−	−	+	+	−	−	−	v	+	−	−	+	+	−	+	−	+	+
1193	*S. subbrunneus*	−	−	−	−	−	−	−	+	−	+	+	−	−	−	+	−	−	−	−	−	−	−	−	−	−	+	−	−	−	+	−	+	−	+	+
1194	*S. symmetricus*	−	−	−	−	−	−	−	+	−	+	−	−	−	−	+	−	+	−	−	+	−	−	−	−	−	−	−	−	−	+	−	+	−	−	−

Symbols: +, positive or weak; −, negative; v, variable (+/−, w/−); n, no data.

Growth reactions and other characteristics

	myo-Inositol	DL-Lactate	Succinate	Citrate	D-Gluconate	D-Glucosamine	*N*-Acetyl-D-glucosamine	Hexadecane	Nitrate	Nitrite	Vitamin-free	2-Keto-D-gluconate	5-Keto-D-gluconate	Saccharate
Spathaspora														
1141	−	+	+	+	+	+	n	n	−	−	−	+	n	−
Sporidiobolus														
1143	−	v	+	+	+	−	n	n	+	+	+	n	n	−
1144	−	−	+	−	+	−	n	n	−	−	+	n	n	−
1145	−	+	+	+	+	−	n	n	+	+	+	n	n	−
1146	−	−	+	+	+	−	n	n	+	+	+	n	n	+
1147	−	v	+	+	+	−	n	n	−	−	+	n	n	−
1148	−	−	+	+	+	−	n	n	+	+	+	n	n	+
1149	−	v	+	+	+	−	n	n	+	+	+	n	n	−
Sporobolomyces														
1151	−	−	+	−	n	−	n	−	+	+	+	n	n	n
1152	−	−	+	−	n	−	n	−	−	−	+	n	n	n
1153	−	+	+	+	n	n	n	n	−	−	−	+	+	n
1154	−	−	+	−	+	−	−	−	+	−	+	−	−	n
1155	−	−	+	+	+	−	n	n	−	−	+	−	−	n
1156	−	−	−	−	n	−	n	−	−	−	−	n	n	n
1157	−	+	+	+	+	−	n	n	−	−	−	+	+	n
1158	−	+	+	+	+	−	n	n	+	+	−	−	−	n
1159	−	−	+	v	−	−	n	n	+	v	−	−	−	n
1160	−	−	+	−	−	−	−	n	−	−	−	−	−	n
1161	−	−	+	−	−	−	n	n	−	−	−	−	−	n
1162	−	−	+	−	−	−	n	n	−	−	−	−	n	n
1163	−	−	+	+	+	+	n	n	+	+	−	+	n	n
1164	−	−	+	−	+	−	n	n	+	+	−	+	n	n
1165	−	−	+	+	−	−	−	−	−	−	−	−	−	−
1166	−	v	+	v	−	−	n	n	−	−	−	−	n	n
1167	−	−	+	+	+	−	n	n	+	+	−	+	n	n
1168	+	−	+	+	+	−	n	n	+	+	−	+	n	n
1169	−	+	+	+	+	−	n	n	−	−	+	−	n	n
1170	−	−	+	−	n	−	n	v	+	+	+	n	n	n
1171	−	−	+	+	+	−	n	n	+	+	−	+	n	n
1172	−	+	+	+	−	−	n	n	+	+	−	−	n	n
1173	−	+	+	+	−	−	n	n	+	+	−	−	−	n
1174	−	+	+	+	−	−	−	n	+	+	−	−	−	−
1175	−	+	+	+	+	v	+	n	+	+	−	+	+	n
1176	−	−	+	+	−	−	n	n	+	v	−	−	−	n
1177	−	−	+	−	+	−	−	−	+	+	+	−	−	n
1178	−	−	+	−	+	−	n	−	+	+	+	n	n	n
1179	v	v	+	v	n	n	n	n	−	−	−	+	+	n
1180	−	+	+	+	+	−	n	n	−	−	−	+	n	n
1181	−	−	+	−	v	−	n	−	+	−	+	n	n	n
1182	−	−	+	−	n	n	n	n	+	+	+	−	−	n
1183	−	−	+	+	+	−	n	n	−	−	−	+	n	n
1184	−	−	+	+	+	−	−	−	+	+	+	−	−	n
1185	−	−	+	−	−	−	−	n	−	−	−	−	−	−
1186	−	+	+	+	+	−	n	n	+	+	+	n	n	n
1187	−	−	+	−	−	−	n	n	−	−	−	v	n	n
1188	−	−	+	+	−	n	n	n	+	+	+	−	n	n
1189	−	−	+	+	−	−	n	n	+	+	−	−	n	n
1190	−	−	+	v	+	−	n	n	v	v	v	−	n	n
1191	−	−	+	−	−	−	n	n	−	−	−	−	n	n
1192	−	+	+	+	+	−	n	n	−	−	−	+	n	n
1193	−	+	+	+	+	−	n	n	+	+	−	−	n	n
1194	−	−	+	−	n	−	n	−	−	−	+	n	n	n

	Xylitol	L-Arabinitol	Arbutin	Propane 1,2 diol	Butane 2,3 diol	Cadaverine	Creatinine	L-Lysine	Ethylamine	50% Glucose	10% NaCl/5% glucose	Starch formation	Urease	Gelatin liquefaction
Spathaspora														
1141	+	−	+	+	−	+	−	+	+	−	−	−	n	n
Sporidiobolus														
1143	+	n	n	n	n	n	n	n	n	n	n	−	+	n
1144	−	n	n	n	n	n	n	n	n	n	n	−	v	n
1145	−	n	n	n	n	n	n	n	n	n	n	−	+	n
1146	+	n	n	n	n	n	n	n	n	n	n	−	+	n
1147	+	n	n	n	n	n	n	n	n	n	n	−	+	n
1148	+	n	n	n	n	n	n	n	n	n	n	−	+	n
1149	+	n	n	n	n	n	n	n	n	n	n	−	+	n
Sporobolomyces														
1151	n	n	n	n	n	−	n	−	−	n	n	−	+	n
1152	n	n	n	n	n	−	n	+	−	+	n	−	+	n
1153	n	n	n	n	n	−	n	+	−	−	n	−	+	n
1154	n	n	n	n	n	+	n	+	−	−	n	−	+	n
1155	n	n	n	n	n	+	n	+	−	+	n	−	+	n
1156	n	n	n	n	n	+	n	−	+	−	n	−	−	n
1157	n	n	n	n	n	−	n	−	−	−	n	−	+	n
1158	n	n	n	n	n	−	n	−	−	−	n	−	+	n
1159	n	n	n	n	n	−	n	−	−	−	n	−	+	n
1160	n	n	n	n	n	−	n	−	−	−	n	−	−	n
1161	n	n	n	n	n	−	n	−	−	−	n	−	+	n
1162	n	n	n	n	n	−	n	−	−	−	n	−	+	n
1163	n	n	n	n	n	−	n	−	+	−	n	−	+	n
1164	n	n	n	n	n	−	n	−	−	−	n	−	+	n
1165	+	−	n	−	−	−	n	+	+	−	n	−	+	n
1166	n	n	n	n	n	−	n	v	−	−	n	−	+	n
1167	n	n	n	n	n	−	n	−	+	−	n	−	+	n
1168	n	n	n	n	n	+	n	v	+	−	n	−	+	n
1169	n	n	n	n	n	+	n	+	+	+	n	−	+	n
1170	n	n	n	n	n	+	n	+	−	−	n	−	+	n
1171	n	n	n	n	n	−	n	v	−	−	n	−	+	n
1172	n	n	n	n	n	+	n	−	+	−	n	−	+	n
1173	n	n	n	n	n	−	n	−	−	−	n	−	+	n
1174	−	+	n	−	−	−	n	−	+	−	n	−	+	n
1175	n	n	n	n	n	−	n	−	−	−	n	−	+	n
1176	n	n	n	n	n	−	n	−	−	−	n	−	+	n
1177	n	n	n	n	n	−	n	−	+	+	n	−	+	n
1178	n	n	n	n	n	−	n	−	−	n	n	−	+	n
1179	n	n	n	n	n	−	n	+	−	−	n	−	+	n
1180	n	n	n	n	n	−	n	−	−	−	n	−	+	n
1181	n	n	n	n	n	v	n	v	+	n	n	−	+	n
1182	n	n	n	n	n	v	n	+	v	n	n	−	+	n
1183	n	n	n	n	n	−	n	−	−	−	n	−	+	n
1184	n	n	n	n	n	−	n	−	+	+	n	−	+	n
1185	+	+	n	+	−	−	n	−	−	−	n	−	−	n
1186	n	n	n	n	n	n	n	n	n	v	n	−	+	n
1187	n	n	n	n	n	−	n	−	−	−	n	−	+	n
1188	n	n	n	n	n	+	n	v	−	−	n	−	n	n
1189	n	n	n	n	n	+	n	−	−	−	n	−	+	n
1190	n	n	n	n	n	v	n	v	v	+	n	−	+	n
1191	n	n	n	n	n	+	n	+	+	−	n	−	+	n
1192	n	n	n	n	n	+	n	−	+	−	n	−	+	n
1193	n	n	n	n	n	−	n	+	−	−	n	−	+	n
1194	n	n	n	n	n	−	n	−	+	−	n	−	+	n

	Cycloheximide 0.01%	Cycloheximide 0.1%	Growth at 19°C	Growth at 25°C	Growth at 30°C	Growth at 35°C	Growth at 37°C	Growth at 40°C	Growth at 45°C	CoQ (Main component)	Mol% G + C (Ave.)	DBB
Spathaspora												
1141	−	−	+	+	+	+	+	n	−	n	n	−
Sporidiobolus												
1143	+	+	+	+	+	+	−	−	−	10	63.0	+
1144	+	−	+	+	−	−	−	−	−	n	n	+
1145	+	−	+	+	−	−	−	−	−	10	52.8	+
1146	+	+	+	+	+	−	−	−	−	n	n	+
1147	v	−	+	+	+	−	−	−	−	10	52.5	+
1148	+	+	+	+	+	−	−	−	−	10	64.7	+
1149	+	+	+	+	+	+	−	−	−	10	63.5	+
Sporobolomyces												
1151	n	n	+	+	+	n	−	−	−	10	n	+
1152	n	n	+	+	+	n	−	−	−	10	n	+
1153	n	n	+	+	+	+	+	n	n	10	49.6	+
1154	n	n	+	+	+	−	−	−	−	10	59.5	+
1155	n	n	+	+	−	−	−	−	−	10	n	+
1156	n	n	+	+	−	−	−	−	−	10	n	+
1157	n	n	+	+	−	−	−	−	−	10	59.6	+
1158	n	n	+	+	−	−	−	−	−	10	68.0	+
1159	n	n	+	+	−	−	−	−	−	10	59.9	+
1160	n	n	+	+	−	−	−	−	−	10	56.3	+
1161	n	n	n	n	−	−	−	−	−	10	49.9	+
1162	n	n	+	+	−	−	−	−	−	10 (H_2)	55.7	+
1163	n	n	+	+	−	−	−	−	−	10	56.5	+
1164	n	n	+	+	v	−	−	−	−	10	56.0	+
1165	n	n	+	+	−	−	−	−	−	10	51.6	+
1166	n	n	+	−	−	−	−	−	−	10	50.9	+
1167	n	n	+	+	−	−	−	−	−	10	60.9	+
1168	n	n	+	+	−	−	−	−	−	10	58.1	+
1169	n	n	+	+	+	−	−	−	−	n	n	+
1170	n	n	+	+	+	n	−	−	−	10	n	+
1171	n	n	+	+	v	−	−	−	−	10	53.8	+
1172	n	n	+	+	+	−	−	−	−	10	55.6	+
1173	n	n	+	+	−	−	−	−	−	10	67.6	+
1174	n	n	+	+	−	−	−	−	−	10	55.6	+
1175	n	n	+	+	+	−	−	−	−	10	50.5	+
1176	n	n	+	+	−	−	−	−	−	10	62.1	+
1177	n	n	+	+	+	+	−	−	−	10	60.8	+
1178	n	n	+	+	v	−	−	−	−	n	n	+
1179	n	n	+	+	−	−	−	−	−	10 (H_2)	51.7	+
1180	n	n	+	+	+	−	−	−	−	10	61.1	+
1181	n	n	+	+	+	−	−	−	−	n	n	+
1182	n	n	+	+	+	−	−	−	−	10	n	+
1183	n	n	+	+	−	−	−	−	−	10	47.4	+
1184	n	n	+	+	+	+	−	−	−	10	62.3	+
1185	n	n	+	+	−	−	−	−	−	10	45.4	+
1186	n	n	+	+	−	−	−	−	−	10	52.9	+
1187	n	n	+	+	−	−	−	−	−	10	49.5	+
1188	n	n	+	+	+	−	−	−	−	n	n	+
1189	n	n	+	+	+	−	−	−	−	10	51.1	+
1190	n	n	+	+	v	−	−	−	−	n	n	+
1191	n	n	+	+	−	−	−	−	−	10	56.9	+
1192	n	n	+	+	−	−	−	−	−	10	58.0	+
1193	n	n	+	+	−	−	−	−	−	10	68.0	+
1194	n	n	+	+	+	−	−	−	−	10	n	+

Symbols: +, positive or weak; −, negative; v, variable (+/−, w/−); n, no data.

Ln. no.	Species	Fermentation: Glucose	Galactose	Sucrose	Maltose	Lactose	Raffinose	Trehalose	Growth reactions and other characteristics: Glucose	Inulin	Sucrose	Raffinose	Melibiose	Galactose	Lactose	Trehalose	Maltose	Melezitose	Methyl-α-D-glucoside	Soluble Starch	Cellobiose	Salicin	L-Sorbose	L-Rhamnose	D-Xylose	L-Arabinose	D-Arabinose	D-Ribose	Methanol	Ethanol	Glycerol	Erythritol	Ribitol	Galactitol	D-Mannitol	D-Glucitol
	Sporobolomyces (*cont'd*)																																			
1195	*S. syzygii*	−	−	−	−	−	−	−	+	−	+	+	+	+	−	+	+	+	+	+	+	+	+	+	+	+	−	−	−	−	+	−	+	−	+	+
1196	*S. taupoensis*	−	−	−	−	−	−	−	+	−	+	+	−	−	−	+	+	−	−	+	+	+	−	−	−	−	−	−	−	−	−	−	+	−	+	+
1197	*S. tsugae*	−	−	−	−	−	−	−	+	−	+	−	−	−	+	+	+	+	v	−	+	+	+	−	+	−	v	−	−	+	+	−	v	−	+	+
1198	*S. vermiculatus*	−	−	−	−	−	−	−	+	−	+	−	−	+	−	+	−	+	−	+	+	−	+	−	+	+	+	+	−	−	+	−	+	−	+	+
1199	*S. xanthus*	−	−	−	−	−	−	−	+	−	+	+	−	+	+	+	+	−	+	+	+	−	−	−	−	+	−	−	−	−	−	−	+	−	+	+
1200	*S. yunnanensis*	−	−	−	−	−	−	−	+	−	+	−	−	+	−	+	+	+	−	+	+	+	+	−	+	+	+	−	−	+	+	−	+	−	+	−
1201	***Sporopachydermia***																																			
1202	*S. cereana*	−	−	−	−	−	−	−	+	−	−	−	−	−	−	+	−	−	−	−	+	+	+	−	+	−	v	v	−	+	+	+	+	−	+	+
1203	*S. lactativora*	−	−	−	−	−	−	−	+	−	−	−	−	−	−	−	−	−	−	−	−	−	+	−	+	−	−	−	−	+	+	−	v	−	v	+
1204	*S. quercuum*	+	−	−	−	−	−	−	+	−	−	−	−	−	−	−	−	−	−	−	−	−	+	−	+	−	−	−	−	+	+	−	−	−	−	+
1205	***Starmera***																																			
1206	*S. amethionina*	−	−	−	−	−	−	−	+	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	+	−	−	−	−	+	+	−	−	−	−	−
1207	*S. caribaea*	+	−	−	−	−	−	−	+	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	v	−	−	−	−	+	+	−	−	−	+	−
1208	*S. dryadoides*	−	−	−	−	−	−	−	+	−	−	−	−	−	−	−	−	−	−	−	+	−	−	−	v	−	−	−	−	+	+	−	−	−	+	+
1209	*S. pachycereana*	−	−	−	−	−	−	−	+	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	+	+	−	−	−	+	−
1210	*S. quercuum*	+	−	−	−	−	−	−	+	−	−	−	−	−	−	−	−	−	−	−	+	+	−	−	−	−	−	−	−	+	+	−	−	−	+	+
1211	***Starmerella***																																			
1212	*S. bombicola*	+	−	+	−	−	v	−	+	−	v	v	−	v	−	−	−	−	−	−	−	−	v	−	−	−	−	−	−	+	+	−	−	−	+	v
1213	*S. meliponinorum*	+	−	v	v	−	v	−	+	−	+	+	−	+	−	−	+	v	v	−	−	−	v	−	−	−	−	+	−	−	+	−	−	−	+	+
1214	***Sterigmatomyces***																																			
1215	*S. elviae*	−	−	−	−	−	−	−	+	−	+	+	−	−	+	+	−	−	−	−	+	+	+	+	+	+	+	+	−	+	+	+	+	+	+	+
1216	*S. halophilus*	−	−	−	−	−	−	−	+	−	−	−	−	v	v	+	−	−	−	−	v	+	v	−	+	v	+	+	−	+	+	+	+	v	+	+
1217	***Sugiyamaella***																																			
1218	*S. americana*	+	−	−	−	−	−	v	+	−	−	−	−	+	−	+	−	−	−	−	+	+	+	−	+	+	+	+	−	+	+	+	+	−	+	+
1219	*S. chiloensis*	−	−	−	−	−	−	−	+	−	+	+	+	+	v	+	v	+	+	−	+	+	+	+	+	+	+	+	−	+	+	+	+	−	+	+
1220	*S. japonica*	+	+	−	−	−	−	+	+	−	−	−	−	+	v	+	−	−	−	−	+	+	+	−	+	+	+	v	−	+	+	+	+	v	+	+
1221	*S. smithiae*	−	−	−	−	−	−	−	+	−	+	+	+	+	+	+	+	+	+	v	+	+	+	+	+	+	+	+	−	+	+	+	+	+	+	+
1222	***Sympodiomycopsis***																																			
1223	*S. paphiopedili*	−	−	−	−	−	−	−	+	−	+	+	+	+	+	+	+	+	+	−	+	−	+	−	+	+	+	+	−	+	+	+	+	−	+	+
1224	***Taphrina***																																			
1225	*T. alni*	−	−	−	−	−	−	−	+	−	+	−	−	−	−	−	−	+	−	+	+	v	−	−	+	−	v	−	−	−	+	−	−	−	+	+
1226	*T. americana*	−	−	−	−	−	−	−	+	+	+	+	−	−	−	−	−	−	−	+	+	+	−	−	−	−	−	−	−	+	+	−	−	−	−	−
1227	*T. betulina*	−	−	−	−	−	−	−	+	v	+	+	−	−	−	+	+	+	−	+	+	+	−	−	v	+	v	v	−	+	+	−	−	−	+	−
1228	*T. caerulescens*	−	−	−	−	−	−	−	+	−	−	−	−	−	−	+	−	−	−	+	+	+	v	−	+	−	−	−	−	−	v	−	v	−	+	v
1229	*T. carpini*	−	−	−	−	−	−	−	+	+	+	−	−	−	−	+	+	+	−	+	+	+	−	−	+	+	+	+	−	+	+	−	+	−	+	+
1230	*T. communis*	−	−	−	−	−	−	−	+	−	−	−	−	−	−	+	−	−	−	+	v	v	v	−	+	−	v	v	−	v	+	−	v	−	+	+
1231	*T. confusa*	−	−	−	−	−	−	−	+	−	+	−	−	−	−	−	−	−	−	+	+	+	−	−	+	−	−	−	−	−	+	−	−	−	+	+
1232	*T. dearnessii*	−	−	−	−	−	−	−	+	v	+	+	−	−	−	+	−	−	−	+	+	v	−	−	v	+	−	−	−	−	+	−	−	−	+	−
1233	*T. deformans*	−	−	−	−	−	−	−	+	−	v	−	−	−	−	v	−	−	−	v	+	+	v	−	+	−	−	−	−	v	v	−	−	−	+	+
1234	*T. epiphylla*	−	−	−	−	−	−	−	+	+	+	+	−	+	−	−	−	+	−	+	+	+	−	−	+	−	−	+	−	−	+	−	−	−	−	+
1235	*T. flavorubra*	−	−	−	−	−	−	−	+	−	+	−	−	−	−	+	−	−	−	+	+	+	−	−	+	−	−	−	−	+	+	−	+	−	+	+
1236	*T. johansonii*	−	−	−	−	−	−	−	+	−	−	−	−	−	−	+	−	−	−	+	+	−	−	−	−	−	−	−	−	−	+	−	−	−	+	−
1237	*T. letifera*	−	−	−	−	−	−	−	+	+	+	+	−	+	−	+	−	−	−	−	+	+	−	−	+	+	−	−	−	−	+	−	−	−	+	−
1238	*T. mirabilis*	−	−	−	−	−	−	−	+	+	−	−	−	+	−	+	+	−	−	+	+	+	−	−	+	−	+	−	−	+	+	−	−	−	+	+
1239	*T. padi*	−	−	−	−	−	−	−	+	−	+	−	−	−	−	+	−	−	−	+	+	+	−	−	+	−	+	−	−	+	+	−	−	−	+	+
1240	*T. populina*	−	−	−	−	−	−	−	+	−	−	−	−	−	−	−	−	−	−	+	+	+	−	−	−	−	v	−	−	−	+	−	−	−	+	−
1241	*T. populi-salicis*	−	−	−	−	−	−	−	+	+	−	−	−	−	−	+	−	−	−	+	+	+	−	−	−	−	−	−	−	−	+	−	−	−	+	−
1242	*T. pruni*	−	−	−	−	−	−	−	+	+	+	−	−	−	−	+	−	−	−	+	+	−	−	−	+	−	−	−	−	−	+	−	−	−	+	+
1243	*T. pruni-subcordatae*	−	−	−	−	−	−	−	+	+	+	+	−	−	−	−	−	−	−	+	+	+	−	−	+	−	−	−	−	+	+	−	−	−	+	+
1244	*T. robinsoniana*	−	−	−	−	−	−	−	+	−	+	−	−	−	−	−	+	v	v	v	+	+	−	−	+	+	−	−	−	v	+	−	v	−	+	−
1245	*T. sacchari*	−	−	−	−	−	−	−	+	+	+	+	−	+	−	+	+	−	−	+	+	+	−	−	+	+	−	−	−	+	+	−	−	−	+	+
1246	*T. sadebeckii*	−	−	−	−	−	−	−	+	+	+	v	−	−	−	−	−	+	−	+	+	+	−	−	+	−	−	−	−	v	+	−	−	−	+	v
1247	*T. tormentillae*	−	−	−	−	−	−	−	+	+	+	+	−	+	−	+	−	−	−	+	+	+	v	−	+	+	+	−	−	+	+	−	−	−	v	+
1248	*T. tosquinetii*	−	−	−	−	−	−	−	+	−	+	−	−	−	−	+	+	−	−	+	+	+	−	−	+	+	−	−	−	v	+	−	−	−	+	+

Symbols: +, positive or weak; −, negative; v, variable (+/−, w/−); n, no data.

Growth reactions and other characteristics

	myo-Inositol	DL-Lactate	Succinate	Citrate	D-Gluconate	D-Glucosamine	*N*-Acetyl-D-glucosamine	Hexadecane	Nitrate	Nitrite	Vitamin-free	2-Keto-D-gluconate	5-Keto-D-gluconate	Saccharate	Xylitol	L-Arabinitol	Arbutin	Propane 1,2 diol	Butane 2,3 diol	Cadaverine	Creatinine	L-Lysine	Ethylamine	50% Glucose	10% NaCl/5% glucose	Starch formation	Urease	Gelatin liquefaction	Cycloheximide 0.01%	Cycloheximide 0.1%	Growth at 19°C	Growth at 25°C	Growth at 30°C	Growth at 35°C	Growth at 37°C	Growth at 40°C	Growth at 45°C	CoQ (Main component)	Mol% G + C (Ave.)	DBB
Sporobolomyces (*cont'd*)																																								
1195	−	+	+	+	n	n	n	n	−	−	−	+	+	n	n	n	n	n	n	−	n	+	−	−	n	−	+	n	n	n	+	+	+	−	−	−	−	10 (H_2)	48.9	+
1196	−	−	+	−	+	−	n	n	+	+	−	−	−	n	n	n	n	n	n	−	n	−	−	−	n	−	+	n	n	n	+	+	−	−	−	−	−	10	60.0	+
1197	−	+	+	+	+	−	n	n	+	+	−	+	n	n	n	n	n	n	n	−	n	v	+	−	n	−	+	n	n	n	+	+	−	−	−	−	−	10	51.0	+
1198	−	−	+	−	−	−	−	−	−	−	−	−	−	n	n	n	n	n	n	−	n	+	−	−	n	−	+	n	n	n	+	+	v	v	v	n	n	10	51.8	+
1199	−	−	+	+	−	−	n	n	+	+	−	−	n	n	n	n	n	n	n	+	n	−	+	−	n	−	+	n	n	n	+	+	−	−	−	−	−	10	59.5	+
1200	−	−	+	+	+	n	n	n	+	+	−	+	+	n	n	n	n	n	n	−	n	−	−	−	n	−	+	n	n	n	+	+	n	−	−	−	−	10 (H_2)	50.0	+
Sporopachydermia																																								
1202	+	−	−	−	−	−	−	−	−	−	−	−	n	n	+	n	n	n	n	+	n	+	+	−	n	−	n	−	+	−	+	+	+	+	+	n	n	9	49.6	−
1203	+	+	v	−	−	−	−	−	−	−	−	−	n	n	+	n	n	n	n	+	n	+	+	−	n	−	n	−	+	+	+	+	+	+	+	n	n	9	46.2	−
1204	+	+	+	−	−	−	−	−	−	−	−	−	n	n	+	n	n	n	n	+	n	+	+	−	n	−	n	−	+	+	+	+	+	+	+	n	n	9	37.8	+
Starmera																																								
1206	−	+	+	−	+	−	−	−	−	n	−	v	−	−	n	n	n	n	n	n	n	n	n	n	−	−	n	−	n	n	+	+	+	+	+	n	n	7	33.1	−
1207	−	+	+	−	+	−	−	−	−	n	−	−	−	−	n	n	n	n	n	n	n	n	n	n	−	−	n	−	n	n	+	+	+	n	v	n	n	7	34.2	−
1208	−	+	+	+	+	−	−	−	+	n	+	−	−	−	n	n	n	n	n	n	n	n	n	n	−	−	n	−	n	n	+	+	+	n	v	n	n	n	31.4	−
1209	−	+	+	−	+	−	−	−	−	n	−	v	−	−	n	n	n	n	n	n	n	n	n	n	−	−	n	−	n	n	+	+	+	+	+	n	n	7	33.2	−
1210	−	+	+	+	−	−	−	−	−	n	−	−	−	−	n	n	n	n	n	n	n	n	n	n	−	−	n	−	n	n	+	+	+	+	+	n	n	7	41.3	−
Starmerella																																								
1212	−	−	v	v	v	−	−	−	−	−	−	−	n	n	−	n	n	n	n	+	n	+	+	+	n	−	n	v	v	−	+	+	+	n	v	n	n	9	49.8	−
1213	−	−	−	−	−	−	−	−	+	+	+	v	n	n	v	n	n	n	n	+	n	+	−	+	n	−	n	−	−	−	+	+	+	n	−	−	−	n	n	−
Sterigmatomyces																																								
1215	−	v	+	+	+	−	v	−	−	−	−	+	+	n	+	n	n	n	n	+	−	+	+	+	n	−	+	n	n	n	+	+	+	+	+	n	−	9	52.0	+
1216	−	−	+	+	−	−	v	−	v	n	−	+	+	n	+	n	n	n	n	−	−	+	+	+	n	−	+	n	n	n	+	+	−	−	−	−	−	9	n	+
Sugiyamaella																																								
1218	−	+	+	−	+	+	+	−	−	n	−	+	+	−	n	n	n	n	n	+	n	n	n	n	−	−	n	−	+	+	+	+	+	+	+	n	n	n	n	−
1219	+	v	+	+	+	+	+	+	+	n	+	+	+	−	n	n	n	n	n	+	n	n	n	n	−	−	n	−	+	+	+	+	+	n	−	−	−	n	43.9	−
1220	−	v	+	+	+	+	+	−	−	n	−	+	+	−	n	n	n	n	n	+	n	n	n	n	v	−	n	−	+	+	+	+	+	n	v	n	n	n	n	−
1221	+	v	+	+	+	+	n	n	+	n	+	+	+	−	n	n	n	n	n	+	n	n	n	n	+	−	n	−	+	+	+	+	+	+	+	n	n	9	47.2	−
Sympodiomycopsis																																								
1223	+	−	+	+	+	−	n	n	+	+	+	+	n	−	+	+	−	+	−	−	−	−	+	+	+	−	n	n	n	n	+	+	+	n	−	−	−	10	56.3	+
Taphrina																																								
1225	−	−	+	+	−	−	n	n	+	−	w	n	n	−	v	n	n	n	n	+	n	−	−	n	n	+	+	n	−	−	+	v	−	−	−	−	−	10	n	−
1226	−	−	+	+	−	−	n	n	+	−	+	n	n	−	−	n	n	n	n	+	n	+	+	n	n	+	+	n	−	−	+	+	−	−	−	−	−	n	n	−
1227	−	−	+	+	+	−	n	n	+	−	v	n	n	−	+	n	n	n	n	+	n	v	−	n	n	+	+	n	−	−	+	v	−	−	−	−	−	n	n	−
1228	−	−	+	+	−	+	n	n	+	v	v	n	n	−	v	n	n	n	n	+	n	v	−	n	n	v	+	n	−	−	+	+	−	−	−	−	−	10	41.0	−
1229	+	+	+	+	+	−	n	n	+	+	+	n	n	−	+	n	n	n	n	+	n	+	−	n	n	+	+	n	−	−	+	+	−	−	−	−	−	n	49.9	−
1230	−	−	+	−	−	v	n	n	+	v	v	n	n	v	+	n	n	n	n	+	n	−	−	n	n	+	+	n	−	−	+	+	−	−	−	−	−	n	49.1	−
1231	−	−	+	+	−	−	n	n	+	+	−	n	n	−	+	n	n	n	n	+	n	−	−	n	n	+	+	n	−	−	+	+	−	−	−	−	−	n	n	−
1232	−	−	+	−	−	v	n	n	+	v	+	n	n	−	+	n	n	n	n	+	n	−	v	n	n	+	+	n	−	−	+	+	−	−	−	−	−	n	n	−
1233	−	−	v	−	−	−	n	n	+	v	v	n	n	v	v	n	n	n	n	v	n	−	−	n	n	v	+	n	−	−	+	+	−	−	−	−	−	10	49.5	−
1234	−	−	+	+	−	−	n	n	+	−	+	n	n	−	+	n	n	n	n	+	n	+	−	n	n	+	+	n	−	−	+	+	−	−	−	−	−	n	n	−
1235	−	−	+	−	−	−	n	n	+	+	+	n	n	−	+	n	n	n	n	+	n	−	−	n	n	+	+	n	−	−	+	+	−	−	−	−	−	10	47.7	−
1236	−	−	+	+	−	+	n	n	+	−	+	n	n	−	+	n	n	n	n	+	n	−	−	n	n	+	+	n	−	−	+	+	−	−	−	−	−	n	n	−
1237	−	−	+	−	−	−	n	n	+	−	−	n	n	−	+	n	n	n	n	+	n	−	+	n	n	+	+	n	−	−	+	−	−	−	−	−	−	n	n	−
1238	−	−	+	−	−	−	n	n	+	+	+	n	n	−	+	n	n	n	n	+	n	−	−	n	n	+	+	n	−	−	+	+	−	−	−	−	−	n	50.2	−
1239	−	−	+	−	−	−	n	n	+	+	−	n	n	−	+	n	n	n	n	+	n	−	+	n	n	+	+	n	−	−	+	+	−	−	−	−	−	n	n	−
1240	−	−	+	−	−	v	n	n	+	+	+	n	n	−	v	n	n	n	n	v	n	v	−	n	n	+	+	n	−	−	+	+	−	−	−	−	−	10	n	−
1241	−	−	+	−	−	−	n	n	+	−	+	n	n	−	−	n	n	n	n	+	n	+	−	n	n	+	+	n	−	−	+	v	−	−	−	−	−	n	n	−
1242	−	−	+	−	−	−	n	n	+	+	−	n	n	−	+	n	n	n	n	−	n	−	−	n	n	+	+	n	−	−	+	v	−	−	−	−	−	n	48.5	−
1243	−	−	+	−	−	−	n	n	+	−	+	n	n	−	+	n	n	n	n	+	n	−	−	n	n	+	+	n	−	−	+	v	−	−	−	−	−	n	51.2	−
1244	−	v	+	+	−	−	n	n	+	−	+	n	n	−	v	n	n	n	n	+	n	+	v	n	n	+	+	n	−	−	+	v	−	−	−	−	−	n	n	−
1245	−	−	+	+	−	−	n	n	+	−	+	n	n	−	+	n	n	n	n	+	n	−	+	n	n	+	+	n	−	−	+	+	−	−	−	−	−	n	n	−
1246	−	−	+	+	−	−	n	n	+	−	−	n	n	−	+	n	n	n	n	+	n	v	−	n	n	+	+	n	−	−	+	+	−	−	−	−	−	n	n	−
1247	−	−	+	+	+	v	n	n	+	+	−	n	n	−	+	n	n	n	n	+	n	+	+	n	n	+	+	n	−	−	+	+	−	−	−	−	−	10	41.0	−
1248	−	−	+	−	−	−	n	n	+	−	+	n	n	−	+	n	n	n	n	+	n	+	−	n	n	+	+	n	−	−	+	+	−	−	−	−	−	10	n	−

Symbols: +, positive or weak; −, negative; v, variable (+/−, w/−); n, no data.

Ln. no.	Species	Fermentation: Glucose	Galactose	Sucrose	Maltose	Lactose	Raffinose	Trehalose	Growth reactions and other characteristics: Glucose	Inulin	Sucrose	Raffinose	Melibiose	Galactose	Lactose	Trehalose	Maltose	Melezitose	Methyl-α-D-glucoside	Soluble Starch	Cellobiose	Salicin	L-Sorbose	L-Rhamnose	D-Xylose	L-Arabinose	D-Arabinose	D-Ribose	Methanol	Ethanol	Glycerol	Erythritol	Ribitol	Galactitol	D-Mannitol	D-Glucitol
	Taphrina (*cont'd*)																																			
1249	*T. ulmi*	−	−	−	−	−	−	−	+	−	+	−	−	−	−	−	−	+	−	+	+	−	−	−	+	−	+	−	−	−	−	−	+	−	+	+
1250	*T. vestergrenii*	−	−	−	−	−	−	−	+	+	+	+	−	+	−	+	−	−	−	+	+	−	−	−	−	−	−	−	−	−	−	−	−	−	+	−
1251	*T. virginica*	−	−	−	−	−	−	−	+	+	+	+	−	+	−	+	+	+	+	+	+	+	−	−	+	+	+	+	−	+	+	−	+	−	+	+
1252	*T. wiesneri*	−	−	−	−	−	−	−	+	v	+	v	−	−	−	+	−	−	−	+	+	+	v	−	+	−	−	−	−	+	+	−	+	−	+	+
1253	***Tausonia***																																			
1254	*T. pamirica*	−	−	−	−	−	−	−	+	−	+	+	+	+	−	+	+	+	−	+	+	+	−	−	+	+	−	−	−	+	−	+	+	−	+	+
1255	***Tetrapisispora***																																			
1256	*T. arboricola*	+	+	−	−	−	−	−	+	−	−	−	−	+	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−
1257	*T. blattae*	+	+	−	−	−	−	−	+	−	−	−	−	+	−	−	−	−	−	−	−	−	−	−	−	−	−	v	−	v	+	−	−	−	−	−
1258	*T. fleetii*	+	−	−	−	−	−	−	+	−	−	−	−	+	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−
1259	*T. iriomotensis*	+	+	−	−	−	−	−	+	−	−	−	−	+	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−
1260	*T. namnaonensis*	+	+	−	−	−	−	−	+	−	−	−	−	+	−	+	−	−	−	−	−	−	−	−	−	−	−	−	−	−	+	−	−	−	−	−
1261	*T. nanseiensis*	+	+	−	−	−	−	−	+	−	−	−	−	+	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	+	−	−	−	−	−
1262	*T. phaffii*	+	+	−	−	−	−	−	+	−	−	−	−	+	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	+	+	−	−	−	−	−
1263	***Tilletiaria***																																			
1264	*T. anomala*	−	−	−	−	−	−	−	+	+	+	+	+	−	+	+	−	−	−	+	+	−	−	−	−	+	−	−	−	−	+	−	−	−	+	−
1265	***Tilletiopsis***																																			
1266	*T. albescens*	−	−	−	−	−	−	−	+	+	+	+	+	+	+	+	+	+	+	+	+	v	+	v	+	+	+	+	−	v	+	+	+	−	+	+
1267	*T. cremea*	−	−	−	−	−	−	−	+	−	+	+	+	+	−	+	+	+	−	+	+	−	−	−	+	+	+	+	−	+	+	+	−	−	+	+
1268	*T. derxii*	−	−	−	−	−	−	−	+	+	+	+	+	+	−	+	+	−	−	+	+	−	+	−	+	+	+	+	−	−	+	+	+	−	+	+
1269	*T. flava*	−	−	−	−	−	−	−	+	+	+	+	+	−	−	+	+	−	−	+	+	−	+	−	+	+	+	+	−	−	+	−	+	−	+	+
1270	*T. fulvescens*	−	−	−	−	−	−	−	+	+	+	+	+	+	+	+	+	+	−	+	+	−	v	−	+	+	+	+	−	v	+	+	+	−	+	+
1271	*T. lilacina*	−	−	−	−	−	−	−	+	−	+	+	+	+	−	+	+	+	+	+	+	−	−	−	+	+	+	+	−	−	+	+	+	−	+	+
1272	*T. minor*	−	−	−	−	−	−	−	+	+	+	+	+	+	+	+	+	+	v	+	+	−	v	−	+	+	+	+	−	v	+	v	+	−	+	+
1273	*T. oryzicola*	−	−	−	−	−	−	−	+	+	+	+	−	−	−	+	+	−	−	+	+	−	−	−	+	+	+	+	−	−	+	−	−	−	+	+
1274	*T. pallescens*	−	−	−	−	−	−	−	+	v	+	+	+	v	v	+	+	+	v	+	+	v	+	−	v	+	v	v	−	v	v	+	+	−	+	+
1275	*T. penniseti*	−	−	−	−	−	−	−	+	−	+	+	−	−	+	+	+	+	−	+	+	−	−	+	+	+	+	v	−	−	v	+	−	−	+	+
1276	*T. washingtonensis*	−	−	−	−	−	−	−	+	−	+	+	v	v	−	+	+	+	v	+	v	v	−	−	+	+	+	+	−	v	+	+	v	−	+	+
1277	***Torulaspora***																																			
1278	*T. delbrueckii*	+	v	v	v	−	v	v	+	v	v	v	−	v	−	+	v	v	v	−	−	−	v	−	v	−	−	−	−	+	v	−	v	−	+	v
1279	*T. franciscae*	+	+	+	+	−	+	−	+	+	+	+	−	+	−	+	+	−	+	−	−	−	−	−	−	−	−	−	−	v	−	−	−	−	+	−
1280	*T. globosa*	+	−	+	−	−	+	−	+	v	+	+	−	−	−	v	−	−	−	−	−	−	−	−	−	−	−	−	−	+	v	−	−	−	+	−
1281	*T. maleeae*	+	v	+	+	v	+	−	+	v	+	+	v	v	−	v	+	+	+	v	−	−	−	−	−	−	−	−	−	v	v	−	−	−	v	v
1282	*T. microellipsoides*	+	+	+	−	−	+	−	+	+	+	+	+	+	−	+	−	−	−	−	−	−	v	−	−	−	−	−	−	+	v	−	−	−	+	v
1283	*T. pretoriensis*	+	v	+	+	−	v	v	+	+	+	+	−	+	−	+	+	v	+	−	−	−	−	−	−	−	−	−	−	+	v	−	−	−	+	v
1284	***Tremella***																																			
1285	*T. aurantia*	−	−	−	−	−	−	−	+	−	+	+	−	+	+	+	+	+	+	+	+	+	v	+	+	+	+	+	−	+	+	−	+	v	+	+
1286	*T. brasiliensis*	−	−	−	−	−	−	−	+	−	−	−	−	+	+	+	+	−	−	−	+	+	+	−	+	v	+	+	−	−	−	+	+	−	+	+
1287	*T. cinnabarina*	−	−	−	−	−	−	−	+	−	+	−	−	+	+	+	+	+	+	−	+	+	+	−	+	+	+	+	−	+	+	+	+	+	+	+
1288	*T. coalescens*	−	−	−	−	−	−	−	+	−	−	−	−	−	−	+	−	+	−	−	−	−	+	−	+	−	+	−	−	−	−	−	+	−	+	+
1289	*T. encephala*	−	−	−	−	−	−	−	+	−	+	v	v	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	−	+	+	−	+	+	+	+
1290	*T. flava*	−	−	−	−	−	−	−	+	−	+	−	−	+	+	+	+	+	+	+	+	+	+	−	+	+	+	+	−	−	+	+	+	+	+	+
1291	*T. foliacea*	−	−	−	−	−	−	−	+	−	−	−	−	v	−	+	+	−	−	−	+	−	v	+	+	+	+	v	+	+	+	v	+	v	+	+
1292	*T. fuciformis*	−	−	−	−	−	−	−	+	−	+	+	+	+	+	+	+	+	+	+	+	+	+	−	+	+	+	+	−	+	+	+	+	+	+	+
1293	*T. giraffa*	−	−	−	−	−	−	−	+	−	−	−	−	+	+	+	−	−	−	−	+	+	+	+	+	+	−	−	−	−	−	−	−	−	−	−
1294	*T. globispora*	−	−	−	−	−	−	−	+	−	+	−	−	+	−	+	+	+	+	+	+	+	+	−	+	+	+	+	−	+	+	+	+	+	+	+
1295	*T. indecorata*	−	−	−	−	−	−	−	+	−	+	v	v	+	v	+	+	+	+	v	+	+	+	+	+	+	+	+	−	+	v	−	+	+	+	+
1296	*T. mesenterica*	−	−	−	−	−	−	−	+	−	−	−	−	−	+	+	−	−	−	−	+	+	+	−	+	−	+	−	−	+	−	+	+	−	+	+
1297	*T. moriformis*	−	−	−	−	−	−	−	+	−	+	+	−	+	+	+	+	+	+	−	+	+	−	+	+	+	+	+	−	−	+	−	+	+	+	+
1298	*T. neofoliacea*	−	−	−	−	−	−	−	+	−	−	−	v	+	−	+	−	−	−	v	+	−	v	+	+	+	+	+	−	v	−	−	+	+	+	+
1299	*T. nivalis*	−	−	−	−	−	−	−	+	−	+	+	+	+	+	+	+	+	−	+	+	+	+	−	+	+	+	+	−	−	−	+	+	+	+	+
1300	*T. resupinata*	−	−	−	−	−	−	−	+	−	−	−	−	−	−	+	−	−	−	+	−	−	+	−	+	−	+	+	−	−	−	+	+	−	+	+
1301	*T. taiwanensis*	−	−	−	−	−	−	−	+	−	−	−	−	−	−	+	−	−	−	−	−	−	−	−	+	−	+	−	−	+	−	−	+	−	+	+
1302	*T. tropica*	−	−	−	−	−	−	−	+	−	−	−	−	−	−	+	−	−	−	−	+	+	+	−	+	−	+	−	−	−	−	−	+	−	+	+

Symbols: +, positive or weak; −, negative; v, variable (+/−, w/−); n, no data.

Growth reactions and other characteristics

	myo-Inositol	DL-Lactate	Succinate	Citrate	D-Gluconate	D-Glucosamine	*N*-Acetyl-D-glucosamine	Hexadecane	Nitrate	Nitrite	Vitamin-free	2-Keto-D-gluconate	5-Keto-D-gluconate	Saccharate	Xylitol	L-Arabinitol	Arbutin	Propane 1,2 diol	Butane 2,3 diol	Cadaverine	Creatinine	L-Lysine	Ethylamine	50% Glucose	10% NaCl/5% glucose	Starch formation	Urease	Gelatin liquefaction	Cycloheximide 0.01%	Cycloheximide 0.1%	Growth at 19°C	Growth at 25°C	Growth at 30°C	Growth at 35°C	Growth at 37°C	Growth at 40°C	Growth at 45°C	CoQ (Main component)	Mol% G + C (Ave.)	DBB
Taphrina (*cont'd*)																																								
1249	−	−	+	+	−	−	n	n	+	−	−	n	n	−	−	n	n	n	n	−	n	−	+	n	n	+	+	n	−	−	+	+	−	−	−	−	−	n	45.0	−
1250	−	−	+	−	−	−	n	n	+	+	+	n	n	−	−	n	n	n	n	+	n	−	−	n	n	+	+	n	−	−	+	−	−	−	−	−	−	10	n	−
1251	+	−	+	+	−	+	n	n	+	+	+	n	n	−	+	n	n	n	n	+	n	−	−	n	n	+	+	n	−	−	+	+	−	−	−	−	−	10	50.0	−
1252	−	−	+	+	v	v	n	n	+	v	+	n	n	−	v	n	n	n	n	+	n	−	v	n	n	+	v	n	−	−	+	+	−	−	−	−	−	10	48.8	−
Tausonia																																								
1254	+	−	+	+	+	−	n	n	+	+	−	n	n	n	−	n	n	n	n	−	−	−	−	n	n	+	n	n	−	−	+	−	−	−	−	−	−	n	63.6	+
Tetrapisispora																																								
1256	−	−	−	−	−	−	−	−	−	−	−	−	n	n	−	n	n	n	n	−	n	−	−	−	n	−	n	−	−	−	+	+	+	n	−	−	−	6	31.0	−
1257	−	−	−	−	−	−	−	−	−	−	−	+	n	n	−	n	n	n	n	−	n	−	−	−	n	−	n	−	−	−	+	+	+	n	−	−	−	6	34.2	−
1258	−	−	−	−	+	−	−	−	−	−	−	−	n	n	−	n	n	n	n	−	n	−	−	−	n	−	n	−	+	−	+	+	+	+	+	n	n	n	n	−
1259	−	−	−	−	+	−	−	−	−	−	−	−	n	n	−	n	n	n	n	−	n	−	−	−	n	−	n	−	−	−	+	+	+	n	−	−	−	6	32.0	−
1260	−	−	−	−	+	−	−	−	−	−	n	n	n	n	n	n	n	n	n	−	n	−	−	−	n	−	n	n	−	−	+	+	+	n	−	−	−	6	36.7	−
1261	−	−	−	−	+	−	−	−	−	−	−	−	n	n	−	n	n	n	n	−	n	−	−	−	n	−	n	−	+	−	+	+	+	n	−	−	−	6	30.0	−
1262	−	−	−	−	+	−	−	−	−	−	−	−	n	n	−	n	n	n	n	−	n	−	−	−	n	−	n	−	−	−	+	+	+	n	−	−	−	6	35.3	−
Tilletiaria																																								
1264	−	−	+	−	−	−	n	n	−	+	+	−	n	n	n	n	n	n	n	n	n	n	n	−	n	−	+	n	n	n	+	+	+	−	−	−	−	10	62.9	+
Tilletiopsis																																								
1266	+	+	+	+	+	−	n	n	+	+	+	v	n	n	n	n	n	n	n	n	n	n	n	−	n	−	+	n	n	n	+	+	−	−	−	−	−	10	56.7	+
1267	−	+	+	+	+	−	n	n	+	+	−	−	n	n	n	n	n	n	n	n	n	n	n	−	n	−	+	n	n	n	+	+	v	−	−	−	−	10	66.8	+
1268	−	−	+	−	−	−	n	v	v	−	−	−	n	n	n	n	n	n	n	n	n	n	n	−	n	−	+	n	n	n	+	+	+	−	−	−	−	10	61.2	+
1269	−	+	+	+	−	−	n	n	+	+	−	−	n	n	n	n	n	n	n	n	n	n	n	−	n	−	+	n	n	n	+	+	+	−	−	−	−	10	63.2	+
1270	−	v	+	+	v	−	n	n	+	+	−	+	n	n	n	n	n	n	n	n	n	n	n	−	n	−	+	n	n	n	+	+	+	−	−	−	−	10	67.1	+
1271	−	+	+	+	+	−	n	n	+	+	−	−	n	n	n	n	n	n	n	n	n	n	n	−	n	−	+	n	n	n	+	+	v	−	−	−	−	10	67.5	+
1272	−	+	+	+	v	−	n	n	+	v	−	v	n	n	n	n	n	n	n	n	n	n	n	−	n	−	+	n	n	n	+	+	v	−	−	−	−	10	56.0	+
1273	−	+	+	−	−	−	n	n	+	−	−	−	n	n	n	n	n	n	n	n	n	n	n	−	n	−	+	n	n	n	+	+	+	−	−	−	−	10	61.5	+
1274	v	v	+	v	v	−	n	n	+	v	+	v	n	n	n	n	n	n	n	n	n	n	n	−	n	−	+	n	n	n	+	+	v	−	−	−	−	10	43.7	+
1275	−	−	+	+	−	−	n	+	+	−	−	+	n	n	n	n	n	n	n	n	n	n	n	−	n	−	+	n	n	n	+	+	+	−	−	−	−	10	61.5	+
1276	−	+	+	+	+	−	n	n	+	+	−	−	n	n	n	n	n	n	n	n	n	n	n	−	n	−	+	n	n	n	+	+	v	−	−	−	−	10	68.2	+
Torulaspora																																								
1278	−	v	v	−	v	−	−	−	−	n	v	+	−	−	n	n	n	n	n	−	n	n	n	n	+	−	n	−	−	−	+	+	+	n	v	n	n	6	43.4	−
1279	−	+	−	−	−	−	−	−	−	n	+	+	−	−	n	n	n	n	n	−	n	n	n	n	+	−	n	−	−	−	+	+	+	+	+	n	n	6	46.0	−
1280	−	+	−	−	v	−	−	−	−	n	+	+	−	−	n	n	n	n	n	−	n	n	n	n	v	−	n	−	+	−	+	+	+	+	+	n	n	6	47.3	−
1281	−	v	−	−	v	−	−	−	−	n	+	+	−	n	n	n	n	n	n	−	n	n	n	n	+	n	n	n	−	−	+	+	+	n	v	n	n	6	44.0	−
1282	−	+	v	−	+	−	−	−	−	n	−	+	−	−	n	n	n	n	n	−	n	n	n	n	−	−	n	−	+	−	+	+	+	n	−	−	−	6	40.4	−
1283	−	+	−	−	v	−	−	−	−	n	−	+	−	−	n	n	n	n	n	−	n	n	n	n	v	−	n	−	−	−	+	+	+	+	+	n	n	6	46.4	−
Tremella																																								
1285	+	+	+	v	+	+	n	n	−	−	−	+	n	n	n	n	n	n	n	n	n	n	n	v	n	+	+	n	n	n	+	+	−	−	−	−	−	10	52.8	+
1286	−	−	+	v	−	+	n	n	−	−	−	−	n	n	n	n	n	n	n	n	n	n	n	−	n	+	+	n	n	n	+	+	−	−	−	−	−	10	56.9	+
1287	−	+	+	+	+	+	n	n	−	−	−	−	n	n	n	n	n	n	n	n	n	n	n	−	n	v	+	n	n	n	+	+	+	n	−	−	−	n	n	+
1288	−	−	+	+	−	−	n	n	−	−	−	−	n	n	n	n	n	n	n	n	n	n	n	−	n	+	+	n	n	n	+	+	−	−	−	−	−	9/10	47.2	+
1289	+	v	+	+	+	+	n	n	−	−	−	+	n	n	n	n	n	n	n	n	n	n	n	−	n	+	+	n	n	n	+	+	+	n	v	n	n	10	47.7	+
1290	−	−	+	+	+	+	n	n	−	−	−	+	n	n	n	n	n	n	n	n	n	n	n	−	n	+	+	n	n	n	+	+	+	n	−	−	−	n	n	+
1291	+	v	+	+	+	v	n	n	−	+	−	+	n	n	n	n	n	n	n	n	n	n	n	−	n	+	+	n	n	n	+	+	+	n	−	−	−	10	49.8	+
1292	−	+	+	+	+	+	n	n	−	−	v	v	n	n	n	n	n	n	n	n	n	n	n	−	n	+	+	n	n	n	+	+	v	n	−	−	−	10	55.9	+
1293	−	−	+	−	+	+	n	n	−	−	−	+	n	n	n	n	n	n	n	n	n	n	n	−	n	+	+	n	n	n	+	+	−	−	−	−	−	n	n	+
1294	−	+	+	+	+	+	n	n	−	−	−	+	n	n	n	n	n	n	n	n	n	n	n	−	n	v	+	n	n	n	+	+	−	−	−	−	−	9	57.2	+
1295	+	+	+	+	+	+	n	n	−	−	−	+	n	n	n	n	n	n	n	n	n	n	n	−	n	+	+	n	n	n	+	+	v	n	−	−	−	n	n	+
1296	−	−	+	+	+	−	n	n	−	−	−	−	n	n	n	n	n	n	n	n	n	n	n	−	n	+	+	n	n	n	+	+	v	n	−	−	−	9/10	46.4	+
1297	+	+	+	+	+	+	n	n	−	+	−	+	n	n	n	n	n	n	n	n	n	n	n	−	n	+	+	n	n	n	+	+	+	n	−	−	−	n	n	+
1298	+	−	+	+	+	−	n	n	−	−	−	+	n	n	n	n	n	n	n	n	n	n	n	−	n	+	+	n	n	n	+	+	+	−	−	−	−	n	n	+
1299	−	−	+	+	+	+	n	n	−	−	−	+	n	n	n	n	n	n	n	n	n	n	n	−	n	+	+	n	n	n	+	+	−	−	−	−	−	n	n	+
1300	−	−	+	−	−	−	n	n	−	−	−	−	n	n	n	n	n	n	n	n	n	n	n	−	n	+	+	n	n	n	+	+	+	n	−	−	−	n	n	+
1301	−	−	+	+	−	−	n	n	−	+	−	−	n	n	n	n	n	n	n	n	n	n	n	−	n	+	+	n	n	n	+	+	+	n	−	−	−	n	n	+
1302	−	−	+	−	−	−	n	n	−	−	−	−	n	n	n	n	n	n	n	n	n	n	n	−	n	+	+	n	n	n	+	+	+	n	−	−	−	n	n	+

Symbols: +, positive or weak; −, negative; v, variable (+/−, w/−); n, no data.

Ln. no.	Species	Fermentation							Growth reactions and other characteristics																																	
		Glucose	Galactose	Sucrose	Maltose	Lactose	Raffinose	Trehalose	Glucose	Inulin	Sucrose	Raffinose	Melibiose	Galactose	Lactose	Trehalose	Maltose	Melezitose	Methyl-α-D-glucoside	Soluble Starch	Cellobiose	Salicin	L-Sorbose	L-Rhamnose	D-Xylose	L-Arabinose	D-Arabinose	D-Ribose	Methanol	Ethanol	Glycerol	Erythritol	Ribitol	Galactitol	D-Mannitol	D-Glucitol				
1303	***Trichomonascus***																																								
1304	*T. apis*	+	+	−	−	−	−	−	+	−	+	v	+	+	v	+	+	v	+	+	+	+	+	+	+	+	+	+	−	+	+	+	+	+	+	+				
1305	*T. ciferrii*	−	−	−	−	−	−	−	+	−	+	+	v	+	−	+	+	−	v	v	v	v	+	+	+	+	+	+	v	−	v	+	+	+	+	+	+				
1306	*T. farinosus*	+	v	−	v	v	−	v	+	−	−	v	v	+	v	+	v	−	v	v	+	v	+	−	v	v	v	v	n	v	+	v	+	v	+	+				
1307	*T. petasosporus*	+	+	−	+	−	−	+	+	−	−	+	+	+	−	+	+	−	+	+	+	+	+	−	+	+	+	−	−	v	+	−	+	−	+	+				
1308	***Trichosporon***																																								
1309	*T. aquatile*	−	−	−	−	−	−	−	+	−	+	−	−	+	+	+	+	v	+	+	+	v	v	−	+	+	v	+	−	+	−	v	−	−	−	−				
1310	*T. asahii*	−	−	−	−	−	−	−	+	−	v	−	−	+	+	+	+	v	+	v	+	+	v	+	+	+	+	+	−	+	v	v	v	−	v	v				
1311	*T. asteroides*	−	−	−	−	−	−	−	+	−	+	−	−	+	+	+	+	+	+	+	+	v	+	v	+	+	v	v	−	+	v	v	v	−	−	v				
1312	*T. brassicae*	−	−	−	−	−	−	−	+	−	+	−	−	+	−	+	+	−	−	+	−	−	+	−	+	+	−	+	−	+	−	−	−	−	+	+				
1313	*T. caseorum*	−	−	−	−	−	−	−	+	−	+	v	−	+	+	+	+	+	+	−	+	+	+	v	+	+	+	+	−	+	+	+	+	+	+	+				
1314	*T. coremiiforme*	−	−	−	−	−	−	−	+	−	+	−	−	+	+	+	+	+	+	+	+	+	v	+	+	+	+	+	−	+	v	+	v	−	v	+				
1315	*T. cutaneum*	−	−	−	−	−	−	−	+	−	+	+	+	+	+	+	+	+	+	+	+	+	v	v	+	+	v	+	−	+	+	+	+	−	+	+				
1316	*T. debeurmannianum*	−	−	−	−	−	−	−	+	−	+	+	+	v	+	+	+	−	+	v	+	+	+	+	+	v	+	+	−	+	+	+	+	−	+	+				
1317	*T. dehoogii*	−	−	−	−	−	−	−	+	−	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	−	+	−	+	+	+	−	+	+	+				
1318	*T. dermatis*	−	−	−	−	−	−	−	+	−	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	−	+	+	+	+	+	+	+				
1319	*T. domesticum*	−	−	−	−	−	−	−	+	−	+	−	−	+	+	+	+	+	+	+	+	v	v	−	+	+	−	+	−	+	+	−	v	−	+	v				
1320	*T. dulcitum*	−	−	−	−	−	−	−	+	−	+	v	−	−	+	+	+	−	−	+	+	v	−	+	+	−	v	−	+	+	−	v	−	+	+				
1321	*T. faecale*	−	−	−	−	−	−	−	+	−	+	−	−	+	+	+	+	+	+	+	+	−	+	+	+	+	+	+	−	+	+	+	+	−	+	+				
1322	*T. gamsii*	−	−	−	−	−	−	−	+	−	+	−	+	+	+	+	+	+	+	+	+	+	+	+	+	+	−	+	−	+	+	−	−	−	+	+				
1323	*T. gracile*	−	−	−	−	−	−	−	+	−	−	−	−	−	v	+	−	−	−	v	+	+	−	−	+	+	−	+	−	+	+	−	−	−	v	v				
1324	*T. guehoae*	−	−	−	−	−	−	−	+	−	+	+	+	+	+	+	+	+	+	−	+	+	+	+	+	+	+	+	−	+	+	−	−	+	+	+				
1325	*T. inkin*	−	−	−	−	−	−	−	+	−	+	−	−	+	+	+	+	+	+	+	+	−	v	−	+	−	v	+	−	+	v	+	−	−	+	−				
1326	*T. japonicum*	−	−	−	−	−	−	−	+	−	+	−	−	+	+	+	+	v	+	+	+	+	+	−	+	+	−	+	−	+	+	+	v	−	−	v				
1327	*T. jirovecii*	−	−	−	−	−	−	−	+	−	+	+	+	+	+	+	+	+	+	+	+	+	+	v	+	+	−	+	−	+	+	+	−	+	+	+				
1328	*T. lactis*	−	−	−	−	−	−	−	+	−	+	−	−	+	+	v	+	−	+	−	+	v	+	v	+	+	v	+	−	+	+	+	−	v	+	+				
1329	*T. laibachii*	−	−	−	−	−	−	−	+	−	+	+	+	+	+	+	+	v	+	+	+	+	+	+	+	+	v	+	−	+	+	−	v	+	v	v				
1330	*T. lignicola*	−	−	−	−	−	−	−	+	−	+	+	+	+	+	+	+	+	+	v	+	+	−	+	+	+	v	+	−	+	+	+	+	−	+	−				
1331	*T. loubieri*	−	−	−	−	−	−	−	+	−	+	+	+	+	+	+	+	−	+	+	+	+	−	+	+	+	−	+	−	+	+	+	−	v	−	+				
1332	*T. moniliiforme*	−	−	−	−	−	−	−	+	−	+	+	+	+	+	+	+	+	+	+	+	+	v	+	+	+	v	+	−	+	+	+	+	−	+	+				
1333	*T. montevideense*	−	−	−	−	−	−	−	+	−	v	−	−	+	+	+	+	v	+	+	+	v	−	−	+	+	v	+	−	+	+	v	v	v	+	+				
1334	*T. mucoides*	−	−	−	−	−	−	−	+	−	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	−	+	+	+	+	+	+	+				
1335	*T. mycotoxinivorans*	−	−	−	−	−	−	−	+	−	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	−	+	+	+	−	+	+	+				
1336	*T. ovoides*	−	−	−	−	−	−	−	+	−	+	v	−	+	+	+	+	v	+	+	+	v	v	+	+	v	v	+	−	+	v	v	−	−	+	v				
1337	*T. porosum*	−	−	−	−	−	−	−	+	−	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	−	+	+	+	+	+	+	+				
1338	*T. scarabaeorum*	−	−	−	−	−	−	−	+	−	+	−	−	+	+	+	+	−	−	+	+	−	+	−	+	−	−	+	−	+	+	−	+	−	+	+				
1339	*T. siamense*	−	−	−	−	−	−	−	+	−	+	−	−	+	+	+	+	+	+	+	+	−	+	+	+	−	−	+	−	+	+	−	+	−	+	+				
1340	*T. smithiae*	−	−	−	−	−	−	−	+	−	+	+	+	+	+	+	+	+	+	+	+	−	−	+	+	+	−	+	−	+	+	+	+	−	+	+				
1341	*T. sporotrichoides*	−	−	−	−	−	−	−	+	−	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	−	+	−	+	+	−	−	+	+	+				
1342	*T. terricola*	−	−	−	−	−	−	−	+	−	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	−	+	+	+	+	+	+	+				
1343	*T. vadense*	−	−	−	−	−	−	−	+	−	+	+	+	+	+	+	+	−	+	−	+	+	−	+	+	+	+	+	−	+	+	−	+	−	+	+				
1344	*T. veenhuisii*	−	−	−	−	−	−	−	+	−	+	+	−	+	+	+	+	+	+	+	+	−	−	−	+	+	−	+	−	+	+	−	+	−	+	+				
1345	*T. wieringae*	−	−	−	−	−	−	−	+	−	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	−	+	−	+	+	+	−	+	+	−				
1346	***Trigonopsis***																																								
1347	*T. californica*	−	−	−	−	−	−	−	+	−	−	−	−	+	−	−	−	−	−	−	−	−	+	−	+	−	−	−	−	+	+	+	−	−	+	+				
1348	*T. cantarellii*	+	−	−	−	−	−	−	+	−	−	−	−	v	−	−	+	−	−	−	−	−	+	−	v	−	−	+	−	+	+	+	v	−	+	+				
1349	*T. variabilis*	−	−	−	−	−	−	−	+	−	−	−	−	+	−	−	+	−	−	−	−	−	+	−	v	−	−	+	−	+	+	−	−	−	+	+				
1350	*T. vinaria*	−	−	−	−	−	−	−	+	−	−	−	−	+	−	−	−	−	−	−	−	−	+	−	v	−	−	v	−	+	+	−	−	−	v	v				
1351	***Trimorphomyces***																																								
1352	*T. papilionaceus*	−	−	−	−	−	−	−	+	−	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	−	−	v	v	+	v	+	+				
1353	***Udeniomyces***																																								
1354	*U. megalosporus*	−	−	−	−	−	−	−	+	−	+	+	−	−	−	+	+	+	−	+	+	+	v	−	v	v	−	v	−	v	v	−	v	v	+	v				
1355	*U. pannonicus*	−	−	−	−	−	−	−	+	−	+	+	+	−	v	+	+	+	+	+	+	+	−	−	+	+	−	+	−	+	+	−	+	+	+	+				
1356	*U. puniceus*	−	−	−	−	−	−	−	+	−	+	+	−	−	−	+	+	−	+	+	+	+	+	+	−	+	+	+	+	+	+	−	+	+	+	+				
1357	*U. pyricola*	−	−	−	−	−	−	−	+	−	+	+	+	+	+	+	+	+	v	+	+	+	+	+	+	+	+	+	+	+	+	−	+	+	+	+				

Symbols: +, positive or weak; −, negative; v, variable (+/−, w/−); n, no data.

Growth reactions and other characteristics

	myo-Inositol	DL-Lactate	Succinate	Citrate	D-Gluconate	D-Glucosamine	*N*-Acetyl-D-glucosamine	Hexadecane	Nitrate	Nitrite	Vitamin-free	2-Keto-D-gluconate	5-Keto-D-gluconate	Saccharate	Xylitol	L-Arabinitol	Arbutin	Propane 1,2 diol	Butane 2,3 diol	Cadaverine	Creatinine	L-Lysine	Ethylamine	50% Glucose	10% NaCl/5% glucose	Starch formation	Urease	Gelatin liquefaction	Cycloheximide 0.01%	Cycloheximide 0.1%	Growth at 19°C	Growth at 25°C	Growth at 30°C	Growth at 35°C	Growth at 37°C	Growth at 40°C	Growth at 45°C	CoQ (Main component)	Mol% G + C (Ave.)	DBB
Trichomonascus																																								
1304	+	+	+	+	+	+	+	v	−	n	−	v	n	−	n	n	v	n	n	n	n	n	n	n	+	−	n	n	+	+	+	+	v	−	−	−	−	n	n	−
1305	+	+	v	v	+	−	n	n	−	n	−	+	+	−	n	n	v	n	n	n	n	n	n	n	+	−	n	−	n	n	+	+	+	+	+	n	n	9	46.6	−
1306	−	−	v	v	−	v	n	n	−	n	−	n	n	n	n	n	v	n	n	n	n	n	n	n	n	n	n	n	n	n	+	+	+	n	−	−	−	9	49.2	−
1307	+	−	+	+	v	+	+	+	−	n	−	n	n	n	n	n	n	n	n	n	n	n	n	n	+	n	n	n	+	+	+	+	+	+	+	n	n	n	n	−
Trichosporon																																								
1309	−	+	+	+	+	−	n	n	−	−	n	+	n	n	−	−	+	+	v	+	−	+	+	+	n	−	+	n	+	+	+	+	+	+	−	n	−	9	62.6	+
1310	v	v	+	+	+	v	n	n	−	v	n	+	n	n	v	+	+	+	v	+	−	+	+	v	n	+	+	n	+	+	+	+	+	+	+	v	−	9	58.2	+
1311	v	+	v	+	+	v	n	n	−	−	n	+	n	n	v	v	+	+	v	+	−	+	v	v	n	−	+	n	+	v	+	+	+	+	+	v	−	9	61.7	+
1312	+	+	+	+	+	+	n	n	−	−	n	+	n	n	−	−	−	+	+	+	−	+	+	−	n	−	+	n	+	−	+	+	+	+	+	−	−	9	55.9	+
1313	v	+	+	+	+	+	n	n	−	+	n	+	n	n	−	+	+	+	+	+	−	−	+	−	n	−	+	n	+	+	+	+	+	+	+	−	−	9	59.5	+
1314	+	+	+	+	+	+	n	n	−	+	n	+	n	n	+	+	+	+	v	+	−	+	v	v	n	v	+	n	+	−	+	+	+	n	v	v	−	9	59.8	+
1315	+	+	+	+	+	v	n	n	−	v	n	+	n	n	+	+	+	+	−	+	−	+	+	−	n	−	+	n	+	v	+	+	+	−	−	−	−	10	62.1	+
1316	+	+	+	+	+	v	n	n	−	−	n	+	n	n	v	−	+	+	+	+	−	+	+	−	n	−	+	n	+	−	+	+	+	+	−	−	−	10	59.5	+
1317	+	+	+	+	+	+	n	n	−	−	n	+	n	n	−	−	+	+	−	+	+	+	+	−	n	−	+	n	+	−	+	+	+	−	−	−	−	9	n	+
1318	+	+	+	+	+	+	n	n	−	+	n	+	n	n	+	+	+	+	+	+	−	+	+	−	n	+	+	n	+	+	+	+	+	+	+	−	−	10	60.3	+
1319	+	+	+	+	−	+	n	n	−	−	n	+	n	n	v	−	+	+	−	+	−	+	+	v	n	−	+	n	+	+	+	+	+	+	+	−	−	9	56.8	+
1320	+	+	+	v	+	v	n	n	−	+	n	+	n	n	+	v	v	+	v	+	−	+	+	−	n	−	+	n	+	v	+	+	−	−	−	−	−	9	56.2	+
1321	+	+	+	+	+	v	n	n	−	−	n	+	n	n	+	+	+	+	+	+	−	+	+	+	n	+	+	n	+	v	+	+	+	+	+	+	−	9	58.7	+
1322	+	+	+	+	+	+	n	n	−	+	n	+	n	n	+	−	+	+	−	+	+	+	+	−	n	−	+	n	−	−	+	+	−	−	−	−	−	9	61.5	+
1323	+	+	+	+	+	v	n	n	−	−	n	+	n	n	v	−	+	+	−	+	−	+	+	−	n	+	+	n	+	+	+	+	+	−	−	−	−	9	58.8	+
1324	+	+	+	+	+	+	n	n	−	+	n	+	n	n	+	+	+	+	+	+	+	+	+	−	n	−	+	n	+	+	+	+	+	+	+	−	−	9	n	+
1325	+	+	+	+	+	−	n	n	−	+	n	+	n	n	−	−	+	+	+	+	−	+	+	−	n	−	+	n	+	−	+	+	+	+	+	+	−	9	58.9	+
1326	−	+	+	+	+	−	n	n	−	−	n	+	n	n	−	−	+	+	+	+	−	+	+	−	n	−	+	n	+	+	+	+	+	+	+	+	−	9	59.8	+
1327	+	+	+	+	+	−	n	n	−	−	n	+	n	n	v	v	+	+	+	+	−	+	+	−	n	v	+	n	+	v	+	+	+	−	−	−	−	10	61.4	+
1328	v	+	+	+	+	+	n	n	−	+	n	+	n	n	v	v	+	+	+	+	−	+	+	−	n	−	+	n	+	−	+	+	+	+	−	−	−	9	n	+
1329	+	v	v	v	+	+	n	n	−	+	n	+	n	n	v	v	+	+	v	+	+	+	+	−	n	+	+	n	+	+	+	+	v	−	−	−	−	9	57.9	+
1330	v	v	+	+	−	−	n	n	−	+	n	+	n	n	−	−	+	+	+	+	−	+	+	−	n	+	+	n	+	+	+	+	+	−	−	−	−	9	n	+
1331	+	+	+	+	+	+	n	n	−	−	n	+	n	n	v	v	+	+	+	+	−	+	+	−	n	v	+	n	+	+	+	+	+	+	+	+	−	9	57.5	+
1332	+	+	+	+	+	v	n	n	−	+	n	+	n	n	+	+	+	+	+	+	−	+	+	−	n	+	+	n	+	v	+	+	+	−	−	−	−	10	59.0	+
1333	+	+	+	+	+	v	n	n	−	v	n	+	n	n	v	v	+	+	v	v	−	+	+	−	n	−	+	n	+	+	+	+	+	+	v	−	−	9	56.2	+
1334	+	+	+	+	+	+	n	n	−	+	n	+	n	n	+	+	+	+	v	+	−	+	+	v	n	+	+	n	+	+	+	+	+	+	+	v	−	10	58.6	+
1335	+	+	+	+	+	+	n	n	−	−	n	+	n	n	+	+	+	−	−	+	+	+	+	−	n	−	+	n	+	+	+	+	+	+	+	−	−	9	n	+
1336	+	+	+	v	+	v	n	n	−	v	n	+	n	n	v	−	+	v	v	+	−	+	+	v	n	−	+	n	+	+	+	+	+	+	v	−	−	9	60.0	+
1337	+	+	+	+	+	+	n	n	−	+	n	+	n	n	+	+	+	+	−	+	−	+	+	−	n	−	+	n	+	+	+	+	−	−	−	−	−	9	n	+
1338	+	+	+	−	+	+	n	n	−	−	n	+	n	n	+	−	−	+	−	+	−	+	+	−	n	−	+	n	+	+	+	+	+	−	−	−	−	9	n	+
1339	+	+	+	+	+	+	n	n	−	+	n	+	n	n	+	−	−	+	+	+	−	+	+	−	n	−	+	n	−	−	+	+	+	+	−	−	−	9	63.4	+
1340	+	+	+	+	+	−	n	n	−	−	n	+	n	n	+	+	+	+	−	+	−	+	+	−	n	−	+	n	+	+	+	+	+	−	−	−	−	10	n	+
1341	+	+	+	+	+	v	n	n	−	+	n	+	n	n	+	+	+	+	+	+	−	+	+	−	n	−	+	n	+	−	+	+	+	−	−	−	−	9	57.3	+
1342	+	+	+	+	+	+	n	n	−	−	n	+	n	n	+	+	+	+	+	+	−	+	+	+	n	−	+	n	+	+	+	+	+	+	+	+	−	10	57.6	+
1343	+	+	+	+	+	−	n	n	−	−	n	+	n	n	+	−	+	+	−	+	−	+	+	−	n	−	+	n	+	+	+	+	+	−	−	−	−	9	n	+
1344	+	+	+	−	+	+	n	n	−	−	n	+	n	n	−	+	+	−	+	+	−	+	+	−	n	−	+	n	+	+	+	+	+	+	+	+	−	9	n	+
1345	+	+	+	+	+	+	n	n	−	+	n	+	n	n	−	−	+	+	−	+	+	+	+	−	n	−	+	n	+	+	+	+	+	−	−	−	−	9	n	+
Trigonopsis																																								
1347	−	+	−	−	+	−	+	−	−	n	+	+	+	+	n	n	n	n	n	−	n	n	n	n	−	−	n	−	+	+	+	+	+	n	−	−	−	n	n	−
1348	−	v	+	v	v	v	+	−	−	n	+	+	n	n	n	n	n	n	n	n	n	n	n	n	+	−	n	−	+	+	+	+	+	n	v	n	n	9	41.9	−
1349	−	+	+	+	−	−	n	n	−	n	−	−	n	n	n	n	n	n	n	n	n	n	n	n	n	n	n	n	n	n	+	+	+	+	+	n	n	n	46.1	−
1350	−	+	+	+	−	+	+	−	−	n	−	−	−	−	n	n	n	n	n	n	n	n	n	n	−	−	n	n	n	n	+	+	+	−	−	−	−	9	44.1	−
Trimorphomyces																																								
1352	v	v	+	+	+	+	n	n	−	−	−	+	n	n	n	n	n	n	n	n	n	n	n	−	n	v	+	n	n	n	+	+	−	−	−	−	−	n	n	+
Udeniomyces																																								
1354	−	−	+	+	+	−	−	−	+	+	−	+	+	−	+	−	n	+	−	−	n	−	−	−	n	+	n	+	n	n	+	−	−	−	−	−	−	10	49.8	+
1355	−	−	+	+	+	−	−	−	+	+	−	+	+	−	+	−	n	+	−	−	n	−	−	n	n	+	n	v	n	n	+	−	−	−	−	−	−	10	58.9	+
1356	+	−	+	+	+	−	−	−	+	+	−	+	+	−	+	+	n	+	−	−	n	−	−	−	n	+	n	+	n	n	+	−	−	−	−	−	−	10	53.9	+
1357	+	−	+	+	+	−	−	−	+	+	−	+	+	−	+	+	n	+	−	−	n	+	−	−	n	+	n	n	n	n	+	−	−	−	−	−	−	10	51.8	+

Symbols: +, positive or weak; −, negative; v, variable (+/−, w/−); n, no data.

Ln. no.	Species	Fermentation							Growth reactions and other characteristics																											
		Glucose	Galactose	Sucrose	Maltose	Lactose	Raffinose	Trehalose	Glucose	Inulin	Sucrose	Raffinose	Melibiose	Galactose	Lactose	Trehalose	Maltose	Melezitose	Methyl-α-D-glucoside	Soluble Starch	Cellobiose	Salicin	L-Sorbose	L-Rhamnose	D-Xylose	L-Arabinose	D-Arabinose	D-Ribose	Methanol	Ethanol	Glycerol	Erythritol	Ribitol	Galactitol	D-Mannitol	D-Glucitol
1358	***Ustilago***																																			
1359	*U. maydis*	−	−	−	−	−	−	−	+	−	+	+	−	−	+	+	+	+	+	+	+	+	+	+	+	+	+	+	−	+	+	+	+	+	+	−
1360	***Vanderwaltozyma***																																			
1361	*V. polyspora*	+	+	+	−	−	+	+	+	−	+	+	−	+	−	v	−	−	−	−	−	−	−	−	−	−	−	−	−	v	+	−	−	−	−	−
1362	*V. yarrowii*	+	+	−	−	−	−	−	+	−	−	−	−	+	−	−	−	−	−	−	−	−	−	−	+	−	−	−	−	v	+	−	−	−	−	−
1363	***Wickerhamia***																																			
1364	*W. fluorescens*	+	+	+	−	−	+	−	+	−	+	+	−	+	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	+	+	−	+	−	+	+
1365	***Wickerhamiella***																																			
1366	*W. australiensis*	−	−	−	−	−	−	−	+	−	−	−	−	+	−	−	−	−	−	−	−	−	+	−	v	−	−	−	−	+	+	−	+	−	+	+
1367	*W. cacticola*	−	−	−	−	−	−	−	+	−	−	−	−	+	−	−	−	−	−	−	−	−	+	−	−	−	v	−	−	+	+	−	v	−	+	+
1368	*W. domercqiae*	−	−	−	−	−	−	−	+	−	v	−	−	v	−	−	−	−	−	−	−	−	+	−	v	−	−	v	−	+	+	−	v	−	+	v
1369	*W. lipophila*	−	−	−	−	−	−	−	+	−	−	−	−	−	−	−	−	−	−	−	−	−	+	−	−	−	−	−	−	−	−	−	−	−	+	+
1370	*W. occidentalis*	−	−	−	−	−	−	−	+	−	−	−	−	+	−	−	−	−	−	−	−	−	+	−	−	−	−	−	−	+	+	−	+	−	+	+
1371	***Wickerhamomyces***																																			
1372	*W. alni*	−	−	−	−	−	−	−	+	−	+	−	−	−	−	+	+	+	+	−	+	+	−	+	+	−	−	v	−	+	+	−	v	−	+	+
1373	*W. anomalus*	+	v	+	v	−	v	−	+	−	+	+	−	v	−	+	+	+	+	+	+	+	−	−	v	v	−	v	−	+	+	+	v	−	+	+
1374	*W. bisporus*	v	−	−	−	−	−	−	+	−	+	−	−	−	−	+	+	+	+	−	+	+	−	+	+	v	−	v	−	+	+	−	v	−	v	+
1375	*W. bovis*	+	−	v	v	−	−	v	+	−	+	−	−	−	−	+	+	+	+	v	+	+	−	v	+	+	−	−	−	+	+	−	−	−	+	+
1376	*W. canadensis*	−	−	−	−	−	−	−	+	−	+	−	−	−	−	+	+	+	v	−	+	+	−	+	+	−	−	−	−	+	+	−	v	−	+	+
1377	*W. chambardii*	−	−	−	−	−	−	−	+	−	−	−	−	+	−	−	−	−	−	−	+	+	−	−	−	−	−	−	−	+	+	−	−	−	−	−
1378	*W. ciferrii*	+	+	+	v	−	+	−	+	−	+	+	−	+	−	+	+	+	+	+	+	+	−	+	+	+	−	+	−	+	+	+	+	−	+	+
1379	*W. hampshirensis*	+	−	−	−	−	−	−	+	−	+	−	−	−	−	+	+	+	+	−	+	+	−	+	+	−	−	−	−	+	+	−	+	−	v	+
1380	*W. lynferdii*	+	−	+	−	−	+	−	+	+	+	+	−	+	−	+	+	+	+	−	+	+	−	−	−	−	−	+	−	+	+	+	+	−	+	+
1381	*W. mucosus*	+	−	−	−	−	−	−	+	−	+	−	−	−	−	+	+	+	+	−	+	+	+	−	+	−	v	−	−	+	+	−	−	−	+	+
1382	*W. onychis*	+	−	+	−	−	+	−	+	v	+	+	−	−	−	+	+	+	+	−	+	+	−	−	+	v	v	−	−	+	+	−	−	−	+	+
1383	*W. pijperi*	+	−	−	−	−	−	−	+	−	−	−	−	−	−	−	−	−	−	−	+	+	+	−	+	−	−	−	−	+	+	−	−	−	+	+
1384	*W. rabaulensis*	+	−	+	−	−	+	+	+	−	+	+	−	−	−	+	+	+	+	−	+	v	−	v	+	+	−	−	−	+	+	−	+	−	+	+
1385	*W. silvicola*	+	+	−	−	−	−	−	+	−	v	−	−	+	−	v	v	v	+	−	+	+	v	+	+	+	−	v	−	+	+	v	+	−	v	+
1386	*W. strasburgensis*	+	+	+	−	−	+	−	+	−	+	+	−	+	−	+	+	+	+	−	+	+	−	+	+	+	−	v	−	+	+	−	+	−	+	+
1387	*W. subpelliculosus*	+	−	+	v	−	v	−	+	−	+	+	−	v	−	+	+	v	+	v	v	+	−	−	v	v	v	v	−	+	+	+	v	−	+	+
1388	*W. sydowiorum*	+	+	+	v	−	+	+	+	−	+	+	+	+	−	+	+	+	+	v	+	+	−	+	v	+	−	+	−	+	+	+	+	−	+	+
1389	***Xanthophyllomyces***																																			
1390	*X. dendrorhous*	+	−	+	v	−	v	+	+	v	v	+	−	−	−	+	+	+	v	+	+	v	v	−	+	+	−	v	−	+	+	−	v	−	v	v
1391	***Yamadazyma***																																			
1392	*Y. akitaensis*	+	−	+	+	−	−	+	+	−	+	−	−	+	−	+	+	+	+	+	+	+	+	−	+	+	+	+	−	+	+	+	+	−	+	+
1393	*Y. mexicana*	+	+	−	−	−	−	+	+	−	+	+	v	+	+	+	+	+	+	−	+	+	−	+	+	+	v	+	−	+	+	+	+	v	+	+
1394	*Y. nakazawae*	+	+	−	+	−	−	+	+	−	+	−	−	+	−	+	+	+	+	+	+	+	+	+	+	+	+	+	−	+	+	+	+	−	+	+
1395	*Y. philogaea*	+	+	−	v	−	−	+	+	−	+	−	−	+	−	+	+	+	+	−	+	−	+	−	+	+	+	+	−	+	+	+	+	−	+	+
1396	*Y. scolyti*	+	+	v	v	−	−	+	+	−	+	+	+	+	v	+	+	+	+	−	+	+	−	+	+	+	v	+	−	+	+	+	+	−	+	+
1397	*Y. triangularis*	v	−	−	−	−	−	−	+	−	+	−	−	+	−	+	+	+	+	−	+	−	−	+	+	+	−	+	−	+	+	+	+	+	+	+
1398	***Yarrowia***																																			
1399	*Y. lipolytica*	−	−	−	−	−	−	−	+	−	−	−	−	v	−	−	−	−	−	−	v	v	v	−	−	−	−	v	−	+	+	+	v	−	+	+
1400	***Zygoascus***																																			
1401	*Z. hellenicus*	v	v	v	v	−	v	v	+	−	+	v	−	+	v	+	+	v	v	+	+	+	+	+	+	v	v	v	−	+	+	−	v	v	+	+
1402	*Z. meyerae*	v	v	v	v	−	v	v	+	−	+	v	−	+	−	+	v	v	v	v	+	+	+	+	+	+	v	v	−	+	+	−	+	+	+	+
1403	*Z. ofunaensis*	+	+	−	−	−	−	+	+	−	v	v	+	+	+	+	v	v	v	−	+	+	+	+	+	+	−	+	−	+	+	v	+	+	+	+
1404	*Z. tannicolus*	+	+	−	−	−	−	+	+	−	−	−	+	+	v	+	−	−	−	−	−	−	−	+	+	+	−	−	−	+	+	v	+	+	+	+
1405	***Zygosaccharomyces***																																			
1406	*Z. bailii*	+	−	v	−	−	−	−	+	−	v	−	−	v	−	+	−	−	−	−	−	−	−	−	−	−	−	−	−	v	+	−	+	−	v	+
1407	*Z. bisporus*	+	−	−	−	−	−	−	+	−	−	−	−	v	−	−	−	−	−	−	−	−	v	−	−	−	−	−	−	+	+	−	v	−	+	v
1408	*Z. kombuchaensis*	+	−	+	−	−	−	−	+	−	+	−	−	+	−	−	v	−	−	−	−	−	v	−	−	−	−	−	−	+	+	−	−	−	v	v
1409	*Z. lentus*	+	−	+	−	−	−	−	+	−	+	v	−	v	−	−	−	−	−	−	−	−	+	−	−	−	−	−	−	+	+	−	v	−	v	v
1410	*Z. mellis*	+	−	−	+	−	−	−	+	−	−	−	−	−	−	v	v	−	−	−	−	−	−	−	−	−	−	−	−	−	+	−	−	−	v	v
1411	*Z. rouxii*	+	−	v	+	−	−	v	+	−	v	−	−	v	−	v	v	−	−	−	−	−	−	−	−	−	−	−	−	v	+	−	−	−	+	v

Symbols: +, positive or weak; −, negative; v, variable (+/−, w/−); n, no data.

Growth reactions and other characteristics

	myo-Inositol	DL-Lactate	Succinate	Citrate	D-Gluconate	D-Glucosamine	*N*-Acetyl-D-glucosamine	Hexadecane	Nitrate	Nitrite	Vitamin-free	2-Keto-D-gluconate	5-Keto-D-gluconate	Saccharate	Xylitol	L-Arabinitol	Arbutin	Propane 1,2 diol	Butane 2,3 diol	Cadaverine	Creatinine	L-Lysine	Ethylamine	50% Glucose	10% NaCl/5% glucose	Starch formation	Urease	Gelatin liquefaction	Cycloheximide 0.01%	Cycloheximide 0.1%	Growth at 19°C	Growth at 25°C	Growth at 30°C	Growth at 35°C	Growth at 37°C	Growth at 40°C	Growth at 45°C	CoQ (Main component)	Mol% G + C (Ave.)	DBB
Ustilago																																								
1359	+	+	+	−	+	+	n	n	+	+	+	+	n	−	n	n	n	n	n	n	n	n	n	−	n	−	+	n	n	n	+	+	+	+	+	n	n	10	n	+
Vanderwaltozyma																																								
1361	−	−	v	+	+	−	−	−	−	−	−	−	n	n	−	n	n	n	n	−	n	−	−	−	n	−	n	−	−	−	+	+	+	n	v	n	n	6	35.3	−
1362	−	−	−	−	−	−	−	−	−	−	−	−	n	n	v	n	n	n	n	−	n	−	−	−	n	−	n	−	v	−	+	+	−	−	−	−	−	6	34.5	−
Wickerhamia																																								
1364	−	+	+	+	+	−	+	+	−	n	−	+	−	−	n	n	n	n	n	n	n	n	n	n	+	−	n	−	+	n	+	+	+	n	−	−	−	9	37.6	−
Wickerhamiella																																								
1366	−	−	+	−	−	−	−	+	+	+	−	−	n	n	+	n	n	n	n	+	n	+	v	+	n	−	n	−	+	+	+	+	+	n	v	n	n	n	n	−
1367	−	−	+	+	−	−	−	−	+	+	−	−	n	n	v	n	n	n	n	+	n	+	+	−	n	−	n	−	+	−	+	+	+	+	+	n	n	n	n	−
1368	−	−	+	+	+	−	−	−	+	+	−	+	−	−	v	n	n	n	n	+	n	+	+	v	n	−	n	−	−	−	+	+	+	n	v	n	n	n	48.6	−
1369	−	−	+	−	−	−	−	+	−	−	−	−	n	n	−	n	n	n	n	+	n	+	−	+	n	−	n	−	v	v	+	+	+	n	−	−	−	n	n	−
1370	−	−	+	−	−	−	−	+	+	+	−	−	n	n	+	n	n	n	n	+	n	+	+	+	n	−	n	−	+	+	+	+	+	+	+	n	n	n	n	−
Wickerhamomyces																																								
1372	−	+	+	+	+	−	−	−	+	n	−	−	−	−	n	n	n	n	n	n	n	n	n	n	v	−	n	−	n	n	+	+	+	n	−	−	−	7	41.9	−
1373	−	+	+	+	v	−	−	−	+	n	+	−	−	−	n	n	n	n	n	n	n	n	n	n	n	−	n	−	n	n	+	+	+	n	v	n	n	7	36.5	−
1374	−	v	+	+	+	−	−	−	+	n	−	−	−	−	n	n	n	n	n	n	n	n	n	n	−	−	n	−	n	n	+	+	+	n	−	−	−	7	36.8	−
1375	−	+	+	+	+	−	−	−	−	n	−	−	−	−	n	n	n	n	n	n	n	n	n	n	−	−	n	−	n	n	+	+	+	+	+	n	n	7	41.0	−
1376	−	+	+	+	+	−	−	−	v	n	−	−	−	−	n	n	n	n	n	n	n	n	n	n	−	−	n	−	n	n	+	+	+	+	+	n	n	7	40.1	−
1377	−	+	+	+	−	−	−	−	−	n	−	−	−	−	n	n	n	n	n	n	n	n	n	n	−	−	n	−	n	n	+	+	+	n	−	−	−	7	32.0	−
1378	−	+	+	+	+	−	−	+	+	n	+	−	−	−	n	n	n	n	n	n	n	n	n	n	+	−	n	+	n	n	+	+	+	n	v	n	n	7	32.2	−
1379	−	+	+	+	v	−	−	−	−	n	−	−	−	−	n	n	n	n	n	n	n	n	n	n	−	−	n	−	n	n	+	+	+	n	−	−	−	n	39.3	−
1380	−	+	+	+	+	−	−	−	+	n	+	−	−	−	n	n	n	n	n	n	n	n	n	n	+	−	n	−	n	n	+	+	+	n	−	−	−	n	39.3	−
1381	−	−	v	−	−	−	−	−	−	n	−	+	−	−	n	n	n	n	n	n	n	n	n	n	v	−	n	−	n	n	+	+	+	n	−	−	−	7	34.0	−
1382	−	+	+	+	+	−	−	−	−	n	−	−	−	−	n	n	n	n	n	n	n	n	n	n	v	−	n	−	n	n	+	+	+	+	+	n	n	7	41.8	−
1383	−	+	+	v	−	−	−	−	−	n	−	−	−	−	n	n	n	n	n	n	n	n	n	n	−	−	n	−	n	n	+	+	+	n	v	n	n	7	41.6	−
1384	−	+	+	+	+	−	−	−	−	n	−	−	−	−	n	n	n	n	n	n	n	n	n	n	+	−	n	−	n	n	+	+	+	+	+	n	n	7	42.8	−
1385	−	v	+	v	+	−	−	−	+	n	−	−	−	−	n	n	n	n	n	n	n	n	n	n	−	−	n	−	n	n	+	+	+	n	v	n	n	7	35.2	−
1386	−	+	+	+	+	−	−	−	−	n	−	−	−	−	n	n	n	n	n	n	n	n	n	n	+	−	n	−	n	n	+	+	+	n	v	n	n	7	40.4	−
1387	−	+	+	+	+	−	−	−	+	n	−	−	−	−	n	n	n	n	n	n	n	n	n	n	+	−	n	v	n	n	+	+	+	n	v	n	n	7	33.7	−
1388	−	+	+	+	+	−	−	−	+	n	+	−	−	−	n	n	n	n	n	n	n	n	n	n	+	−	n	v	n	n	+	+	+	n	−	−	−	n	36.2	−
Xanthophyllomyces																																								
1390	−	v	+	v	+	−	−	−	−	−	−	+	+	n	v	v	+	v	v	v	−	+	−	+	−	+	+	+	−	−	+	+	−	−	−	−	−	10	48.3	+
Yamadazyma																																								
1392	−	−	+	+	+	+	+	+	−	n	−	+	−	−	n	n	n	n	n	n	n	n	n	n	+	−	n	−	n	n	+	+	+	n	−	−	−	n	39.7	−
1393	−	−	+	+	+	+	+	+	−	n	−	+	−	−	n	n	n	n	n	n	n	n	n	n	+	−	n	+	n	n	+	+	+	+	+	n	n	9	42.3	−
1394	−	+	+	+	+	+	+	+	−	n	−	+	−	−	n	n	n	n	n	n	n	n	n	n	+	−	n	−	n	n	+	+	+	n	−	−	−	9	39.0	−
1395	−	−	+	+	+	+	+	+	−	n	−	+	−	−	n	n	n	n	n	n	n	n	n	n	+	−	n	v	n	n	+	+	+	+	+	n	n	9	42.0	−
1396	−	−	+	+	+	v	+	+	−	n	−	+	−	−	n	n	n	n	n	n	n	n	n	n	v	−	n	v	n	n	+	+	+	n	v	n	n	9	38.2	−
1397	−	−	+	v	+	−	+	−	−	n	−	−	−	−	n	n	n	n	n	n	n	n	n	n	+	−	n	−	n	n	+	+	+	n	−	−	−	9	34.5	−
Yarrowia																																								
1399	−	+	+	+	v	−	+	+	−	n	−	−	−	−	n	n	n	n	n	n	n	n	n	n	−	−	−	+	n	n	+	+	+	n	v	n	n	9	49.9	−
Zygoascus																																								
1401	+	v	+	+	+	+	n	n	−	n	−	v	n	n	+	n	n	n	n	n	n	n	n	v	n	−	n	n	+	+	+	+	+	+	+	−	−	9	44.2	−
1402	+	v	v	v	v	+	n	n	−	n	−	v	n	n	+	n	n	n	n	n	n	n	n	v	n	−	n	n	+	+	+	+	+	+	+	v	n	n	44.1	−
1403	+	+	+	+	+	+	+	−	+	n	−	+	n	−	+	n	n	n	n	n	n	n	n	−	+	−	n	−	−	−	+	+	+	+	+	n	n	n	32.6	−
1404	v	+	+	+	v	+	+	−	−	n	−	−	n	−	−	n	n	n	n	n	n	n	n	−	−	−	n	−	+	+	+	+	+	n	−	−	−	n	43.2	−
Zygosaccharomyces																																								
1406	−	−	−	−	n	−	n	n	−	n	−	n	n	n	n	n	n	n	n	n	n	n	n	+	+	−	n	−	n	−	+	+	+	n	v	−	−	6	43.3	−
1407	−	−	−	−	n	−	n	n	−	n	−	n	n	n	n	n	n	n	n	n	n	n	n	+	+	−	n	−	n	−	+	+	+	n	−	−	−	6	44.5	−
1408	−	−	−	−	n	−	n	n	−	n	−	n	n	n	n	n	n	n	n	n	n	n	n	+	−	−	n	n	n	−	+	+	−	−	−	−	−	n	n	−
1409	−	−	−	−	n	−	n	n	−	n	−	n	n	n	n	n	n	n	n	n	n	n	n	+	v	−	n	n	n	−	+	+	−	−	−	−	−	n	n	−
1410	−	−	−	−	n	−	n	n	−	n	−	n	n	n	n	n	n	n	n	n	n	n	n	+	+	−	n	n	n	−	+	+	v	n	−	−	−	6	41.5	−
1411	−	−	−	−	n	−	n	n	−	n	−	n	n	n	n	n	n	n	n	n	n	n	n	+	+	−	n	n	n	−	+	+	+	n	v	−	−	6	41.2	−

Symbols: +, positive or weak; −, negative; v, variable (+/−, w/−); n, no data.

Ln. no.	Species	Fermentation							Growth reactions and other characteristics																																	
		Glucose	Galactose	Sucrose	Maltose	Lactose	Raffinose	Trehalose	Glucose	Inulin	Sucrose	Raffinose	Melibiose	Galactose	Lactose	Trehalose	Maltose	Melezitose	Methyl-α-D-glucoside	Soluble Starch	Cellobiose	Salicin	L-Sorbose	L-Rhamnose	D-Xylose	L-Arabinose	D-Arabinose	D-Ribose	Methanol	Ethanol	Glycerol	Erythritol	Ribitol	Galactitol	D-Mannitol	D-Glucitol				
1412	***Zygotorulaspora***																																							
1413	*Z. florentina*	+	+	+	+	−	+	+	+	+	+	+	+	+	−	+	+	+	+	−	−	−	+	−	−	−	−	−	−	+	v	−	−	−	+	+				
1414	*Z. mrakii*	+	+	+	−	−	+	−	+	−	+	+	+	+	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	v	+	−	−	−	+	+				

Symbols: +, positive or weak; −, negative; v, variable (+/−, w/−); n, no data.

Growth reactions and other characteristics

	myo-Inositol	DL-Lactate	Succinate	Citrate	D-Gluconate	D-Glucosamine	*N*-Acetyl-D-glucosamine	Hexadecane	Nitrate	Nitrite	Vitamin-free	2-Keto-D-gluconate	5-Keto-D-gluconate	Saccharate	Xylitol	L-Arabinitol	Arbutin	Propane 1,2 diol	Butane 2,3 diol	Cadaverine	Creatinine
Zygotorulaspora																					
1413	−	−	+	−	v	−	−	−	−	n	v	+	−	−	n	n	n	n	n	n	n
1414	−	−	+	−	−	−	−	−	−	n	−	+	−	−	n	n	n	n	n	n	n

	L-Lysine	Ethylamine	50% Glucose	10% NaCl/5% glucose	Starch formation	Urease	Gelatin liquefaction	Cycloheximide 0.01%	Cycloheximide 0.1%	Growth at 19°C	Growth at 25°C	Growth at 30°C	Growth at 35°C	Growth at 37°C	Growth at 40°C	Growth at 45°C	CoQ (Main component)	Mol% G + C (Ave.)	DBB
Zygotorulaspora																			
1413	n	n	n	−	−	n	−	+	+	+	+	+	n	−	−	−	6	42.8	−
1414	n	n	n	v	−	n	−	+	+	+	+	+	n	−	−	−	n	41.7	−

Symbols: +, positive or weak; −, negative; v, variable (+/−, w/−); n, no data.

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Glossary of Terms Used in This Book[1,2]

abaxial: the side away from the main axis of a structure; e.g., the abaxial surface of a basidiospore is the side away from the long axis of a basidium (cp. adaxial)

abstriction: the combination of abjunction and constriction, i.e., cutting off of a spore from the sporophore or hypha by a septum, followed by abscission, especially by constriction

acerose: shape that resembles a pine needle with ends tapered and the long central part with parallel sides; see filiform (Fig. 1251.8)

acicular: needle-shaped; see acerose

acropetal: produced successively in the direction of the apex, e.g., production of mitospores (conidia); the apical part is youngest (cp. basipetal)

aculeate: surface spiny, with long spines (Fig. 1251.9D)

adaxial: the side toward the main axis of a structure, i.e., for basidiospores the side toward the basidial axis; the flattened or less strongly curved side of the basidiospore; (cp. abaxial)

aerobic: organisms that require free oxygen for growth; also, an atmosphere with free oxygen

agglutinate: to clump or bind together; if occurring with suspensions of compatible mating cells, referred to as sexual agglutination

airplane figure: configuration of cells similar to an airplane in shape (in *Metschnikowia* spp.)

alignment of sequences: a linear arrangement of DNA or amino acid sequences of two or more taxa in a way that homologous positions appear in one column. This linear arrangement is the basis for most methods of molecular phylogenetic analysis

allantoid: curved with rounded ends, sausage-shaped (Fig. 1251.18) (cp. botuliform)

allele: any of the alternative versions of a gene

allochthonous: derived from outside a system (exotic or introduced); an accidental member of a community; see also autochthonus

allopolyploid: a polyploid species with individual sets of chromosomes originating from different species

allotype: paratype of the opposite (compatible) mating type to the holotype

amphigenous hymenium: hymenial layer covering all exposed surfaces of the basidiome

amphidiploid: special case of an allopolyploid species, which has originated by the fusion of the genomes of two separate but usually related species with different chromosome numbers; see allopolyploid

ampulliform: ampoule-like or flask-like form (Fig. 1251.12); see also amygdaliform (amygdalate): almond-shaped

anaerobic: living and reproducing in the absence of free oxygen

anamorph (anamorphic state, conidial state, imperfect state, mitospore state): asexual part of life cycle

anastomosis: fusion between hyphae of the same mycelium or different mycelia; see also somatogamy

annellation: formation of ring-like protrusions near the apex of a cell resulting from successive formation of conidia or buds at the same locus (Fig. 1251.21)

annellidic: with annellations; see annellation

apex: the end of a cell or other structure farthest from its point of attachment or base

apical: referring to apex, tip

apiculate: with a short projection (apiculus) at one or both ends of a cell

apiculus (pl. = apiculi): a short terminal projection on a spore by which the spore was fixed to the sterigma

arthroconidium (pl. = -conidia; arthrospore): an anamorphic (asexual) spore resulting from the division of a hypha or a single cell by fission, e.g., in *Trichosporon*

ascoma (pl. = ascomata): ascocarp structure in which asci are produced; the sexual reproductive structure of an ascomycete

ascophore: an ascus-bearing hypha, e.g., in *Cephaloascus*

ascospore: spore produced by free cell formation in an ascus, typically after karyogamy and meiosis

ascostromatic: of ascomata in which asci are produced in unwalled locules (see pseudothecium)

ascus (pl. = asci): the sac-like cell in which ascospores develop following karyogamy and meiosis

aseptate: of hyphae, basidia or other structure without internal cross-walls

asexual state, conidial state, imperfect state, mitosporic state: now generally referred to as the **anamorphic state**, or anamorph, in which reproduction is by mitotic cell division

[1] Prepared by Robert J. Bandoni, Michael Weiss, Teun Boekhout, Jack W. Fell and Cletus P. Kurtzman.

[2] See also Kirk et al. (2008) and McNeill et al. (2006).

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asperulate: spores that are minutely roughened with projections or points; see punctuate (Fig. 1251.9B)
asporogenous: yeasts that have no known teleomorphic state (asci, basidia)
attenuate: of a gradually narrowed structure; of parasitic strains, diminished disease-causing capacity
authentic strain: non-type material believed to genetically represent the species
autochthonous: derived from inside a system (native or indigenous); a fundamental member of a community; see also allochthonous
autogamy: fusion of nuclei within a cell in the absence of cell fusion
auxotrophic: growth factor dependent (cp. prototrophic)
automictic: self-fertile
axenic culture: a culture of one organism, i.e., not contaminated by other organisms

bacilliform: cylindrical, rod-shaped, the ends rounded or truncate (Fig. 1251.35, 42)
ballistoconidium (pl. = -conidia): an anamorphic spore produced in a manner similar to an abstricted basidiospore, but not borne on a basidium (Fig. 1251.34)
ballistospore: spore that is forcibly projected from a basidium (Fig. 1251.34)
base composition of DNA: molar ratio of guanine + cytosine (G + C) or adenine + thymine (A + T) expressed as the percent that the particular base pair comprises in a genome or nucleic acid sequence
basidiocarp: see basidioma
basidioma (pl. = basidiomata), basidiome: the structure of Basidiomyetes, which bears or contains teleomorphic reproductive cells, the basidia and basidiospores
basidiophore: basidium-bearing hypha
basidiospore: a spore produced by a basidium following karyogamy and meiosis
basidium (pl. = basidia): cell, initially dikaryotic, then diploid, in the teleomorphic (sexual) state of a basidiomycete; following meiosis, it bears basidiospores
basionym: the first validly given name for a species
basipetal: produced successively in the direction of the base; the apical-most part matures first (cp. acropetal)
basitonous: with dense branching at the base of the conidiophores, compared to more widely spaced branching in the apical part
biallelic compatibility: see mating loci
bifactorial mating system: see mating loci
bifurcate: with two branches
bilaterally symmetrical: with a single plane of symmetry, the halves being mirror images of one another
bipodal: of asci; asci arising from two basal cells
bipolar: of budding, buds that develop at both ends of a cell; mating systems (see also mating loci), biallelic compatibility, as above, the progeny of crosses fall into two distinct groups; bipolar geographical distribution, species occurring in both polar areas
bisexual: having two opposite (compatible) mating alleles in the genome of a single cell or thallus, a heterothallic diploid
blastese: non-septate cells that resemble true mycelium, e.g., as in the species of *Brettanomyces* and *Dekkera*
blastoconidium (pl. = -conidia): an asexual spore formed by budding from a yeast cell or conidiogenous hyphal cell by septal formation, and secession; see also budding
blastospore: see blastoconidium
bootstrap: statistical procedure to study the variance by resampling from the original sample. In phylogenetic analysis the bootstrap is used to measure how homogeneously a certain branch in a phylogenetic tree is supported by the data. In each bootstrap replicate, columns from the original data matrix (e.g., from a sequence alignment) are randomly drawn with repetition and assembled to a matrix of the same length, which is subsequently analyzed using some method of phylogenetic inference. A bootstrap value is the percentage with which a certain branch in a phylogenetic tree is present in the trees inferred in the bootstrap replicates.
botuliform: cylindrical, curved, with rounded ends (Fig. 1251.18), also "sausage-shaped" or allantoid
bracket fungi: basidiomycetes that form shelf- or bracket-shaped fruiting bodies
bud: a new cell formed from an outgrowth (a "bleb") on the parent cell on a broad or narrow base; see budding (Fig. 1251.21, 22)
budding: reproduction of anamorphic yeast states of many basidiomycetes and ascomycetes; budding involves formation of a bubble-like protrusion or bleb on a parent cell, transfer of organelles, and the abscission of the new cell (Fig. 1251.21, 22); monopolar budding: forming buds at only one pole of the cell, often on a broad base; bipolar budding: forming buds at both poles of the cell, usually on a broad base; multipolar (multilateral) budding: forming buds, usually on a narrow base, over nearly the entire surface of the cell
bud-fission: bud formation on a broad base with cross-wall development at the constriction between bud and parent cell, e.g., in *Hanseniaspora*, *Nadsonia*, *Saccharomycodes*, *Wickerhamia*, and their anamorphic genera
bullate: pileus with a rounded, raised, knob-like center; also spores or other structures with rounded blister- or knob-like projections; also verrucose or verruculose if projections are small (Fig. 1251.9E)
bulliform: cells that appear globoid in abaxial view, knob-shaped in lateral view with the apiculus situated almost midway along the flattened adaxial surface; once described as "jug-shape" by some mycologists

capitate: with a swollen tip or head, the capitulum (Fig. 1251.1)
capitulum: a tight cluster of branches resembling a head or flower; also swollen tip of hyphae as in sphaaropedunculate
capsule: a hyaline sheath of polysaccharide surrounding the yeast cell, e.g., as in *Cryptococcus* spp.; capsules are not easily stained and usually shown by the use of negative staining (India ink mounts)
catenate: in chains
catenulate: in short chains
cerebriform: with a brain-like appearance, often spheroidal or hemispherical and with surface grooves and ridges
chlamydospore: a resistant structure developing in an intercalary or terminal cell, the protoplast contracting, rounding up, and a usually thick wall then forming around it (within the old cell wall); considered not primarily a disseminule, but a survival structure which remains viable over dry or cold periods. Many teliospores have similar development but these structures are a part of the sexual phase
cicatrize: to form a scar
clade: a monophyletic group of any size (corresponding to subtrees in a rooted cladogram)

cladogram: graphical visualization of the topology of a phylogenetic tree

clamp connection: in basidiomycetes, a hyphal outgrowth formed during cell division of dikaryotic hyphae that makes a connection between the two cells by anastomosis. The function is to separate dividing nuclei during cell division; one of the daughter nuclei passes through the clamp (Fig. 1251.24)

clavate: club-shaped, broadest at the apex (Fig. 1251.4); see also obclavate

clone: the asexual offspring from a single cell; a genetically identical copy of an individual

closure line: the site in the center of the septum where, during growth, the septum has closed; a double layer of plasmalemma is visible (by electron microscopy) in a longitudinal section through the center of the hypha

cluster analysis: an iterative procedure to gradually cluster a set of objects according to known distances between these objects. In molecular phylogenetic inference, trees may be constructed using UPGMA cluster analysis if substitution rates are assumed to be constant for the dataset to be analyzed

coalesce: to join by fusion; in many species, crowded basidiocarps arise from a single mycelium and grow together (coalesce), where they contact one another, to form a large basidiocarp

coenzyme Q number: the number of isoprene units in the side-chain of coenzyme Q (ubiquinone)

colacosome: minute organelles associated with parasitism of host fungus in *Colacogloea* and allied species; also known as a lenticular body

collarette: cup-shaped structure found at the apex of certain conidiogenous cells such as on the conidiophores of *Phialophora* or after successive budding at the same site on the cells of certain yeasts (Fig. 1251.21)

colony: a mass of cells, generally of one species, growing together

comb. nov., combinatio nova: name of a taxon that has been transferred in rank or position, such as from one genus to another; a transferred specific epithet is followed by comb. nov. when the change is published

compatible mating types: see complementary mating types

complementary mating types: of two haploid strains capable of mating to initiate a fertile dikaryotic or diploid state

congeneric: of species that belong to the same genus (analogously used for other levels of the classification hierarchy, i.e., conspecific, confamilial, etc.)

conidioma (pl. = conidiomata): a macroscopically visible accumulation of conidiophores

conidiophore: formerly, any specialized hypha on which conidia are produced; a distinction is now made between conidiophores and conidiogenous cells, the latter term is used for the cells that give rise to the conidia

conidium (pl. = conidia), conidiospore: an anamorphic spore (also called a mitospore, asexual spore, "imperfect" spore) produced following mitosis

conjugated ascus: ascus developed from the fusion of two cells, here yeast cells, e.g., in *Pichia*, *Saccharomyces* and many other genera

conjugation: fusion of two cells during the mating process; the cells may fuse directly or via mating tubes ("mating" is a more common term for most yeast species)

consensus network: a phylogenetic network that contains splits that are present in a given set of phylogenetic trees or phylogenetic networks; generalization of the consensus tree concept

consensus tree: a single tree that summarizes information contained in a set of trees; e.g., majority-rule consensus tree or strict consensus tree

conspecific: individuals of the same species

context: "flesh" of a sporocarp supporting the hymenium and subhymenium (not a "tissue" in the biological sense of this word, being composed of interwoven hyphae)

coralloid: coral-like in form; of sporocarps that are composed of (usually) erect, branched or unbranched structures

coremium (pl. = coremia): anamorphic structure, a compact fascicle of conidiophores arranged in a dish-like form when sessile; if borne on a stalk and clavate or capitate, referred to as a synnema; see also stilbelloid

cornute: horned, horn-shaped

corticolous: living superficially on bark; see also subcortical

crenate (=, diminutive = crenulate): of colonies with margins that are toothed, the teeth rounded apically (Fig. 1251.36C)

crescentiform: crescent shaped; see lunate (Fig. 1251.19)

crisped, crispulate: margin repeatedly bent into a wavy or minutely wavy-form

cross: to mate; to bring together genetic material from different individuals

cross-wall: see septum

cruciate-septate: term once widely used to describe the tremelloid basidial septation (in the Tremellales and Auriculariales with four-celled globoid basidia, and in the Sebacinales). The cross-like appearance results from the positions of the appressed walls of the four compartments; they do not "cross" one another. In many taxa in these orders, often with clavate, capitate, fusiform or cylindrical basidia in a single basidiocarp, the arrangement does not yield a cruciate appearance.

cupulate: cup-shaped sporocarps as in pezizoid and helotioid ascomycetes and in some basidiomycetes

cylindrical: structures with the shape of a cylinder, i.e., round in cross-section, elongate, the sides parallel, the ends truncate or rounded (Fig. 1251.35, 41, 42); see also oblong

cymbiform: boat-like in outline, biconvex, bilaterally symmetrical (Fig. 1251.5)

cystidium (pl. = cystidia): a sterile cell situated among the basidia and usually projecting beyond them in basidiomycetes

cystosome: a membranous septum-associated organelle that occurs in some basidiomyces

cytocidal: causing cell death

dacryoid: teardrop, tear-shaped; one end rounded and the other more or less pointed (Fig. 1251.20)

dactyloid: finger-like

dangeardien: see meiosporangium (in ascomycetes and basidiomycetes)

Dauer cells: from *Dauerzellen* (German); the Dauer cell is a thick-walled, microscopically refractive, lasting or resting yeast-like cell stage

degree Balling: the gravity of wort that indicates sugar content by weight. The measurement is made with a saccharometer graduated with a scale constructed in 1843 by Carl Joseph Napoleon Balling. Degree Balling is similar to degree Brix, but the latter was determined at 15°C, whereas Balling was determined at 17.5°C. A saccharometer is a hydrometer consisting of a long graduated stem attached to an elongated bulb, which is weighted at the bottom. The hydrometer is placed in the wort and the gravity can be read on the

graduated stem; the lower the content of sugar the deeper the meter sinks into the liquid

dehiscent, dehiscing: of ascocarps or asci that open at maturity, either by formation of pores or by breaking apart

deletion: loss of one or more nucleotides or amino acids in a nucleic acid or protein sequence

deliquescent: in heterobasidiomycetes, the liquefaction of gelatinous basidiomes as they age; deliquescent ascus: see evanescent ascus

dentate: with tooth-like projections (Fig. 1251.36D, E)

denticle: a small tooth-like projection

depedunculate: having or supported on a peduncle

diclavate: club-shaped at both ends, narrowest toward the middle

dikaryon: hyphae or cells containing two genetically distinct nuclei, or sometimes numerous such pairs; also refers to the paired nuclei of such cells

dikaryotic: see dikaryon

dimitic: composed of two types of hyphae

dimorphic: having two forms (morphs), e.g., unicellular (budding cells) and filamentous (hyphae)

diobovate: broadly rounded at both ends and narrowing centrally

diplo-haplontic life cycle: asexual cells may be haploid or diploid, e.g., in *Saccharomyces cerevisiae*

diploid: nucleus or cell with a double set (2n) of chromosomes

diplontic life cycle: the asexual cells are diploid, e.g., in *Saccharomycodes ludwigii*

diplophase: the part of the life cycle in which the cells are diploid

distal: a point away from the center or away from the point of origin

distance analysis: a family of methods of phylogenetic reconstruction (e.g., neighbor joining, UPGMA) where phylogenetic trees are derived from a set of pairwise distances between the taxa to be analyzed (the distance matrix). Distances may be derived from morphological or molecular data according to various procedures

DNA reassociation: the pairing or reannealing of complementary single strands of DNA to form a double-stranded molecule (duplex)

DNA sequence homology: the extent of homology or relatedness between the nucleotide sequences of different taxa or specimens

DNA sequence relatedness: see DNA sequence homology

doliiform: barrel-like in form (Fig. 1251.31)

dolipore septum: a septal pore complex (basidiomycetes) in which the pore margin is slightly enlarged into a barrel-like form (dolipore); the paraseptal cytoplasm on either side is delimited by endoplasmic-reticulum-derived membrane domes called parenthesomes or septal pore caps

dormant: in a state of "rest" or reduced physiological activity

echinate (spinose): with more or less pointed spines (Fig. 1251.9C)

echinulate (spinulose): echinate, but with finer spines in higher density

effused: growing flat, extending at the margin; commonly used for thin, closely attached basidiomata growing on wood or other substrates (sometimes called "crusts")

ellipsoidal: elliptical in optical section (Fig. 1251.39, 40; the latter narrowly ellipsoidal)

ellipsoidopedunculate: stalk-like basally with an ellipsoidal capitulum (cp. sphaeropedunculate)

endospore: a spore formed within a cell

endosymbiont: an organism that lives inside another organism

enteroblastic: involvement of the inner part of the cell wall of the parent cell in the formation of the bud

entire margin: margin even, neither crenate nor with lobes, teeth, etc. (Fig. 1251.36A)

epibasidium (prosterigma): a structure located between a probasidium and basidiospores

epithet: the second (specific) part of a Latin binomial

erose: delicate tooth-like projections from the margin or edge, especially of colonies

erumpent: used to describe subepidermal or subcortical sporocarps that break through the outer layers (epidermis, bark) at maturity

eurybiotic: relative to the distribution of an organism, describes species that are ubiquitous

evanescent ascus: an ascus the wall of which breaks down (dissolves, disappears) when mature, thus liberating the ascospores

exosporium: the outer layer of the spore wall

falcate: sickle-shaped (Fig. 1251.26)

farinose: of surfaces, with a powdery appearance (i.e., as if dusted with flour)

fascicle: bundle, as in a sheaf of hyphae bearing conidiogenous cells in a synnema

fasciculate: growth in fascicles

filament: thread-like hyphal or pseudohyphal cell

filiform: thread-like, elongate, sides parallel, often used for straight, narrow spores (Fig. 1251.8)

filamentous: a fungus that grows with hyphae (as opposed to yeast-like growth); a life stage of a fungus, which consists of hyphal growth

fimbriate: with a torn or minutely fringed margin

fission: reproduction by cell elongation, deposition of a septum and separation of the two parts, as in *Schizosaccharomyces* spp. (Fig. 1251.23A–C)

foliaceous: leaf-like, flat, thin, broad

foliicolous: living on leaves, e.g., species of *Sporobolomyces*, *Bullera* and other fungi

funiculose: with hyphae aggregated into rope-like strands

fusiform: spindle-like, tapered toward both ends (Fig. 1251.16)

G + C content: mol percent guanine + cytosine (G + C) of DNA; see also base composition of DNA

galeate: of hat-shaped ascospores (Fig. 1251.28)

gametangiogamy: fusion of gametangia

gametangium (pl. = gametangia): gamete-producing cell; alternatively, when gametes are not formed, copulation or conjugation of gametangia occurs

gap: a symbol (mostly a hyphen) for insertions or deletions that is introduced into an alignment of nucleic acid or amino acid sequences to ensure that putatively homologous positions are arranged in columns

gastroid: a basidiome in which the sporulating parts are not exposed; also used to designate a type of sporulation in which the spores are not forcibly discharged, independent of whether or not the basidiome is of the gastroid type; see statismospore

gelatinous: gelatin- or jelly-like, as in the matrix in which basidia and structural hyphae of jelly fungi (Tremellales,

Auriculariales, etc.) are embedded; rapidly hydrating in wet weather, permitting rapid sporulation after dry periods. Gelatinous ascomata of similar constitution (also revivable on wetting) are found in some discomycetes

genetic distance: distance between two taxa derived from the comparison of DNA or amino acid sequences

genotype: the genetic constitution of an individual (cell, organism, or taxon)

germination by repetition: germination of basidiospores by the production of a ballistoconidium closely resembling its parent (sometimes referred to as secondary basidiospores)

glabrous: smooth, not hairy or roughened

globose: spherical; subglobose; almost globose, spheroidal (Fig. 1251.37, 38)

gonotocont: structure or cell in which meiosis takes place; see also meiosporangium

guild: a group of populations that use the same resources in a similar manner

habitat: the place and environmental conditions where a population occurs or lives

halophilic: of organisms requiring an increased salt concentration for growth

halotolerant: of organisms adapted to high saline environments that may require increased salt concentration for survival tolerant of high salt concentrations

haploid: nucleus or cell having a single set (n) of chromosomes

haplontic life cycle: the asexual cells are haploid

haustorium: a special hyphal branch, some portion of which penetrates a host cell wall (but usually not through the host plasma membrane); haustoria function in nutrient absorption (Fig. 1251.33, tremelloid haustorium or haustorial branch)

heritable: the proportion of the phenotypic variation that is attributable to genetic variation

heterobasidiomycetes: formerly used as a taxon name, now an informal name for basidiomycetes with plastic germination of basidiospores, i.e., with basidiospores that are capable of germinating with repetitive spores or by budding, and often have septate basidia. Heterobasidiomycetes occur in the Pucciniomycotina, Ustilaginomycotina and Agaricomycotina

heterogamous conjugation: conjugation of compatible cells, the strains consistently differing in form or size

heteropolar: cells with polar asymmetry, e.g., cells shaped like an egg or a baseball bat (cp. homopolar)

heterothallic: (see also mating loci; homothallic, bipolar, tetrapolar) in yeasts and many other fungi that lack secondary sexual features, the cells or hyphae of compatible strains are morphologically similar, but capable of mating and producing sexual spores only when compatible pairs of cells or hyphae come together. These can be bipolar or tetrapolar, the first commonly having two alternative alleles regulating mating (e.g., "a" and "α"); tetrapolar species have two separate *MAT* loci (A, and B) on separate chromosomes. *MAT* A can consist of an allelic pair, as above, but *MAT* B typically bears multiple alleles at one locus or several subloci

hispid: with short rigid hairs

hirsute: with long hairs

holoblastic: involvement of the entire cell wall of the parent cell in the formation of the bud

holometabasidium: non-septate metabasidium

holomorph: all stages of a fungus, comprising the teleomorph and all anamorphs

holotype: material or strain indicated as nomenclatural type by the original author

homokaryon: a strain in which all nuclei are of the same genotype

homokaryotic "fruiting": formation of basidia and often basidiomata in the absence of a dikaryophase (the mycelial cells typically are uninucleate and lack clamp connections, but pseudoclamps are sometimes present)

homonym: the same name given to two or more different taxa of the same rank based on different nomenclatural types (cp. synonym)

homopolar: cells with polar symmetry, e.g., cells shaped like a football or a sausage (cp. heteropolar)

homothallic: (see also mating loci, heterothallic) of species in which thalli are all alike morphologically and can reproduce sexually without mating (i.e., without the preceding interaction of complementary mating types). *Saccharomyces cerevisiae* has "a" and "α" types which can mate; each produces a complementary peptide pheromone that acts on the opposite mating type, which initiates the steps leading to sexual reproduction. This yeast is unusual, however, in that each cell carries two additional (but inactive "silenced") copies of the mating type alleles at a separate location on the same chromosome. In cells that have budded at least once, mating type switching can occur via recombination between the active and the silenced *MAT* alleles. This is thought to promote mating among sibling cells to re-establish the diploid state

horizontal gene transfer (lateral gene transfer): the transfer of DNA from a genome of one species to the genome of a different species independent of sexual recombination, or from one organelle of a cell into another organelle

hyaline: transparent, glassy, not necessarily colorless

hybrid: progeny of a cross involving parents that belong to different species or genotypes

hymenium (pl. = hymenia): spore-bearing fertile layer of an ascoma or basidioma; it consists of a layer or layers of basidia or asci plus sterile cells (cystidia, paraphyses, hyphidia) and hyphae producing these

hypha (pl. = hyphae): a tubular filament, branched or simple, septate in ascomycetes and basidiomycetes, but the septa are perforate, which often allows movement of organelles between the cells of the hypha

hyphidium (pl. = hyphidia): sterile dikaryotic hymenial structures in heterobasidiomycetes, most hypha-like and often resembling ascomycetous paraphyses

ICBN, International Code of Botanical Nomenclature: the regulations directed at consistency in describing, naming and classifying plants and fungi (the current edition is the Vienna code, McNeill et al. 2006)

imperfect state: see asexual state and conidium

incompatibility: inability of two strains of a species to mate and reproduce sexually

incompatibility system: a system in which cross-breeding is favored over inbreeding, e.g., as in the complex tetrapolar and bipolar systems of many basidiomycetes

indel: an insertion or a deletion in a DNA sequence or amino acid sequence

ingroup: the set of terminal taxa included in a phylogenetic analysis minus the outgroup taxa

insertion: gain of one or more nucleotides or amino acids in a nucleic acid or protein sequence

intercalary cell: a cell between two other cells in a hypha
interfertility: mating of individuals of separate taxa with production of fertile offspring
intramatrical: living in the matrix or substratum
invalid name: see nom. inval.
isogamous mating: direct fusion, either by mating tubes, or of cells of like morphology and size
isotype: a duplicate of the holotype from the same, single collection as the holotype

jackknife: statistical procedure related to the bootstrap to study the variance by subsampling. In phylogenetic reconstruction used to estimate the degree with which a branch of a phylogenetic tree is supported by the data. In contrast to the bootstrap, in each jackknife replicate a certain percentage (often 50%) of the columns in the original data matrix is randomly deleted. The jackknife matrices are then evaluated according to some specified method of phylogenetic inference. A jackknife value is the percentage with which a certain branch in a phylogenetic tree is present in the trees inferred in the jacknife replicates
jelly fungi: polyphyletic assemblage of heterobasidiomycetes that form gelatinous basidiomata

karyogamy: the fusion of the two compatible nuclei in an ascus or a basidium
killer toxin: see mycocin
killer yeasts: yeast species that produce mycocins

lacrymoid: shaped like a teardrop (Fig. 1251.20)
lageniform: basally enlarged, narrowed above, resembling a Florence flask (Fig. 1251.3)
lanceolate: flat objects, such as leaves, feathers, some sporocarps: narrow, tapering to the apex and sometimes toward the base
lateral: at the side of a structure
lateral gene transfer: see horizontal gene transfer
lectotype: a specimen designated as the nomenclatural type when no holotype was indicated at the time of publication of a species, or if the holotype is missing or if the holotype is found to consist of more than one taxon
lenticular: with the shape of a double convex lens in lateral view (Fig. 1251.29A)
lenticular body: see colacosome
life cycle: series of stages or events between the zygote of one generation and the subsequent zygote of the next generation
lobate: lobed
lobiform: in the shape of a lobe
locus (pl. = loci): the site of a gene on a chromosome; also, the site(s) of budding on a cell (budding loci)
lunate: crescent moon shape; see crescentiform (Fig. 1251.19)
lyophilization: a method of preserving viable, metabolically inactive cells by rapid freezing and drying under a vacuum

majority-rule consensus tree: a tree including all subtrees that are present in more than 50% of a given set of phylogenetic trees (e.g., the set of trees derived by application of the bootstrap procedure)
margin: the outer edge of a colony, e.g., on an agar plate
mating: fusion of two cells that are sexually reactive (either directly or via mating tubes)
mating loci (*MAT* loci): unique regions of the fungal genome that govern cell type identity and control developmental sequences when compatible cell types are mixed. DNA sequences of the *MAT* loci differ between cells of opposite (compatible) mating types. These differences regulate the developmental "cascades" or sequences that occur when mating is initiated. The *MAT* loci encode global transcription factors and species differ in the numbers of mating strains. In homothallic species, all genes required for sexual reproduction are present in every strain, or there is the ability to switch mating types in some cells of a population. Heterothallic species require bringing together of compatible strains; these species occur as bipolar (unifactorial) types, i.e., in which there are two compatible mating types, and as tetrapolar (bifactorial) types, which can have hundreds or possibly thousands of compatible strains. Compatible strains in bipolar species have typically been designated as "A" and "a", "α" and "a" or "+" and "−" and mating occurs only between strains differing for these alleles ("A $\times$ a" or "a $\times$ α" are compatible; "A $\times$ A", "a $\times$ a" or "$\alpha \times \alpha$" are all incompatible). In tetrapolar basidiomycetous yeast states, the alleles regulating mating are in two distinct, unlinked regions of the genome known as the "A" and "B" loci; strains must differ at *MAT* B (as with *MAT* A) for mating to occur. In the tetrapolar Tremellales, *MAT* A locus may be characterized by only two alternative alleles (e.g., A1, A2) which regulate formation of complementary pheromones initiating tube development. The *MAT* B multiple alleles control establishment of viable dikaryotic hyphae. Heterothallism promotes outbreeding in that compatible mating strains are numerous; in bipolar species, the existence of only two allelic alternatives limits outbreeding
mating types: see mating loci
maximum likelihood: statistical principle according to which a set of unknown parameters is estimated in a way that the probability of observing the data is maximized. In molecular phylogenetic reconstruction the unknown parameters are the phylogenetic tree and the parameters of the DNA or amino-acid substitution model; the observable data are represented by the sequence alignment
maximum parsimony: philosophical principle according to which the explanation is favored that uses the fewest assumptions. In phylogenetic reconstruction a phylogenetic tree is considered optimal according to the maximum parsimony principle if it requires the least possible number of character changes along its branches
medallion clamp: a clamp connection with a space between the main hypha and the hook
meiosis: reduction division, associated with sexual reproduction; the chromosome complement is reduced to the haploid number
meiosis bud: in some yeasts, a bud develops on a parent cell: the bud contains two nuclei, which will undergo fusion and subsequent meiosis
meiosporangium: the cell in which meiosis takes place, e.g., the ascus in ascomycetes, and the basidium in basidiomycetes
meiospore: a spore that has arisen from division by meiosis, e.g., an ascospore or a basidiospore
mesophilic: species with optimum temperature for growth at 20–40°C (most fungi) (cp. thermophilic and psychrophilic)
metabasidium (pl. = metabasidia): the part of the basidium in which meiosis occurs; it is also the site of karyogamy in many taxa

micropore: narrow pore-like structure in a septum
minimum evolution: a distance method in phylogenetic analysis; here, a phylogenetic tree is considered optimal when it minimizes total branch length
mitospore: see conidium
mitosporic state: see asexual state
mitosis: nuclear division with retention of the original number of chromosomes in each daughter nucleus; also, the process by which a cell replicates. The resulting cells each contain a complete copy of the parental cell chromosomes (cp. meiosis)
monokaryotic: see haploid
monophyletic group, monophylum: a taxon that consists of all species that are derived from a common ancestor; also called a natural group
monopolar budding: see budding
multiallelic compatibility: the presence of more than two alleles in a *MAT* locus
multipolar (multilateral) budding: see budding
mycangium (pl. = mycangia): a structure in the body of insects/animals that aids in the transport of symbiotic fungi; common in xylophagous insects
mycelium (pl. = mycelia): a mass of assimilative hyphae making up the "body" (soma) of an individual fungus; see also true mycelium and pseudomycelium
mycocin: a toxin produced by a fungus that kills another fungus
mycoparasitism: parasitism of a fungus by another fungus
mycoses: infections in humans/animals that are caused by fungi

napiform: form that is turnip root-like in outline (Fig. 1251.13)
natural group: see monophyletic group
navicular: boat-like in form, e.g., similar to fusiform, the ends broader, rounded, sometimes truncate at one end (Fig. 1251.15)
necrotrophic: a form of parasitism where an organism uses killed tissues of a living organism as a source of nutrients
neighbor joining: a method of distance analysis in which taxa are subsequently joined into groups using minimal evolution as an objective function in each step
neotype: strain or material designated as type when the material or strain on which the original description was based no longer exists
new combination: see comb. nov.
niche: an abstraction that describes the multidimensional environmental space in which a population lives
nom. cons., nomen conservandum: name of a taxon which has been conserved or saved over an earlier name by an International Botanical Congress committee
nom. inval., nomen invalidum: invalid name, i.e., one that has not been validly published (i.e., in accordance with the ICBN)
nom. nud., nomen nudum: a name published without an adequate description or diagnosis, i.e., not in accordance with the ICBN rules
nuclear segregation: the segregation of genetically different nuclei contained in a heterokaryotic multikaryon. Hyphae of some fungi contain several genetically distinct types of nuclei (heterokaryosis). These nuclei may segregate differently into anamorphic propagules (part of a cycle referred to as parasexuality)
numerical analysis, numerical taxonomy: taxonomic arrangement based on quantitation of phenotypic similarities and differences

obclavate: club-shaped with the broadest part at the base (Fig. 1251.4, right)
oblate: ellipsoidal, elongated at right angles to the polar axis; see also prolate
oblong: twice as long as wide and having somewhat truncate ends (Fig. 1251.35, 41, 42, the latter with truncate ends)
obovoid: see obovate
obovate: inversely ovate, narrowest at the base (Fig. 1251.6)
obpyriform: pear-shaped but attached at the broad end (Fig. 1251.7)
obtuse: rounded or blunt
ogival: pointed like a Gothic arch
orbicular: spherical, round, rounded
osmophilic: growing best in media with elevated concentrations of osmotically active substances (i.e., sugars, salts)
osmotic medium: medium with elevated sugar or salt concentration
osmotolerance: resistance to osmotic pressure (i.e., able to grow in higher than normal concentrations of sugars or salts)
outgroup: a set of terminal taxa in a phylogenetic analysis that does not belong to the group of interest; this set of outgroup taxa is used to root trees resulting from phylogenetic analysis
ovoid: egg-like, i.e., with narrowest end distal from the attachment or base (Fig. 1251.6)

papilionoid: butterfly-shaped
paraphyletic taxon: a non-monophyletic taxon that does not contain all species derived from a common ancestor
paraphysis (pl. = paraphyses): simple or branched, sterile filaments in hymenia of many ascomata. Analogous structures in basidiomata are dikaryotic; they are referred to as cystidia (structure distinct from hyphae) or hyphidia (often hypha-like)
parasexuality: recombination of hereditary properties based not on sexual reproduction (meiosis) but on occasional fusions of unlike haploid nuclei in heterokaryotic hyphae, mitotic non-disjunction and segregation into anamorphic spores (events random rather than in orderly series)
parasitoid: the immature life stage of an insect that develops on or within a single insect host, ultimately killing the host
paratype: a specimen (strain) cited in the original description of a species that is neither the holotype nor an isotype
parenthesome: in basidiomycetes, a curved, double membrane-derived system differentiated from the endoplasmic reticulum and present on either side of the septal dolipore
parsimony: see maximum parsimony
pedicel: a small stalk-like structure
peduncle: stalk
pellucid: translucent
peltate: tack-like in outline, the central stipe often rudimentary (Fig. 1251.11)
percurrent: successive budding at one locus, usually leaving distinct bud scars
perfect state: former designation of the sexual state of a fungus, now referred to as the teleomorph
perithecium: a subglobose or flask-like ascoma
persistent ascus: ascus not evanescent (dissolving) at maturity
phenotype: the totality of characteristics of an individual as a result of the interaction between expressed genotype and environment; the visible or measurable properties of an

individual as determined by both environment and genetic makeup

phragmobasidium, phragmometabasidium (pl. = -basidia): a basidium divided by septa (the septate portion of a basidium is often designated as the metabasidium)

phylloplane: the surface of a leaf

phylogenetic network: generalization of a phylogenetic tree that allows either the visualization of conflicting phylogenetic signal as represented by conflicting splits or the inclusion of hybridization events

phylogenetic tree: an unrooted or rooted graph illustrating the phylogenetic relationships between several taxa. In most cases the graph also includes information about the degree of relatedness between taxa as expressed by branch lengths; see also phylogram

phylogram: graphical visualization of a phylogenetic tree, including information on branch lengths

pileus: the cap or hymenium-supporting part of complex basidiomata or ascomata, e.g., in agarics, morels, jelly fungi

plasmodesma (pl. = plasmodesmata): isthmus-like strand of protoplasm connecting adjacent cells via pores in the septum; see also micropore

plasmogamy: fusion of the cytoplasm of two compatible cells, as distinct from karyogamy (nuclear fusion)

pleomorphic: with variable morphology

plicate: folded into pleats, pleated

polar budding: see budding

polyphyletic taxon: a non-monophyletic taxon based on traits that have evolved separately in different clades

polyploid: cell or individual with more than two sets of chromosomes in each nucleus

polytomy: in a phylogenetic tree an inner node that gives rise to more than two branches

polytrophic: organisms that can utilize various types of organic material for maintenance and growth

probasidium: the morphological part or developmental stage of the basidium in which karyogamy often occurs if distinct from the site of meiosis (i.e., the metabasidium) in some dimorphic basidiomycetes

prolate: ellipsoidal, elongated in the direction of the polar axis; see also oblate

promycelium (pl. = promycelia): formerly used for the metabasidium with which a teliospore germinates in smut fungi

protosterigma (pl. = protosterigmata): see epibasidium

prototrophic: growth factor-independent; of a yeast strain that can produce any necessary vitamins or other growth factors it requires for growth (in axenic culture) (cp. auxotrophic)

proximal: close to the point of origin or the center (cp. distal)

pseudoclamp, false clamp: a clamp-like loop, the tip of which does not fuse back with the parent hypha, typical of some homokaryotic hyphae or those developing when some hemicompatible strains are mated

pseudohyphae: a linear or branched arrangement of budding cells that remain attached to each other; also referred to as pseudomycelium

pseudomycelium (pl. = pseudomycelia): see pseudohyphae

pseudothecium: an ascostromatic ascoma with asci in unwalled locules

psychrophilic: species with optimum temperatures for growth below 20°C and capable of growth at 4°C or less (cp. thermophilic and mesophilic)

pulcherrima cells: round cells containing a large oil drop as in *Metschnikowia* (*Candida*) *pulcherrima*

pulcherrimin: a red iron-containing compound produced by some strains of *Metschnikowia*, *Kluyveromyces* and certain other yeasts

pulvinate: cushion-like; strongly convex cushion- or pillow-like sporocarp form

punctuate: surface marked by minute raised points (Fig. 1251.9B)

pyriform: pear-shape (Fig. 1251.7)

reannealing experiments: see DNA reassociation

reniform: kidney-like shape (Fig. 1251.17)

repetitive spore germination: see germination by repetition

reticulate: netted pattern, e.g., spore wall surface pattern (Fig. 1251.9F)

retraction septum: septum that occurs after the cytoplasm retracts from (part of) the hypha

root of a phylogenetic tree: the most basal branch of a rooted phylogenetic tree; in most instances the evidence that a certain branch is most basal comes from external data and cannot be derived directly from the phylogenetic analysis itself

rotational symmetry: with all planes of symmetry through the length axis

rugose: wrinkled (Fig. 1251.9G)

saccate: sac- or bag-like

saturnine: ascospores that are broadly ellipsoidal with a ledge around the middle, i.e., Saturn-like in appearance (Fig. 1251.32)

scolecoconidium (pl. = scolecoconidia): long and thin conidium that may or may not be septate

self-fertile: see homothallic

septate: with septa

Septal pore cap: see parenthesone

septum (pl. = septa): a cross-wall between neighboring cells (e.g., of a hypha)

serrate: margin with teeth; diminutive = serrulate (Fig. 1251.36D, E)

serrulate: see serrate

sessile: structure lacking a stem or stalk; also of basidiospores borne directly on the basidium or nearly so (many statismospores)

seta (pl. = setae): a stiff hair- or bristle-like cell in hymenia of some asco- or basidiomycetes; sterile, typically thick-walled and often pointed

sib mating: mating or crossing of siblings, e.g., crossing of progeny arising from the same meiotic division

sibling species: species that are genetically distinct and not interbreeding, but are not morphologically distinct

siderophore: an iron-chelating compound secreted by microorganisms

sigmoid: curved like the letter S (Fig. 1251.25)

simple pore: septal pore, the wall tapering toward the opening and without a parenthesome (ascomycetes and Pucciniomycotina)

sinuous: margin wavy, neither flat nor indented (Fig. 1251.36B)

sister species: species derived from a common ancestral species shared by no other species

smut fungi, smuts: polyphyletic assemblage of heterobasidiomycetes belonging to Ustilaginomycotina or Pucciniomycotina that parasitize vascular plants and produce teliospores ("smut spores") in dusty, usually black masses within the host tissues

soma: the mass of assimilative hyphae (mycelium) making up the body of a fungus

somatogamous conjugation: fusion of two somatic cells (yeasts)

somatogamy: fusion of monokaryotic hyphae followed by nuclear transfer and initiation of the dikaryotic state (basidiomycetes)

spathulate: stalked, the tip broadened, flat and spoon-like in outline (Fig. 1251.10)

sphaeropedunculate (stalked-capitate): a sphaeroidal capitulum on a narrow, stalk-like base (Fig. 1251.1, 2)

spinose: see echinate

spinulose: see echinulate

split: bipartition of a set of terminal taxa involved in a phylogenetic analysis. Any branch in a phylogenetic tree induces a split by removing that branch from the tree. Phylogenetic networks allow the visualization of conflicting splits (i.e., splits that cannot be included in the same tree)

sporangiospore: a spore produced in a sporangium

sporangium: a structure that produces asexual endospores by cytoplasmic cleavage

sporidium (pl. = sporidia): budding basidiospores, i.e. the blastic statismospores produced by basidia of many smuts, *Agaricostilbum* spp. and similar fungi

sporocarp: ascocarp or basidiocarp

sporophore: a spore-producing or supporting structure

stalagmoid: like a long tear or drop; see also lacrymoid, dacryoid (Fig. 1251.20)

statismospore: a passively released basidiospore (also sometimes called a gastroid basidiospore)

stauroconidium (pl. stauroconidia): star-shaped conidium that may or may not be septate

stemonitoid: of a synnema with an elongate fertile "head" e.g., that resembles the sporangia of *Stemonitis* spp. (fertile portion typically elongate, cylindrical)

sterigma: an extension (process) of a basidium that supports a basidiospore; also used for similar structures supporting ballistoconidia

sterigmate: originating on or gives rise to a sterigma

sterigmatoconidia: conidia that are formed on elongated sporangiophores

stilbelloid: of a minute basidiome having the simple stipitate-capitate characteristic of *Stilbum* and *Agaricostilbum* spp.

stipitate-capitate: similar to sphaeropedunculate (Fig. 1251.1, 2); the capitulum is often not spherical

strict consensus tree: a tree that contains exactly those splits that are present in each tree of a given set of phylogenetic trees

stroma (pl. = stromata): often hard and dark-colored parenchyma-like pseudotissue in fungi (term mostly used for ascomycetes)

subcortical: grows under bark (cortex), and either remains concealed or often breaks through the bark (erumpent)

subglobose: not completely globose (Fig. 1251.38)

subhymenium: the anatomical structure adjacent to the hymenium in a sporocarp

substitution: the replacement of a nucleotide in a certain position of a DNA sequence by another nucleotide or of an amino acid in a certain position within a protein by another amino acid during evolution

substitution rate: the rate at which substitution events occur during evolution of a certain DNA or amino acid sequence

subulate, subuliform: awl-shaped, narrow, pointed at one end, curved (Fig. 1251.27)

supertree: a phylogenetic tree that unites information derived from a set of trees which have different sets of terminal taxa (cp. consensus tree)

symplechiosome: organelle consisting of stacked membranes that occurs in the cells of some basidiomycetes

sympodial proliferation: see sympodium

sympodium (pl. = sympodia): a conidiogenous cell that grows apically, producing a succession of apices; each bearing a conidium, then elongating to one side of the conidial base, often resulting in a zigzag or scorpioid appearance

synanamorph: two or more anamorphs with the same teleomorph

syngamy: fusion of gametes; in yeasts, fusion of compatible undifferentiated cells followed by karyogamy and zygote formation

synnema (pl. = synnemata): anamorphic structures consisting of a compact sheaf of conidiophores bearing conidiogenous cells and conidia; see also coremium

synnematoid: of synnema-like basidiomes see stilbelloid

synonym: another taxonomic name for a species or group, especially a later or illegitimate name not currently in use for the taxon

syntype: one of several descriptive elements cited by an author when originally proposing a name but where no holotype was selected

taxon (pl. = taxa): a taxonomic unit of any type, e.g., species, genus, family or higher classification

teleomorph, teleomorphic state: the life state in which sexual spores (e.g., ascospores or basidiospores) are formed after nuclear fusion and meiosis

teliospore: in Puccinio- and Ustilaginomycotina, a thick-walled resting spore that germinates by producing a metabasidium, the teliospore vestige then referred to as a probasidium

tetrapolar compatibility: see mating loci

thermophilic: organisms with minimum temperatures for growth above 20°C and extending to 60–62°C, which is likely to be the maximum for yeasts (cp. mesophilic and psychrophilic)

topology: as used in phylogenetic analysis, the branching pattern of a phylogenetic tree. The graphical visualization is often referred to as a cladogram and can be obtained by stripping a phylogenetic tree of its branch length information

tremelloid: of a sporocarp; gelatinous, jelly-like; of a basidium: mostly sphaeroidal phragmobasidium, the septa longitudinal to oblique, dividing the basidium into two or four cells (formerly often referred to as cruciate septate)

true hyphae: septate hyphae, the growth in length of which is restricted to the apical cells; see also true mycelium

true mycelium: a body (thallus) of usually septate, branched hyphae

truncate: ending abruptly as though the end was cut off (as in Fig. 1251.42)

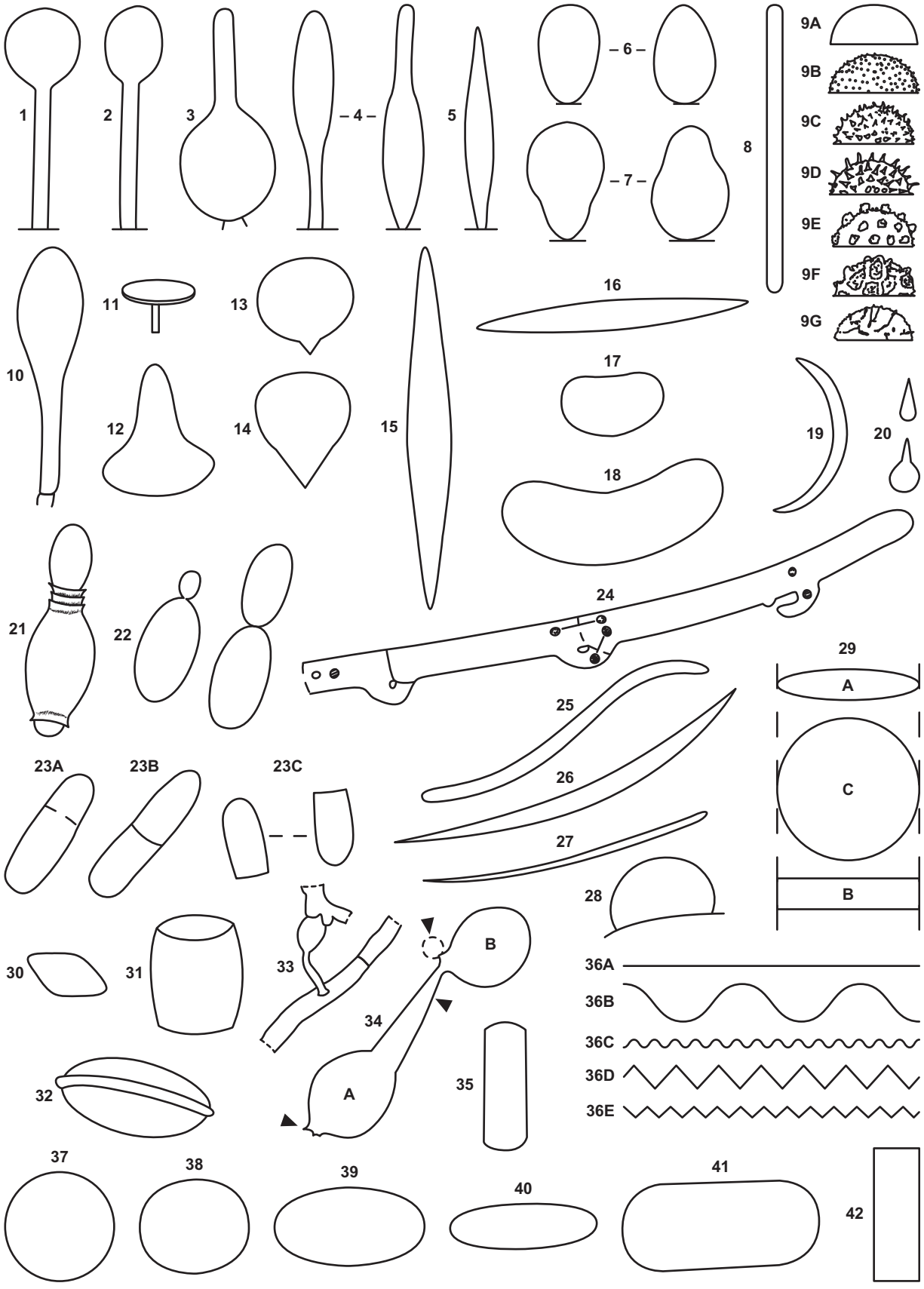
tubercle: a small wart-like structure

tuberculate: with tubercles (Fig. 1251.9E)

turbinate: top-like in form (Fig. 1251.14)

twin buds: two buds that are formed side by side

type material: material on which the name of a species or subspecific category is based; may be dried herbarium material or a viable, metabolically inactive culture preserved by lyophilization or liquid nitrogen freezing


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◀ **FIGURE 1251** 1. Stalked-capitate, sphaeropedunculate; 2. ellipsoidopedunculate; 3. lageniform; 4. clavate (left), obclavate (right); 5. lanceolate; 6. obovoid (left), ovoid (right); 7. obpyriform (left), pyriform (right); 8. filiform; 9. surface textures (spore surfaces, etc.), A. smooth, B. punctuate, C. echinate; diminutive, echinulate, D. aculeate, spines large, E. bullate, F. reticulate, G. rugose; diminutive, rugulose; 10. spathulate (spatulate); 11. peltate; 12. ampulliform; 13. napiform; 14. turbinate; 15. navicular; 16. fusiform; 17. reniform; 18. allantoid (also botuliform); 19. lunate (also crescentiform); 20. dacryoid (also lacrymoid); 21. budding: cell showing bipolar budding; annelations at poles marking sites of earlier buds, as in *Nadsonia*; 22. budding: (on a narrow base) a bleb develops (left), enlarges, receives organelles and cytoplasm from parent cell and is abstricted at maturity, leaving a bud scar on the parent cell and a birth scar on the new cell, e.g., *Saccharomyces*; 23. fission: A, growth of a new yeast cell commences on a broad base; B, it elongates and becomes separated from the parent by a septum; C, the two cells separate; e.g., *Schizosaccharomyces*; 24. clamp connection formation (basidiomycetous hypha): apical cell produces a backward directed branch (top, right); the paired nuclei move one each into the branch and the main axis just adjacent to the branch (middle). The two nuclei undergo mitosis, walls form at right angles to the nuclear spindles, cutting off the branch near its origin, and producing the endwall of a new cell in the hypha. The lateral branch tip continues to grow during the process, its tip anastomosing with the parent filament, and the nucleus in it moving into that cell close to the nucleus produced by mitosis in the main axis. Each cell produced becomes walled off from the previous and next cell and each contains a compatible nuclear pair (a dikaryon); 25. sigmoid; 26. falcate; 27. subulate, subuliform; 28. hat-shaped (galeate) ascospore; 29. A. lenticular (biconvex), edge view, B. discoid, edge view, C. face view of both A and B; 30. rhomboidal, rhombus; 31. doliiform; 32. saturnine: resembling the planet Saturn and its rings; 33. tremelloid haustorial branch (upper, vertical hypha), consisting of a swollen parent cell subtended by a clamp connection and with a terminal filament, the tip of which penetrates the wall of its hyphal fungus host (diagonal simple septate hypha); 34. A. ballistospore germinating by repetition, producing a sterigma and ballistoconidium (basidiomycetes). B. the upper arrowhead marks the liquid droplet which appears immediately preceding forcible abstriction. The second arrowhead (right-hand side) indicates the sterigma which is similar to that on a basidium. The lower arrowhead points to the hilar scar of the basidiospore, the point where it was attached to the basidial sterigma; 35. oblong (cylindrical); 36. margin types (yeast colonies, basidiocarps, etc.), A. straight, entire, B. sinuous, wavy; C. crenate (diminutive, crenulate), D. serrate, E. serrulate; 37. globose, spherical; 38. subglobose, spheroidal; 39. ellipsoidal; 40. narrowly ellipsoidal; 41. oblong, ends rounded truncate; 42. cylindrical, ends truncate, as in an arthroconidium.

type species: a species which was designated as the nomenclatural type of a genus

type strain: the preserved original strain (a culture) originally designated as the nomenclatural type

unifactorial mating system: see mating loci

unisexual: of yeast cells that are of a single mating type

unrooted tree: a phylogenetic tree for which a root has not been designated

UPGMA: method of cluster analysis that may be applied in molecular phylogenetic inference if a constant substitution rate can be assumed for the alignment under analysis

velvety: a velutinous appearance, i.e., the surface is densely covered by fine hairs

ventricose: swelling out in the middle or at one side; inflated (Fig. 1251.5)

verrucose: small rounded processes or wart-like bumps (Fig. 1251.9E)

verticil: a whorl of branches or spores around a single point on a hypha, conidiophore or similar structure

verticillate: arranged in whorls, verticils

vesicle: a small bladder-like sac within a cell or, alternatively, a hyphal cell of similar form

vesiculate, vesiculose: composed of or covered with vesicles

wale-like: ascospore ornamentation comprised of short ridges; they may be irregularly placed

Woronin bodies: membrane-bound refractive spherical bodies that are peroxisomes occurring on either side of the septal pore in hyphae of some ascomycetes

xanthochroic: having a reddish-brown or yellowish-brown content that darkens with potassium hydroxide

zygote: a diploid cell resulting from syngamy of two sexual cells or nuclei

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Index to Taxa by Genus and Species

The names of genera, species and varieties accepted by the authors are indicated in bold type. The numbers of the pages referring to diagnoses and standard descriptions are printed in bold type as well.

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Recurrent use of species and variety names, as well as new combinations from taxonomic changes, result in placement of the same name with different genera. Combinations accepted by authors of the present edition are given in bold type. Page numbers in each combination are given following the genus name.

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References

Aa, E., J.P. Townsend, R. Adams, K.M. Nielsen and J.W. Taylor. 2006. Population structure and gene evolution in *Saccharomyces cerevisiae*. FEMS Yeast Res. 6, 702–715.

Aalbaek, B., J. Stenderup, H.E. Jensen, J. Valbak, B. Nylin and A. Huda. 1994. Mycotic and algal bovine mastitis in Denmark. APMIS 102, 451–456.

Abadias, M., A. Benabarre, N. Texidó, J. Usall and I. Viñas. 2001a. Effect of freeze drying and protectants on viability of the biocontrol yeast *Candida sake*. Int. J. Food Microbiol. 65, 173–182.

Abadias, M., N. Teixidó, J. Usall, A. Benabarre and I. Viñas. 2001b. Viability, efficacy, and storage stability of freeze-dried biocontrol agent *Candida sake* using different protective and rehydration media. J. Food Prot. 64, 856–861.

Abadias, M., N. Texidó, J. Usall, I. Viñas and N. Magan. 2001c. Improving water stress tolerance of the biocontrol yeast *Candida sake* grown on molasses-based media by physiological manipulation. Can. J. Microbiol. 47, 123–129.

Abadie, F. 1961. Intérêt systématique de la recherche de l'urease chez les levures et organismes. C.R. Acad. Sci. 252, 2122–2124.

Abadie, F. 1967. L'Uréase chez les levures. Ann. Inst. Pasteur 113, 791–813.

Abadie, F., M.C. Pignal and J.L. Jacob. 1963. Les levures á spores verruqueuses. Bull. Soc. Mycol. Fr. 79, 16–70.

Abe, F., T. Miura, T. Nagahama, R. Usami, A. Inoue and K. Horikoshi. 2001. Isolation of a highly copper-tolerant yeast, *Cryptococcus* sp., from the Japan Trench and the induction of superoxide dismutase activity by Cu^{2+}. Biotechnol. Lett. 23, 2027–2034.

Abe, F., H. Minegishi, T. Miura, T. Nagahama, R. Usami and K. Horikoshi. 2006. Characterization of cold- and high-pressure-active polygalacturonases from a deep-sea yeast, *Cryptococcus liquefaciens* strain N6. Biosci. Biotechnol. Biochem. 70, 296–299.

Abeliovich, H. 2007. Mitophagy: the life-or-death dichotomy includes yeast. Autophagy 3, 275–277.

Abercrombie, M.J., J.K.N. Jones, M.V. Lock, M.B. Perry and R.J. Stoodley. 1960. The polysaccharides of *Cryptococcus laurentii* (NRRL Y-1401). Can. J. Chem. 38, 1617–1624.

Abou-Gabal, M., and J.A. Fagerland. 1979. Electron microscopy of *Pityrosporum canis* "*pachydermatis*". Mykosen 22, 85–90.

Abou-Gabal, M., C.B. Chastain and R.M. Hongle. 1979. *Pityrosporum* (*pachydermatis*) *canis* as a major cause of otitis externa in dogs. Mykosen 22, 192–199.

Abranches, J., P.B. Morais, C.A. Rosa, L.C. Mendonça-Hagler and A.N. Hagler. 1997. The incidence of killer activity and extracellular proteases in tropical yeast communities. Can. J. Microbiol. 43, 328–336.

Abranches, J., P. Valente, H.N. Nobrega, F.A.S. Fernandez, L.C. Mendonça-Hagler and A.N. Hagler. 1998. Yeast diversity and killer activity dispersed in fecal pellets from marsupials and rodents in a Brazilian tropical habitat mosaic. FEMS Microb. Ecol. 26, 27–33.

Abranches, J., M.J.S. Vital, W.T. Starmer, L.C. Mendonça-Hagler and A.N. Hagler. 2000. The yeast community and mycocin producers of guava fruit in Rio de Janeiro, Brazil. Mycologia 92, 16–22.

Abranches, J., W.T. Starmer and A.N. Hagler. 2001. Yeast–yeast interactions in guava and tomato fruits. Microb. Ecol. 42, 186–192.

Aciole de Queiroz, L. 1970. *Pichia faecalis* nov. comb. Revisión de una cepa de levadura nombrada *Kloeckera faecalis* Batista & Silveira, 1959. Mycopathol. Mycol. Appl. 41, 327–329.

Aciole de Queiroz, L. 1973. *Endomycopsis montevidensis* n. sp. Mycopath. Mycol. Appl. 51, 307–314.

Acton, H.W. 1919. Mycotic infections of the throat due to the *Endomyces tropicalis*. Indian J. Med. Res. 6, 591–600.

Acton, H.W., and G. Panja. 1949. Seborrhoeic dermatitis or pityriasis capitis: a lesion caused by the *Malassezia ovale*. Indian Med. Gaz. 62, 603–614.

Adachi, J., and M. Hasegawa. 1996. Model of amino acid substitution and applications to mitochondrial protein evolution. J. of Mol. Evol. 42, 459–468.

Adam, H., M. Groenewald, S. Mohan, S. Richardson, U. Bunn, C.F.C. Gibas, S. Poutanen and L. Sigler. 2009. Identification of a new species, *Candida subhashii*, as a cause of peritonitis. Med. Mycol. 47, 305–311.

Addis, E., G.H. Fleet, J.M. Cox, D. Kolak and T. Leung. 2001. The growth, properties and interactions of yeasts and bacteria associated with the maturation of Camembert and blue-veined cheeses. Int. J. Food Microbiol. 69, 1–2.

Adler, A., C. Hidalgo-Grass, T. Boekhout, B. Theelen, E. Sionov and I. Polacheck. 2007. *Pichia farinosa* bloodstream infection in a lymphoma patient. J. Clin. Microbiol. 45, 3456–3458.

Adrio, J.L., and A.L. Demain. 2003. Fungal biotechnology. Int. Microbiol. 6, 191–199.

Aehle, W. (Ed.) 2004. Enzymes in Industry. Production and Applications, 2nd edn. Wiley VCH, Weinheim.

Agirbasli, H., H. Bilgen, S.K. Ozcan, B. Otlu, G. Sinik, N. Cerikçioglu, R. Durmaz, E. Can, N. Yalman, G. Gedikoglu and T. Sugita. 2008. Two possible cases of *Trichosporon* infections in bone-marrow-transplanted children: the first case of *T. japonicum* isolated from clinical specimens. Jpn. J. Infect. Dis. 61, 130–132.

Agrawal, R., N.R. Singh, F.H. Ribeiro and W.N. Delgrass. 2007. Sustainable fuel for the transportation sector. Proc. Natl. Acad. Sci. USA 104, 4828–4833.

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Agrios, G.N. 1997. Plant Pathology, 4th edn. Academic Press, San Diego, CA.

Aguedo, M., M.H. Ly, I. Belo, J.A. Teixeira, J.-M. Belin and Y. Waché. 2004. The use of enzymes and microorganisms for the production of aroma compounds from lipids. Food Technol. Biotechnol. 42, 327–336.

Aguilar-Uscanga, B., and J.M. Francois. 2003. A study of the yeast cell wall composition and structure in response to growth conditions and mode of cultivation. Lett. Appl. Microbiol. 37, 268–274.

Ahearn, D.G., and R.B. Simons. 1998. *Malassezia* Baillon. In: C.P. Kurtzman and J.W. Fell (Eds), The Yeasts, A Taxonomic Study, 4th edn. Elsevier, Amsterdam, pp. 782–784.

Ahearn, D.G., F.J. Roth, J.W. Fell and S.P. Meyers. 1960. Use of shaken cultures in the assimilation test for yeast identification. J. Bacteriol. 79, 369–371.

Ahearn, D.G., J.R. Jannach and F.J. Roth. 1966. Speciation and densities of yeasts in human urine specimens. Sabouraudia 5, 110–119.

Ahearn, D.G., F.J. Roth Jr. and S.P. Meyers. 1968. Ecology and characterization of yeasts from aquatic regions of South Florida. Mar. Biol. 1, 291–308.

Ahearn, D.G., D. Yarrow and S.P. Meyers. 1970. *Pichia spartinae* sp. n. from Louisiana marshland habitats. Antonie van Leeuwenhoek 36, 503–508.

Ahearn, D.G., S.A. Meyer, G. Mitchell, M.A. Nicholson and A.I. Ibrahim. 1977. Sucrose-negative variants of *Candida tropicalis*. J. Clin. Microbiol. 5, 494–496.

Ahmad, K., S. Koul, S.C. Taneja, A.P. Singh, M. Kapoor, Riyaz-ul-Hassan, V. Verma and G.N. Qazi. 2004. Enzyme directed diastereoselectivity in chemical reductions: studies towards the preparation of all four isomers of 1-phenyl-1,3-butanediol. Tetrahedron Asymmetry 15, 1685–1692.

Ahmad, S., M. Al-Mahmeed and Z.U. Khan. 2005. Characterization of *Trichosporon* species isolated from clinical specimens in Kuwait. J. Med. Microbiol. 54, 639–646.

Ahrazem, O., A. Prieto, G. San-Blas, J.A. Leal, J. Jimenez-Barbero and M. Bernabe. 2003. Structural differences between the alkali-extracted water-soluble cell wall polysaccharides from mycelial and yeast phases of the pathogenic dimorphic fungus *Paracoccidioides brasiliensis*. Glycobiology 13, 743–747.

Aidoo, K.E., M.J.R. Nout and P.K. Sarkar. 2006. Occurrence and function of yeasts in Asian indigenous fermented foods. FEMS Yeast Res. 6, 30–39.

Aime, M.C., P.B. Matheny, D.A. Henk, E.M. Frieders, R.H. Nilsson, M. Piepenbring, D.J. McLaughlin, L.J. Szabo, D. Begerow, J.P. Sampaio, R. Bauer, M. Weiss, F. Oberwinkler and D. Hibbett. 2006. An overview of the higher level classification of Pucciniomycotina based on combined analyses of nuclear large and small subunit rDNA sequences. Mycologia 98, 896–905.

Ainsworth, G.C. 1971. Ainsworth & Bisby's Dictionary of the Fungi, 6th edn. Commonwealth Mycological Institute, Kew.

Ainsworth, G.C. 1973. Introduction and keys to higher taxa. In: G.C. Ainsworth, F.K. Sparrow and A.S. Sussman (Eds), The Fungi. Academic Press, New York, pp. 1–7.

Airola, K., L. Petman and S. Makinen-Kiljunen. 2006. Clustered sensitivity to fungi: anaphylactic reactions caused by ingestive allergy to yeasts. Ann. Allergy Asthma Immunol. 97, 294–297.

Ajello, L. 1958. Occurrence of *Cryptococcus neoformans* in soil. Am. J. Hyg. 67, 72–77.

Akagi, S. 1929. Über eine neue mykotische Hautkrankheit "Trichosporiacutis psoriatiformis progressiva Asahi et Akagi". Jpn. J. Dermatol. Urol. 29, 53–55, 733–774.

Akaike, H. 1974. A new look at the statistical model identification. IEEE Trans. Autom. Control 19, 716–723.

Akhtar, P., J.I. Gray and A. Asghar. 1998. Chemical characterization and stereospecific analysis of lipids synthesized by certain yeast strains. J. Food Lipids 5, 299–311.

Aki, T., T. Yamasaki, M. Nanko, M. Shionsaki, S. Kawawato and K. Ono. 2007. Xanthophylls and polyunsaturated acids produced by matine thraustochytrids. In: C.T. Hou and J.-F. Shaw (Eds), Biocatalysis and Biotechnology for Functional Foods and Industrial Products. CRC Press, Boca Raton, FL, pp. 187–198.

Akoh, C., G. Lee and J. Shaw. 2004. Protein engineering and applications of *Candida rugosa* lipase isoforms. Lipids 39, 513–526.

Alcade, M., M. Ferrer, F.J. Plou and A. Ballesteros. 2006. Environmental biocatalysis: from remediation with enzymes to novel green processes. Trends Biotechnol. 24, 281–287.

Alcoba-Flórez, J., S. Méndez-Álvarez, J. Cano, J. Guarro, E. Pérez-Roth and M. Arévalo. 2005. Phenotypic and molecular characterization of *Candida nivariensis* sp. nov., a possible new opportunistic fungus. J. Clin. Microbiol. 43, 4107–4111.

Aldhous, P. 2000. Modified yeast fine for food. Nature 344, 186.

Alexandre, H., and M. Guilloux-Benatier. 2006. Yeast autolysis in sparkling wine – a review. Aust. J. Grape Wine Res. 12, 119–217.

Alexopoulos, C.J., and C.W. Mims. 1979. Introductory Mycology, 3rd edn. Wiley, New York.

Alexopoulos, C.J., C.W. Mims and M. Blackwell. 1996. Introductory Mycology, 4th edn. John Wiley & Sons, New York.

Aliouat, E.M., E. Mazars, E. Dei-Cas, P. Delcourt, P. Billaut and D. Camus. 1994. *Pneumocystis* cross infection experiments using SCID mice and nude rats as recipient host, showed strong host-species specificity. J. Eukaryot. Microbiol. 41, 71S.

Aliouat, E.M., L. Dujardin, A. Martinez, T. Duriez, I. Ricard and E. Dei-Cas. 1999. *Pneumocystis carinii* growth kinetics in culture systems and in host: involvement of each life cycle parasite stage. J. Eukaryot. Microbiol. 46, 116S–117S.

Allen, T.W., L.L. Burpee and J.W. Buck. 2004a. *In vitro* attachment of phylloplane yeasts to *Botrytis cinerea, Rhizoctonia solani*, and *Sclerotinia homoeocarpa*. Can. J. Microbiol. 50, 1041–1048.

Allen, T.W., H.A. Quayyum, L.L. Burpee and J.W. Buck. 2004b. Effect of foliar disease on the epiphytic yeast communities of creeping bentgrass and tall fescue. Can. J. Microbiol. 50, 853–860.

Almeida, J.M.G.C.F. 2005. Yeast community survey in the Tagus estuary. FEMS Microbiol. Ecol. 53, 295–303.

Almeida, M.J., and C.S. Pais. 1996. Characterization of the yeast population from traditional corn and rye bread doughs. Lett. Appl. Microbiol. 23, 154–158.

Aloj, B., B. Nanni and F. Marziano. 1999. Osservazioni su un caso di bolla dell'albicocco in Campania. Inform. Fitopatol. 49, 35–37.

Alper, H., J. Moxley, E. Nevoigt, G.R. Fink and G. Stephanopolous. 2006. Engineering yeast transcription machinery for improved ethanol tolerance and production. Science 314, 1565–1568.

Alsina, A., M. Mason, R.A. Uphoff, W.S. Riggsby, J.M. Becker and D. Murphy. 1988. Catheter-associated *Candida utilis* fungemia in a patient with acquired immunodeficiency syndrome: species verification with a molecular probe. J. Clin. Microbiol. 26, 621–624.

Alstrup, V. 1993. News on lichens and lichenicolous fungi from the Nordic countries. Graphis Scripta 5, 97–98.

Altschul, S.F., T.L. Madden, A.A. Schäffer, J. Zhang, Z. Zhang, W. Miller and D.J. Lipman. 1997. Gapped BLAST and PSI-Blast: a new generation of protein database search programs. Nucleic Acids Res. 25, 3389–3402.

Álvarez, V., M. Rodriguez-Sáiz, J.L. de la Fuente, E.J. Gudiña, R.P. Godio, J.F. Martín and J.L. Barredo. 2007. The crtS gene of *Xanthophyllomyces dendrorhous* encodes a novel cytochrome-P450 hydroxylase involved in the conversion of beta-carotene into astaxanthin and other xanthophylls. Fungal Genet. Biol. 43, 261–272.

Alves-Araújo, C., M.J. Almeida, M.J. Sousa and C. Leão. 2004. Freeze tolerance of the yeast *Torulaspora delbrueckii*; cellular and biochemical basis. FEMS Microbiol. Lett. 240, 7–14.

Alves-Araújo, C., A. Pacheco, M.J. Almeida, I. Spencer-Martins, C. Leão and M.J. Sousa. 2007. Sugar utilization patterns and respiro-fermentative metabolism in the baker's yeast *Torulaspora delbrueckii*. Microbiology 153, 898–904.

Amano, Y., S. Goto and M. Kagami. 1975. A strongly ethanol-assimilating new yeast *Candida brassicae* nov. sp. J. Ferment. Technol. 53, 311–314.

Amberg, D.C., D.J. Burke and J.N. Strathern (Eds). 2005. Methods in Yeast Genetics: A Cold Spring Harbor Laboratory Course Manual. Cold Spring Harbor Laboratory Press, Cold Spring Harbor, New York.

Amerine, M.A., H.W. Berg, R.E. Kunkee, C.S. Ough, V.L. Singleton and A.D. Webb. 1980. The Technology of Winemaking, 4th edn. AVI Publishing, Westport, CT.

Amoresano, A., A. Andolfo, M.M. Corsaro, I. Zocchi, I. Petrescu, C. Gerday and G. Marino. 2000. Structural characterization of a xylanase from psychrophilic yeast by mass spectrometry. Glycobiology 10, 451–458.

Am-In, S., S. Limtong, W. Yongmanitchai and S. Jindamorakot. 2010. *Candida andamanensis* sp. nov., *Candida laemsonensis* sp. nov., and *Candida ranongensis* sp. nov., three anamorphic yeast species isolated from estuarine waters in a mangrove forest in Ranong Province, Thailand. Int. J. Syst. Evol. Microbiol. doi: 10.1099/ijs.0.022038-0.

An, G.-H., and E.A. Johnson. 1990. Influence of light and growth on pigmentation of the yeast *Phaffia rhodozyma*. Antonie van Leeuwenhoek 57, 191–203.

An, G.-H., D.B. Schuman and E.A. Johnson. 1989. Isolation of *Phaffia rhodozyma* mutants with increased astaxanthin content. Appl. Environ. Microbiol. 55, 116–124.

An, G.-H., J. Bielich, R. Auerbach and E.A. Johnson. 1991. Isolation and characterization of carotenoid hyperproducing mutants of yeast by flow-cytometry and cell sorting. Bio/Technol. 9, 70–73.

An, K.-D., H. Nishida, Y. Miura and A. Yokota. 2002. Aminoadipate reductase gene: a new fungal-specific gene for comparative evolutionary analyses. BMC Evol. Biol. 2, 6.

Anaissie, E.J., M.R. McGinnis and M.A. Pfaller. 2003. Clinical Mycology. Churchill Livingstone, New York.

Andersen, T.F. 1996. A comparative taxonomic study of *Rhizoctonia sensu lato* employing morphological, ultrastructural and molecular methods. Mycol. Res. 100, 1117–1128.

Anderson, E.H. 1945. Nature of the growth factor for the colorless alga *Prototheca zopfii*. J. Gen. Physiol. 28, 287–296.

Anderson, H.W. 1917. Yeast-like fungi of the human intestinal tract. J. Infect. Dis. 21, 341–385.

Anderson, H.W. 1918. The influence of illumination gas and its constituents on certain bacteria and fungi. Am. J. Bot. 5, 1–31.

Anderson, I.C., C.D. Campbell and J.I. Prosser. 2003a. Diversity of fungi in organic soils under a moorland–Scots pine (*Pinus sylvestris* L.) gradient. Environ. Microbiol. 5, 1121–1132.

Anderson, I.C., C.D. Campbell and J.I. Prosser. 2003b. Potential bias of fungal 18S rDNA and internal transcribed rDNA and internal transcribed spacer polymerase chain reaction primers for estimating fungal biodiversity in soil. Environ. Microbiol. 5, 36–47.

Anderson, K.W., and C.E. Skinner. 1947. Yeasts in decomposing fleshy fungi. Mycologia 39, 165–170.

Anderson, M.B., T. Roemer and R. Fabrey. 2003. Progress in antifungal drug discovery. Annu. Rep. Med. Chem. 38, 163–172.

Anderson, T.M., M.A. Lachance and W.T. Starmer. 2004. The relationship of phylogeny to community structure: the cactus yeast community. Am. Nat. 164, 709–721.

Andersson, A., A. Scheynius and O. Rasool. 2003. Detection of Mala f and Mala s allergen sequences within the genus *Malassezia*. Med. Mycol. 41, 479–485.

Ando, A., F. Tanaka, Y. Murata, H. Takagi and J. Shima. 2006. Identification and classification of genes required for tolerance to high-sucrose stress revealed by genome-wide screening of *Saccharomyces cerevisiae*. FEMS Yeast Res. 6, 249–267.

Ando, M., T. Sakata, K. Yoshida, H. Yamasaki, S. Araki, K. Onoue and T. Shinoda. 1990. Serotype-related antigen of *Trichosporon cutaneum* in the induction of summer-type hypersensitivity pneumonitis: correlation between serotype of inhalation challenge-positive antigen and that of the isolates from patients' homes. J. Allergy Clin. Immunol. 85, 36–44.

Andrade, M.J., M. Rodriguez, B. Sanchez, E. Aranda and J.J. Cordoba. 2006. DNA typing methods for differentiation of yeasts related to dry-cured meat products. Int. J. Food Microbiol. 107, 48–58.

Andrewes, A.G., and M.P. Starr. 1976. (3R, 3′R) Astaxanthin from the yeast *Phaffia rhodozyma*. Phytochemistry 15, 1009–1011.

Andrewes, A.G., H.J. Phaff and M.P. Starr. 1976. Carotenoids of *Phaffia rhodozyma*, a red-pigmented fermenting yeast. Phytochemistry 15, 1003–1007.

Andrews, A.T. 1986. Electrophoresis. Theory, Techniques, and Biochemical and Clinical Applications, 2nd edn. Clarendon Press, Oxford.

Andrews, J.H. 1984. Comparative Ecology of Microorganisms and Macroorganisms. Springer, New York, 302pp.

Andrews, R.K., R.L. Blakeley and B. Zerner. 1984. Urea and urease. In: G.L. Eichhorn and L.G. Marzilli (Eds), Advances in Inorganic Biochemistry, Vol. 6. Elsevier, New York, pp. 245–253.

Andrews, J.H. 1991. Comparative Ecology of Microorganisms and Macroorganisms. Springer-Verlag, New York.

Andrews, J.H. 1992a. Biological control in the phyllosphere. Annu. Rev. Phytopathol. 30, 603–635.

Andrews, J.H. 1992b. Fungal life-history strategies. In: G.C. Carroll and D.T. Wicklow (Eds), The Fungal Community: Its Organization and Role in the Ecosystem, 2nd edn. Marcel Dekker, New York, pp. 119–145.

Andrews, J.H., and R.F. Harris. 2000. The ecology and biogeography of microorganisms on plant surfaces. Annu. Rev. Phytopathol. 38, 145–180.

Andrews, J.H., L.H. Kinkel, F.M. Berbee and E.V. Nordheim. 1987. Fungi, leaves, and the theory of island biogeography. Microb. Ecol. 14, 277–290.

Andrews, R.K., R.L. Blakeley and B. Zerner. 1984. Urea and urease. In: G.L. Eichhorn and L.G. Marzilli (Eds), Advances in Inorganic Biochemistry, Vol. 6. Elsevier, New York, pp. 245–253.

Angerbauer, C., M. Siebenhofer, M. Mittelbach and G.M. Guebitz. 2008. Conversion of sewage sludge into lipids by *Lipomyces starkeyi* for biodiesel production. Bioresour. Technol. 99, 3051–3056.

Anonymous. 2004. Citrus. European and Mediterranean Plant Protection Organization Bulletin 34, 43–56.

Antachopoulos, C., T.J. Walsh and E. Roilides. 2007. Fungal infections in primary immunodeficiencies. Eur. J. Pediatr. 166, 1099–1117.

Antoni, D., V.V. Zverlov and W.H. Schwarz. 2007. Biofuels from microbes. Appl. Microbiol. Biotechnol. 77, 23–35.

Antoni, J.L., B. Chaufer and G. Daufin. 2003. Non-food applications of milk components and dairy co-products: a review. Lait 83, 417–438.

Anupama and P. Ravindra. 2000. Value-added food: single cell protein. Biotechnol. Adv. 18, 459–479.

Aono, R. 1990. Taxonomic distribution of alkali-tolerant yeasts. System. Appl. Microbiol. 13, 394–397.

Aquilanti, L., S. Santarelli, S. Silvestri, A. Osimani, A. Petruzzelli and F. Clementi. 2007. The microbial ecology of a typical Italian salami during its natural fermentation. Int. J. Food Microbiol. 120, 136–145.

Araujo, C., M.J. Sousa, M.F. Ferreira and C. Leao. 2003. Activity of essential oils from Mediterranean Lamiaeae species against food spoilage yeasts. J. Food Prot. 66, 625–632.

Ardhana, M.M., and G.H. Fleet. 2003. The microbial ecology of cocoa bean fermentations in Indonesia. Int. J. Food Microbiol. 86, 8799.

Arenz, B.E., B.W. Held, J.A. Jurgens, R.L. Farrell and R.A. Blanchette. 2006. Fungal diversity in soils and historic wood from the Ross Sea region of Antarctica. Soil Biol. Biochem. 38, 3057–3064.

Arias, C.R., J.K. Burns, L.M. Friedrich, R.M. Goodrich and M.E. Parish. 2002. Yeast species associated with orange juice: evaluation of different identification methods. Appl. Environ. Microbiol. 68, 1955–1961.

Aristidou, A., and M. Pentilä. 2000. Metabolic engineering applications to renewable research applications. Curr. Opin. Biotechnol. 11, 187–198.

Armour, C.D., and P.K. Lum. 2005. From drug to protein: using yeast genetics for high-throughput drug discovery. Curr. Opin. Chem. Biol. 9, 20–24.

Armstrong, T.P. 1992. Olfaction and habitat selection in *Drosophila buzzatii*. PhD Thesis, University of New England, Armidale, NSW, Australia.

Arnaud, G. 1913. Sur le genre *Eremothecium* Borzi. Bull. Trim. Soc. Mycol. Fr. 29, 572–576.

Arnaud, M.B., M.C. Costanzo, M.S. Skrzypek, P. Shah, G. Binkley, C. Lane, S.R. Miyasato and G. Sherlock. 2007. Sequence resources at the *Candida* Genome Database. Nucleic Acids Res. 35, D452–D456.

Arneborg, N., H. Siegumfeldt, G.H. Andersen, P. Nissen, V.R. Daria, P.J. Rodrigo and J. Gluckstad. 2005. Interactive optical trapping shows that confinement is a determinant of growth in a mixed yeast culture. FEMS Microbiol. Lett. 245, 155–159.

Arras, G. 1996. Mode of action of an isolate of *Candida famata* in biological control of *Penicillium digitatum* in orange fruits. Postharvest Biol. Technol. 8, 191–198.

Arras, G., V. de Cicco, S. Arru and G. Lima. 1998. Biocontrol by yeasts of blue mould of citrus fruits and the mode of action of an isolate of *Pichia guilliermondii*. J. Hortic. Sci. Biotechnol. 73, 413–418.

Arroyo-López, F.N., M.C. Durán-Quintana, J.L. Ruiz-Barba and A. Garrido-Fernández. 2006. Use of molecular methods for the identification of yeast associated with table olives. Food Microbiol. 23, 791–796.

Asadzadeh, M., S. Ahmad, N. Al-Sweih and Z.U. Khan. 2009. Rapid molecular differentiation and genotypic heterogeneity among *Candida parapsilosis* and *Candida orthopsilosis* strains isolated from clinical specimens in Kuwait. J. Med. Microbiol. 58, 745–752.

Asai, T. 1918. Physiologische Untersuchungen über eine neue, in der Gerbbrühe gedeihende Kahmhefe. J. Coll. Sci. Imp. Univ. Tokyo 39, 1–42.

Asai, Y., N. Makiguichi, M. Shimada and Y. Kurimura. 1976. New species of methanol-assimilating yeasts. J. Gen. Appl. Microbiol. 22, 197–202.

Asehraou, A., C. Peres, D. Brito, M. Faid and M. Serhrouchni. 2000. Characterization of yeast strains isolated from bloaters of fermented green table olives during storage. Grasas y Aceites 51, 225–229.

Ashbee, H.R. 2006. Recent developments in the immunology and biology of *Malassezia* species. FEMS Immunol. Med. Microbiol. 47, 14–23.

Ashbee, H.R. 2007. Update on the genus *Malassezia*. Med. Mycol. 45, 287–303.

Ashbee, H.R., and E.G.V. Evans. 2002. Immunology of diseases associated with *Malassezia* species. Clin. Microbiol. Rev. 15, 21–57.

Ashbee, H.R., E. Ingham, K.T. Holland and W.J. Cunliffe. 1993. The carriage of *Malassezia furfur* serovar A, B and C in patients with pityriasis versicolor, seborrheic dermatitis and controls. Br. J. Dermatol. 129, 533–540.

Ashby, S.F., and W. Nowell. 1926. The fungi of stigmatomycosis. Ann. Bot. 40, 69–84.

Ashenafi, M. 1994. Microbial flora and some chemical properties of ersho, a starter for teff (*Eragrostis tef*) fermentation. World J. Microbiol. Biotechnol. 10, 69–73.

Ashford, B.K. 1917. The etiology of sprue. Am. J. Med. Sci. 154, 157–176.

Ashford, B.K. 1928. Certain conditions of the gastro-intestinal tract in Porto Rico and their relation to tropical sprue. Am. J. Trop. Med. 8, 507–538.

Ashford, B.K., and R. Ciferri. 1930. A new species of *Torulopsis: Torulopsis nitrophila* Cif. and Ashf. Zentralbl. Bakteriol. Parasitenkd., Abt. II, 81, 63–67.

Ashton, M.L., and P.B. Moens. 1979. Ultrastructure of sporulation in the Hemiascomycetes *Ascoidea corymbosa, A. rubescens, Cephaloascus fragrans*, and *Saccharomycopsis capsularis*. Can. J. Bot. 57, 1259–1284.

Aspiroz, C., L.A. Moreno, A. Rezusta and C. Rubio. 1999. Differentiation of three biotypes of *Malassezia* species on normal human skin. Correspondence with *M. globosa, M. sympodialis* and *M. restricta*. Mycopathologia 145, 69–74.

Aspiroz, C., M. Ara, M. Varea, A. Rezusta and C. Rubio. 2002. Isolation *of Malassezia globosa* and *M. sympodialis* from patients with pityriasis versicolor in Spain. Mycopathologia 154, 111–117.

Assadi, M.M., and M. Khazaee. 2003. Isolation and identification of oil degrading yeast from Caspian Sea (Shafarood Anzali and Astara stations). Pajouhesh-va-Sazandegi. In: Natural Resources, No. 56/57, 95–103 (article in Arabic; abstract from CAB Abstracts).

Attfield, P.V. 1997. Stress response: the key to effective strains of industrial baker's yeast. Nat. Biotechnol. 15, 1351–1357.

Auch, A.F., S.R. Henz, B.R. Holland and M. Göker. 2006. Genome BLAST distance phylogenies inferred from whole plastid and whole mitochondrion genome sequences. BMC Bioinform. 7, 350.

Aucott, J.N., J. Fayan, H. Grossnicklas, A. Morrissey, M.M. Lederman and R.A. Salata. 1990. Invasive infection with *Saccharomyces cerevisiae*, report of three cases and review. Rev. Infect. Dis. 12, 406–411.

Augustyn, O.P.H. 1992. Capillary GC-MS fatty acid analysis and yeast identification. PhD Thesis, University of the Orange Free State, Bloemfontein, South Africa.

Augustyn, O.P.H., J.L.F. Kock and D. Ferreira. 1989. *Saccharomyces cerevisiae*. S. Afr. J. Enol. Vit. 10, 8–17.

Augustyn, O.P.H., J.L.F. Kock and D. Ferreira. 1990. Differentiating between yeast species and strains, by cellular long chain fatty acid analysis. 3. *Saccharomyces sensu lato*, *Arxiozyma* and *Pachytichospora*. Syst. Appl. Microbiol. 13, 44–55.

Augustyn, O.P.H., D. Ferreira and J.L.F. Kock. 1991. Differentiation between yeast species and strains within species, by cellular fatty acid analysis. *Saccharomyces sensu stricto*, *Hanseniaspora*, *Saccharomycodes* and *Wickerhamiella*. Syst. Appl. Microbiol. 14, 324–334.

Aulakh, H.S., S.E. Straus and K.J. Kwon-Chung. 1981. Genetic relatedness *of Filobasidiella neoformans (Cryptococcus neoformans*) and *Filobasidiella bacillispora (Cryptococcus bacillisporus*) as determined by deoxyribonucleic acid base composition and sequence homology studies. Int. J. Syst. Bacteriol. 31, 97–103.

Averbuch, D., T. Boekhout, R. Falk, D. Engelhard, M. Shapiro, C. Block and I. Polacheck. 2002. Fungemia in a cancer patient caused by fluconozole-resistant *Cryptococcus laurentii*. Med. Mycol. 40, 479–484.

Avigad, G., and M. Kalina. 1979. Effect of the orthophosphate limitation on the production of phosphomannan by *Hansenula capsulata*. FEMS Microbiol. Lett. 6, 111–114.

Avis, T.J., and R.R. Bélanger. 2001. Specificity and mode of action of the antifungal fatty acid cis-9-heptanoic acid produced by *Pseudozyma flocculosa*. Appl. Environ. Microbiol. 67, 956–960.

Avis, T.J., and R.R. Bélanger. 2002. Mechanisms and means of detection of biocontrol activity of *Pseudozyma* yeasts against plant-pathogenic fungi. FEMS Yeast Res. 2, 5–8.

Avis, T.J., S.J. Caron, T. Boekhout, R.C. Hamelin and R.R. Bélanger. 2001. Molecular and physiological analysis of the powdery mildew antagonist *Pseudozyma flocculosa* and related fungi. Phytopathology 91, 249–254.

Avis, T.J., Y.L. Cheng, Y.Y. Zhao, S. Bolduc, B. Neveu, R. Anguenot, C. Labbe, F. Belzile and R.R. Bélanger. 2005. The potential of *Pseudozyma* yeastlike epiphytes for the production of heterologous recombinant proteins. Appl. Microbiol. Biotechnol. 69, 304–311.

Axel, R. 1995. The molecular logic of smell. Sci. Am. 273, 154–159.

Ayala, F.J., J.R. Powell, M.L. Tracey, C.A. Mourao and S. Perez-Salas. 1972. Enzyme variability in the *Drosophila willistoni* group IV. Genetic variability in natural populations of *Drosophila willistoni*. Genetics 70, 113–139.

Ayoub, M.J., J.L. Legras, R. Saliba and C. Gaillardin. 2006. Application of multi locus sequence typing to the analysis of the biodiversity of indigenous *Saccharomyces cerevisiae* wine yeasts from Lebanon. J. Appl. Microbiol. 100, 699–711.

Bab′eva, I.P. 1998. *Tausonia pamirica* gen. nov. sp. nov., a psychrophilic yeast-like micromycete from the soils of Pamir. Mikrobiologiia 67, 189–194.

Babjeva, I.P., and V.M. Blagodatskaya. 1972. Physiological characteristics and ecology of the yeast *Schizoblastosporion starkeyi-henricii* Ciferri. Mikrobiologiia 41, 99–104.

Bab′eva, I.P., and I.Yu. Chernov. 1995. Geographic aspects of yeast ecology. Physiol. Gen. Biol. Rev. 9, 1–54.

Bab′eva, I.P., and S.E. Gorin. 1975. *Lipomyces anomalus* sp. nov. Antonie van Leeuwenhoek 41, 185–191.

Bab′eva, I.P., and A.V. Kartintsev. 1974. Occurrence of the yeast *Rhodosporidium diobovatum* on plants. Mosc. Univ. Soil Sci. Bull. (English translation of Vestn. Mosk. Univ. Pichuoved) 29, 56.

Bab′eva, I.P., and S.V. Levin. 1979. The yeast *Mastigomyces philippovi* Imsch. et Kriss detected anew in nature and description of the neotype. Mikrobiologiia 48, 541–544.

Bab′eva, I.P., and G.A. Lisichkina. 2000. A new species of psychrophilic basidiomycetous yeasts *Leucosporidium fasciculatum* sp. nov. Mikrobiologiia 69, 801–804. In Russian.

Bab′eva, I.P., and K. Meavadh. 1966. Two types of spore formation in *Lipomyces*. Mikrobiologiia 35, 824–828.

Bab′eva, I.P., and I.S. Reshetova. 1975. A new yeast species *Candida podzolica* sp. n. from the soil. Microbiology 44, 294–333. (translated from Mikrobiologiia)

Bab′eva, I.P., W.I. Golubev, I.S. Reshetova, E.B. Azieva and V.M. Blagodatskaya. 1976. Yeasts in high-latitude regions of the northern and southern hemispheres. Vestn. Mosk. Univ. Biol. Pichuoved. 31, 76–82. In Russian.

Bab′eva, I.P., M.M. Vustin, G.I. Naumov and M.E. Vinovarova. 1985. *Arthroascus schoenii* nov. comb., a yeast-like organism. Mikrobiologiia 54, 724–729.

Bab′eva, I.P., I.S. Reshetova, V.M. Blagodatskaya and L.M. Galimova. 1989. New yeast species *Candida odintsovii* sp. nov. Mikrobiologiia 58, 631–634. In Russian.

Bab′eva, I.P., G.A. Lisichkina, I.A. Maksimova, I.S. Reshetova, E.E. Terenina and I.I. Chernov. 2000. A new yeast species *Candida anutae* sp. nov. from the fruiting bodies of *Agaricus*. Microbiology 69, 225–228. (translated from Mikrobiologiia, 69, 276–278)

Bab′eva, I.P., G.A. Lisichkina, L.S. Reshetova and V.N. Danilevich. 2002. *Mrakia curviuscula* sp. nov.: a new psychrophilic yeast from forest substrates. Microbiology (Moscow) 71, 449–454 (translated from Mikrobiologiia 71, 526–632).

Bachinskaya, A.A. 1914. Entwicklungsgeschichte und Kultur des neuen Hefepilzes *Saccharomyces paradoxus*. J. Microbiol. Epidémiol. Immunobiol. 1, 231–250 (cited by Kudryavtsev 1960).

Bachinskaya, A.A. 1941. History of the development of a yeast fungus *Saccharomycodes lipophora*. Mikrobiologiia, 10, 200–207. In Russian.

Bacigálová, K. 1992a. *Taphrina potentillae* on *Parageum montanum* – a new species in Slovakia. Czech Mycol. 46, 138–142.

Bacigálová, K. 1992b. New localities of *Taphrina carpini* on *Carpinus betulus* in Slovakia. Czech Mycol. 46, 296–302.

Bacigálová, K. 1994a. Species of *Taphrina* on *Alnus* in Slovakia. Czech Mycol. 47, 223–236.

Bacigálová, K. 1994b. Species of *Taphrina* on *Populus* in Slovakia. Czech Mycol. 47, 277–283.

Bacigálová, K. 1997a. Species of *Taphrina* on *Betula* in Slovakia. Czech Mycol. 50, 107–118.

Bacigálová, K. 1997b. Ecological notes to the distribution of *Taphrina*les fungi in Slovakia. Biologia (Bratislava) 52, 7–10.

Bacigálová, K. 2008. *Protomyces buerenianus* (Protomycetaceae) – a new species for Slovakia. Biologia 63, 40–43.

Bacigálová, K., W. Mulenko and H. Prillinger. 2002. A *Taphrina* on *Dryopteris carthusiana* in Slovakia. Mycotaxon 84, 387–390.

Bacigálová, K., K. Lopandic, M.G. Rodrigues, Á. Fonseca, M. Herzberg, W. Pinsker and H. Prillinger. 2003. Phenotypic and genotypic identification and phylogenetic characterisation of *Taphrina* fungi on alder. Mycol. Prog. 2, 179–196.

Bacigálová, K., M. Piatek and M. Wolkowycki. 2005. *Protomyces cirsii-oleracei* (Fungi, Protomycetales), a new species for Poland. Pol. Bot. J. 50, 77–82.

Baehrecke, E.H. 2005. Autophagy: dual roles in life and death? Nat. Rev. Mol. Cell Biol. 6, 505.

Baetz, K., L. McHardy, K. Gable, T. Tarling, D. Reberioux, J. Bryan, R.J. Andersen, T. Dunn, P. Hieter and M. Roberge. 2004. Yeast genome-wide induced haploinsufficiency screen to determine drug mode of action. Proc. Natl. Acad. Sci. USA 101, 4525–4530.

Baha, C.S. (Ed.) 2003. Fermentation Biotechnology. ACS Symp. Series 862. American Chemical Society, Washington, DC.

Bahadur, K. 1957. Isolation and morphological studies of the Dhar yeast. Zentralbl. Bakteriol. Parasitenkd., Abt. II, 110, 305–308.

Baharaeen, S., and H.S. Vishniac. 1982. *Cryptococcus lupi* sp. nov., an Antarctic basidioblastomycete. Int. J. Syst. Bacteriol. 32, 229–232.

Baharaeen, S., and H.S. Vishniac. 1984. 25S ribosomal RNA homologies of basidiomycetous yeasts: taxonomic and phylogenetic implications. Can. J. Microbiol. 30, 613–621.

Baharaeen, S., J.A. Bantle and H.S. Vishniac. 1982. The evolution of Antarctic yeasts: DNA base composition and DNA-DNA homology. Can. J. Microbiol. 28, 406–413.

Bai, F.-Y. 1996. Separation of *Candida fermentati* comb. nov. from *Candida guilliermondii* by DNA base composition and electrophoretic karyotyping. Syst. Appl. Microbiol. 19, 178–181.

Bai, F.-Y., H.-Y. Liang and J.-H. Jia. 2000. Taxonomic relationships among the taxa in the *Candida guilliermondii* complex, as revealed by comparative electrophoretic karyotyping. Int. J. Syst. Evol. Microbiol. 50, 417–422.

Bai, F.-Y., M. Takashima and T. Nakase. 2001a. Phylogenetic analysis of strains originally assigned to *Bullera variabilis*: descriptions of *Bullera pseudohuiaensis* sp. nov., *Bullera komagatae* sp. nov. and *Bullera pseudoschimicola* sp. nov. Int. J. Syst. Evol. Microbiol. 51, 2177–2187.

Bai, F.-Y., M. Takashima and T. Nakase. 2001b. Description of *Bullera kunmingensis* sp. nov., and clarification of the taxonomic status of *Bullera sinensis* and its synonyms based on molecular phylogenetic analysis. FEMS Yeast Res. 1, 103–109.

Bai, F.Y., M. Takashima, M. Hamamoto and T. Nakase. 2001c. *Sporobolomyces yunnanensis* sp. nov., a Q-10(H2)-containing yeast species with a close phylogenetic relationship to *Erythrobasidium hasegawianum*. Int. J. Syst. Evol. Microbiol. 51, 231–235.

Bai, F.-Y., M. Takashima, J.-H. Jia and T. Nakase. 2002a. *Dioszegia zsoltii* sp. nov., a new ballistoconidium-forming yeast species with two varieties. J. Gen. Appl. Microbiol. 48, 17–23.

Bai, F.-Y., J.-H. Zao, M. Takashima, J.-H. Jia, T. Boekhout and T. Nakase. 2002b. Reclassification of the *Sporobolomyces roseus* and *Sporidiobolus pararoseus* complexes, with the description of *Sporobolomyces phaffii* sp. nov. Int. J. Syst. Evol. Microbiol. 52, 2309–2314.

Bai, F.-Y., M. Takashima, J.-H. Zhao, J.-H. Jia and T. Nakase. 2003. *Bullera anomala* sp. nov. and *Bullera pseudovariabilis* sp. nov., two new ballistoconidium-forming yeast species from Yunnan, China. Antonie van Leeuwenhoek 83, 257–263.

Bai, F.-Y., Y. Cai, Q.-M. Wang and H. Ohkubo. 2004. *Rhodotorula oryzae* sp. nov., a novel basidiomycetous yeast species isolated from paddy rice. Antonie van Leeuwenhoek 86, 295–299.

Baillon, E.H. 1889. Traité de Botanique Médicale Cryptogamique. O. Doin, Paris.

Bailly, J., L. Fraissinet-Tachet, M.C. Verner, J.C. Debaud, M. Lemaire, M. Wesolowski-Louvel and R. Marmeisse. 2007. Soil eukaryotic functional diversity, a metatranscriptomic approach. ISME J. 1, 632–642.

Bakalinsky, A., and R. Snow. 1990. The chromosomal constitution of wine strains of *Saccharomyces cerevisiae*. Yeast 6, 367–382.

Baker, G.C., T.J. Beebee and M.A. Ragan. 1999. *Prototheca richardsii*, a pathogen of anuran larvae, is related to a

clade of protistan parasites near the animal–fungal divergence. Microbiology 145, 1777–1784.
Baker, J.G., I.F. Salkin, D.H. Pincus and R.F. D'Amato. 1981. *Candida paratropicalis*, a new species of *Candida*. Mycotaxon 13, 115–119.
Baker, J.M., and N.J.W. Kreger-van Rij. 1964. *Endomycopsis platypodis* sp. n. (Ascomycetes): an auxiliary ambrosia fungus of *Platypus cylindrus* Fab. (Col. Platypodidae). Antonie van Leeuwenhoek 30, 433–441.
Baker, J.M., and D.M. Norris. 1968. A complex of fungi mutualistically involved in the nutrition of the ambrosia beetle *Xyleborus ferrugineus*. J. Invertebr. Pathol. 11, 246–250.
Baker, R.H., and R. DeSalle. 1997. Multiple sources of character information and the phylogeny of Hawaiian Drosophilids. Syst. Biol. 46, 654–673.
Baker, R.H., X.B. Yu and R. DeSalle. 1998. Assessing the relative contribution of molecular and morphological characters in simultaneous analysis trees. Mol. Phylogenet. Evol. 9, 427–436.
Baker, W.L. 1972. Eastern Forest Insects. U.S. Department of Agriculture Forest Service, Washington, DC, 642 pp.
Bakkeren, G., J.W. Kronstad and C.A. Lévesque. 2000. Comparison of AFLP fingerprints and ITS sequences as phylogenetic markers in Ustilaginomycetes. Mycologia 92, 510–521.
Balakrishnan, R., K.R. Christie, M.C. Costanzo, K. Dolinski, S.S. Dwight, S.R. Engel, D.G. Fisk, J.E. Hirschman, E.L. Hong, R. Nash, R. Oughtred, M. Skrzypek, C.L. Theesfeld, G. Binkley, Q. Dong, C. Lane, A. Sethuraman, S. Weng, D. Botstein and J.M. Cherry. 2005. Fungal BLAST and Model Organism BLASTP Best Hits: new comparison resources at the *Saccharomyces* Genome Database (SGD). Nucleic Acids Res. 33, D374–D377.
Baldi, F., M. Pepi and F. Fava. 2003. Growth of *Rhodosporidium toruloides* strain DBVPG 6662 on dibenzothiophene crystals and orimulsion. Appl. Environ. Microbiol. 69, 4689–4696.
Balloni, W., R. Materassi and M.C. Margheri. 1971. *Saccharomyces* (*Torulaspora*) *florenzanii* sp. n., a new wine fermenting yeast from Sardegna (Italia). Zentralbl. Bakteriol. Parasitenkd., Abt. II, 126, 386–388.
Balloni, W., G. Florenzano and R. Materassi. 1974. A new species of *Sporidiobolus* (*Spor. veronae*) isolated from a tropical bitumenous soil. Ann. Microbiol. Enzimol. 24, 233–240.
Balloni, W., G. Florenzano, G. Mazza and M. Polsinelli. 1987. *Candida amidevorans* sp. nov., a new ascomycetous anamorph yeast from soil. Antonie van Leeuwenhoek 53, 99–106.
Ballou, C.E. 1970. A study of the immunochemistry of three yeast mannans. J. Biol. Chem. 245, 1197–1203.
Ballou, C.E. 1976. Structure and biosynthesis of the mannan component of the yeast cell envelope. Adv. Microb. Physiol. 14, 93–157.
Bamforth, C.W. 2000. Brewing and brewing research: past, present, future. J. Sci. Food Agric. 80, 1371–1378.
Bamforth, C.W. (Ed.) 2005. Food, Fermentation and Microorganisms. Blackwell Publishing, Oxford.
Bamforth, C.W., and M. Kanauchi. 2004. Enzymology of vicinal diketone reduction in brewer's yeast. J. Inst. Brew. 110, 83–93.
Banat, I.M., R.S. Makkar and S.S. Cameotra. 2000. Potential commercial applications of microbial surfactants. Appl. Microbiol. Biotechnol. 53, 495–508.
Bandelt, H.J. 1995. Combination of data in phylogenetic analysis. Plant Syst. Evol. 9 (Suppl.), 355–361.
Bandoni, R.J. 1957. The spores and basidia of *Sirobasidium*. Mycologia 49, 250–255.
Bandoni, R.J. 1958. Some Tremellaceous fungi in the C.G. Lloyd collection. Lloydia 21, 137–151.
Bandoni, R.J. 1961. The genus *Naematelia*. Am. Midl. Nat. 66, 319–328.
Bandoni, R.J. 1963. Conjugation in *Tremella mesenterica*. Can. J. Bot. 41, 467–474.
Bandoni, R.J. 1965. Secondary control of conjugation in *Tremella mesenterica*. Can. J. Bot. 43, 627–630.
Bandoni, R.J. 1973. Epistolae mycologicae II. Species of *Platygloea* from British Columbia. Syesis 6, 229–232.
Bandoni, R.J. 1979. *Fibulobasidium*: a new genus in the Sirobasidiaceae. Can. J. Bot. 57, 264–268.
Bandoni, R.J. 1984. The Tremellales and Auriculariales: an alternative classification. Trans. Mycol. Soc. Jpn 25, 489–530.
Bandoni, R.J. 1985. On an undescribed, pleomorphic hyphomycete from litter. Bot. J. Linn. Soc. 91, 37–43.
Bandoni, R.J. 1986a. On an undescribed basidiomycetous anamorph. Windahlia 16, 53–58.
Bandoni, R.J. 1986b. *Sirotrema*: a new genus in the Tremellaceae. Can. J. Bot. 64, 668–676.
Bandoni, R.J. 1987. Taxonomic overview of the Tremellales. In: G.S. de Hoog, M.Th. Smith and A.C.M. Weijman (Eds), The Expanding Realm of Yeast-like Fungi. Elsevier, Amsterdam, pp. 87–110 (Stud. Mycol. 30, 87–110).
Bandoni, R.J. 1995. Dimorphic heterobasidiomycetes: taxonomy and parasitism. Stud. Mycol. 38, 13–27.
Bandoni, R.J. 1998a. On an undescribed species of *Fibulobasidium*. Can. J. Bot. 76, 1540–1543.
Bandoni, R.J. 1998b. On some species of *Mycogloea*. Mycoscience 39, 31–36.
Bandoni, R.J., and T. Boekhout. 1998. Tremelloid genera with yeast phases. In: C.P. Kurtzman and J.W. Fell (Eds), The Yeasts, A Taxonomic Study, 4th edn. Elsevier, Amsterdam, pp. 705–717.
Bandoni, R.J., and P.K. Buchanan. 1990. Two new species of *Tremella* from New Zealand. N. Z. J. Bot. 28, 451–454.
Bandoni, R.J., and J. Ginns. 1998. Notes on *Tremella mesenterica* and allied species. Can J. Bot. 76, 1544–1557.
Bandoni, R.J., and B.N. Johri. 1972. *Tilletiaria*: a new genus in the Ustilaginales. Can. J. Bot. 50, 39–43.
Bandoni, R.J., and J.C. Krug. 2000. Two undescribed heterobasidiomycetes from Ontario. Mycoscience 41, 371–377.
Bandoni, R.J., and F. Oberwinkler. 1983. On some species of *Tremella* described by A. Möller. Mycologia 75, 854–863.
Bandoni, R.J., and M. Zang. 1990. On an undescribed *Tremella* from China. Mycologia 82, 270–273.
Bandoni, R.J., K.J. Lobo and S.A. Brezden. 1971. Conjugation and chlamydospores in *Sporobolomyces odorus*. Can. J. Bot. 49, 683–686.
Bandoni, R.J., J. Krug and J. Ginns. 2002. On some *Colacogloea* species from Canada. Czech Mycol. 54, 31–43.
Bandoni, R.J., B.N. Johri and S.A. Reid. 1975. Mating among isolates of three species of *Sporobolomyces*. Can. J. Bot. 53, 2942–2944.

Bandoni, R.J., F. Oberwinkler and A.A. Bandoni. 1991. On species of *Filobasidium* associated with yuccas. Syst. Appl. Microbiol. 14, 98–101.

Bandoni, R.J., J. Carranza and A.-A. Bandoni. 1996. Four new species of *Tremella* (Tremellales: Basidiomycotina) from Costa Rica. Rev. Biol. Trop. 44 (Suppl. 4), 15–24.

Banno, I. 1963. Preliminary report on cell conjugation and mycelial stage in *Rhodotorula* yeasts. J. Gen. Appl. Microbiol. 9, 249–251.

Banno, I. 1967. Studies on the sexuality of *Rhodotorula*. J. Gen. Appl. Microbiol. 13, 167–196.

Banno, I., and K. Mikata. 1985. Scanning electron microscopy of ascospores from various strains of *Debaryomyces hansenii* (Zopf) Lodder et Kreger-van Rij. Inst. Ferment. Osaka Res. Commun. 12, 63–69.

Banno, I., and Y. Yamada. 1998a. *Fellomyces* Y. Yamada & Banno. In: C.P. Kurtzman and J.W. Fell (Eds), The Yeasts, A Taxonomic Study, 4th edn. Elsevier, Amsterdam, pp. 768–772.

Banno, I., and Y. Yamada. 1998b. *Sterigmatomyces* Fell emend Yamada & Banno. In: C.P. Kurtzman and J.W. Fell (Eds), The Yeasts, A Taxonomic Study, 4th edn. Elsevier, Amsterdam, pp. 844–845.

Bao, K., T. Wen, F. Chen, H. Song and C. Zhao. 2005. Isolation of a gene greatly expressed in *Kluyveromyces marxianus* at high temperature. World J. Microbiol. Biotechnol. 21, 1083–1086.

Baptist, J.N., and C.P. Kurtzman. 1976. Comparative enzyme patterns in *Cryptococcus laurentii* and its taxonomic varieties. Mycologia 68, 1195–1203.

Baral, H.-O. 1999. A monograph of *Helicogonium* (=*Myriogonium*, Leotiales), a group of nonascocarpous intrahymenial mycoparasites. Nova Hedwigia 69, 171.

Barbosa, A.C., R.M. Cadete, F.C.O. Gomes, M.A. Lachance and C.A. Rosa. 2009. *Candida materiae* sp. nov., a yeast species isolated from rotting wood in the Atlantic rain forest. Int. J. Syst. Evol. Microbiol. 59, 2104–2106.

Bard, M., M.A. Sturm, C.A. Pierson, S. Brown, K.M. Rogers, S. Nabinger, J. Eckstein, R. Barbuch, N.D. Lees, S.A. Howell and K.C. Hazen. 2005. Sterol uptake *in Candida glabrata*: rescue of sterol auxotrophic strains. Diagn. Microbiol. Infect. Dis. 52, 285–293.

Bareetsang, A.S., J.L.F. Kock, C.H. Pohl, E.E. Pretorius, P.J. Botes, P.W.J. van Wijk and S. Nigam. 2005a. The presence of novel 3-hydroxy oxylipins on the surfaces of hat-shaped ascospores of *Ascoidea africana* Batra & Francke-Grosmann. Can. J. Microbiol. 51, 99–103.

Bareetseng, A., J. Kock, C. Pohl, E. Pretorius and P. Wyk. 2005b. Uncovering the first double brimmed hat-shaped ascospores in *Ambrosiozyma platypodis* van der Walt. Antonie van Leeuwenhoek 87, 169–170.

Bareetseng, A.S., J.L.F. Kock, C.H. Pohl, E.E. Pretorius, C.J. Strauss, P.J. Botes, P.W.J. van Wyk and S. Nigam. 2006. Mapping the distribution of 3-hydroxy oxylipins in the ascomycetous yeast *Saturnispora saitoi*. Syst. Appl. Microbiol. 29, 446–449.

Barker, B.T.P. 1901. A conjugating "yeast". Philos. Trans. R. Soc. Lond. B 194, 467–485.

Barker, H.A. 1935. The metabolism of the colorless alga, *Prototheca zopfii* Krüger. J. Cell. Comp. Physiol. 7, 73–93.

Barker, H.A. 1936. The oxidative metabolism of the colorless alga, *Prototheca zopfii*. J. Cell. Comp. Physiol. 8, 231–250.

Barker, J.S.F., and W.T. Starmer. 2000. Environmental effects and genetics of oviposition site preference for natural yeast substrates in *Drosophila buzzatii*. Hereditas 130, 145–175.

Barker, J.S.F., G.L. Toll, P.D. East, M. Miranda and H.J. Phaff. 1983. Heterogeneity of the yeast flora in the breeding sites of cactophilic *Drosophila*. Can. J. Microbiol. 29, 6–14.

Barker, J.S.F., P.D. East, H.J. Phaff and M. Miranda. 1984. The ecology of the yeast flora in necrotic *Opuntia* cacti and of associated *Drosophila* in Australia. Microb. Ecol. 10, 379–399.

Barker, J.S.F., P.D. East and B.S. Weir. 1986a. Temporal and microgeographic variation in allozyme frequencies in a natural population of *Drosophila buzzatii*. Genetics 112, 577–611.

Barker, J.S.F., D.C. Vacek, P.D. East and W.T. Starmer. 1986b. Allozyme genotypes of *Drosophila buzzatii*: feeding and oviposition preferences for microbial species, and habitat selection. Aust. J. Biol. Sci. 39, 47–58.

Barker, J.S.F., W.T. Starmer and D.C. Vacek. 1987. Analysis of spatial and temporal variation in the community structure of yeasts associated with decaying *Opuntia* cactus. Microb. Ecol. 14, 267–276.

Barker, J.S.F., W.T. Starmer and J.C. Fogleman. 1994. Genotype-specific habitat selection for oviposition sites in the cactophilic species *Drosophila buzzatii*. Heredity 72, 384–395.

Bar-Meir, M., D.A. Sutton, B. Wickes, C.P. Kurtzman, S. Goldman and X. Zheng. 2006. Catheter-related fungemia due to *Candida thermophila*. J. Clin. Microbiol. 44, 3035–3036.

Barnett, H.L. 1964. Mycoparasitism. Mycologia 56, 1–19.

Barnett, J.A. 1998. The history of research on yeasts 1: work by chemists and biologists. Yeast 14, 1439–1451.

Barnett, J.A. 2000. A history of research on yeasts 2: Louis Pasteur and his contemporaries. Yeast 16, 755–771.

Barnett, J.A. 2001. A history of research on yeasts 3: Emil Fischer, Eduard Büchner and their contemporaries, 1880–1900. Yeast 18, 363–368.

Barnett, J.A. 2004. A history of research on yeasts 8: taxonomy. Yeast 21, 1141–1193.

Barnett, J.A., and R.W.M. Buhagiar. 1971. *Torulopsis fragaria species nova*, a yeast from fruit. J. Gen. Microbiol. 67, 233–238.

Barnett, J.A., and M. Ingram. 1955. Technique in the study of yeast assimilation reactions. J. Appl. Microbiol. 18, 131–148.

Barnett, J.A., R.W. Payne and D. Yarrow. 1983. Yeasts: Characteristics and Identification. Cambridge University Press, Cambridge, 811pp.

Barnett, J.A., R.W. Payne and D. Yarrow. 1990. Yeasts: Characteristics and Identification, 2nd edn. Cambridge University Press, Cambridge, 1002pp.

Barnett, J.A., R.W. Payne and D. Yarrow. 2000. Yeasts: Characteristics and Identification, 3rd edn. Cambridge University Press, Cambridge, 1139pp.

Barns, S.M., D.J. Lane, M.L. Sogin, C. Bibeau and W.G. Weisburg. 1991. Evolutionary relationships among pathogenic *Candida* species and relatives. J. Bacteriol. 173, 2250–2255.

Baronian, K.H.R. 2004. The use of yeasts and moulds as sensing elements in biosensors. Biosens. Bioelectron. 19, 953–962.

Bar-Peled, M., C.L. Griffith and T.L. Doering. 2001. Functional cloning and characterization of a UDP-glucuronic acid

decarboxylase: the pathogenic fungus *Cryptococcus neoformans* elucidates UDP-xylose synthesis. Proc. Natl. Acad. Sci. USA 98, 12003–12008.

Barras, S.J. 1973. Reduction of progeny and development in the southern pine beetle following removal of symbiotic fungi. Can. Entomol. 105, 1295–1299.

Barras, S.J., and T.J. Perry. 1965–1974. Interrelationships among microorganisms, bark or ambrosia beetles, and woody host tissue: an annotated bibliography. South. For. Exp. Stn., New Orleans, LA, 34pp. (USDA For. Serv. Gen. Tech. Rep. SO-10).

Barre, P., and P. Galzy. 1960. Etude et détermination d'une levure osmophile. Ann. Technol. 4, 345–348.

Barre, P., F. Vezinhet, S. Dequin and B. Blondin. 1993. Selection and commercial cultivation of wine yeast and bacteria. In: G.H. Fleet (Ed.), Wine Microbiology and Biotechnology. Harwood Academic Publishers, New York, pp. 421–447.

Barret, A., P. Bidan and L. André. 1955. Sur quelques accidents de vinification dûs à des levures à voile. C.R. Acad. Agric. Fr. 41, 426–431.

Bar-Shimon, M., H. Yehuda, L. Cohen, B. Weiss, A. Kobeshnikov, A. Daus, M. Goldway, M. Wisniewski and S. Droby. 2004. Characterization of extracellular lytic enzymes produced by the yeast biocontrol agent *Candida oleophila*. Curr. Genet. 45, 140–148.

Barthe, P., and C. Bulard. 1974. Identification d'une cytokinine par chromatographie en phase gazeuse a partir de cultures pures de *Taphrina cerasi*. Can. J. Bot. 52, 1515–1518.

Bartnicki-Garcia, S. 1968. Cell wall chemistry, morphogenesis, and taxonomy of fungi. Annu. Rev. Microbiol. 22, 87–108.

Bartnicki-Garcia, S. 1970. In: J.B. Harborne (Ed.) Academic Press, New York, pp. 81–103.

Basak, S., H.S. Ramaswamy and J.P.G. Piette. 2002. High pressure destruction kinetics of *Leuconostoc mesenteroides* and *Saccharomyces cerevisiae* in single strength and concentrated orange juice. Innov. Food Sci. Emerg. Technol. 3, 223–231.

Basch, J., T. Franceschini, S. Tonzi and S.J. Chiang. 2004. Expression of a cephalosporin C esterase gene in *Acremonium chrysogenum* for the direct production of deacetylcephalosporin C. J. Ind. Microbiol. Biotechnol. 31, 531–539.

Basgal, W. 1931. Contribuição ao estudo das blastomicoses pulmonares. Thesis, Institute Oswaldo Cruz, Rio de Janeiro.

Batista, A.C., and J.S. Silveira. 1960. *Trichosporon figueirae* n. sp. assinalado como fungo intestinal. Mycopathol. Mycol. Appl. 12, 196–198.

Batista, A.C., and J.S. Silveira. 1962. Micose pulmonar e *Candida genitalis nobis* n. sp. Univ. de Recife, Inst. Micol. 170, 3.

Batista, A.C., and J.S. Silveira. 1959a. *Kloeckera faecalis*, n. sp. isolado de fezes humanas. O. Hospital 56, 505–507.

Batista, A.C., and J.S. Silveira. 1959b. Una variedade nova de *Endomycopsis mali* (Lewis) Dekker assinalada sôbre fezes humanas. Rev. Assoc. Med. Bras. 5, 353–354.

Batista, A.C., and J.S. Silveira. 1959c. Alqumas novas espécies de *Candida* do aparelho digestivo e orgãos anexos do homen. O. Hospital 56, 293–299.

Batista, A.C., J.R. Vieira and R.P. Coêlho. 1959. *Schwanniomyces hominis* n. sp. como causa de lesion epidermica en recien nacido. Rev. Ecuatoriana Hig. Med. Trop. 16, 136–141.

Batista, A.C., R.P. Coelho and J.R. Vieira. 1960. The incidence of *Hanseniaspora valbyensis* Kloecker in the human cecal appendix and epidermal lesions. Mycopathologia 31, 185–195. In Portuguese.

Batista, A.C., J.S. Silveira and R.P. Coêlho. 1961. *Debaryomyces artagaveytiae* n. sp. assinalado em secreção genital de mulher. Mycopathol. Mycol. Appl. 14, 1923.

Batista, A.C., S.T.C. Campos and S. Oliveira. 1963. Epidermomicose devida a *Trichosporon loboi* n. sp. Publ. Inst. Micol. Recife 207, 3–9.

Batra, L.R. 1959. A comparitive morphological and physiological study of the species of *Dipodascus*. Mycologia 51, 329–355.

Batra, L.R. 1963a. Ecology of ambrosia fungi and their dissemination by beetles. Trans. Kans. Acad. Sci. 66, 213–236.

Batra, L.R. 1963b. Contribution to our knowledge of ambrosia fungi. II. *Endomycopsis fasciculata* nom. nov. (Ascomycetes). Am. J. Bot. 50, 481–487.

Batra, L.R. 1963c. Life history of species of *Ascoidea*. Am. J. Bot. 50, 624.

Batra, L.R. 1963d. Habitat and nutrition of *Dipodascus* and *Cephaloascus*. Mycologia 55, 508–520.

Batra, L.R. 1966. Ambrosia fungi: extent of specificity to ambrosia beetles. Science 153, 193–195.

Batra, L.R. 1967. Ambrosia fungi: a taxonomic revision, and nutritional studies of some species. Mycologia 59, 976–1017.

Batra, L.R. 1971. Two new Hemiascomycetes: *Pichia crossotarsi* and *P. microspora*. Mycologia 63, 994–1001.

Batra, L.R. 1973. Nematosporaceae (Hemiascomycetidae): taxonomy, pathogenicity, distribution and vector relations. Tech. Bull. No. 1469, ARS, US Department of Agriculture, Washington, DC, 71pp.

Batra, L.R. 1978. Taxonomy and systematics of the Hemiascomycetes (Hemiascomycetidae). In: C.V. Subramanian (Ed.), Taxonomy of Fungi, Proc. Int. Symp. on Taxonomy of Fungi, Madras.

Batra, L.R., and H. Francke-Grosmann. 1961. Contributions to our knowledge of ambrosia fungi. I. *Ascoidea hylecoeti* sp. nov. (Ascomycetes). Am. J. Bot. 48, 453–456.

Batra, L.R., and H. Francke-Grosmann. 1964. Two new ambrosia fungi – *Ascoidea asiatica* and *A. africana*. Mycologia 56, 632–636.

Batra, R., T. Boekhout, E. Guého, F.J. Cabañes, T.L. Dawson Jr. and A.K. Gupta. 2005. *Malassezia* Baillon, emerging clinical yeasts. FEMS Yeast Res. 5, 1101–1113.

Battacharjee, A.K., K.J. Kwon-Chung and C.P.J. Glademans. 1978. The structure of the capsular polysaccharide from *Cryptococcus neoformans* serotype D. Carbohydr. Res. 73, 183–192.

Battacharjee, A.K., K.J. Kwon-Chung and C.P.J. Glaudemans. 1979. The structure of the capsular polysaccharide from *Cryptococcus neoformans* serotype C II. Mol. Immunol. 16, 531–532.

Battey, A.S., S. Duffy and D.W. Schaffner. 2002. Modelling yeast spoilage in cold-filled ready-to-drink beverages with *Saccharomyces cerevisiae, Zygosaccharomyces bailii* and *Candida lipolytica.* Appl. Environ. Microbiol. 68, 1901–1906.

Bauch, R. 1925. Untersuchungen über die Entwicklungsgeschichte und Sexualphysiologie der *Ustilago bromivora* und *U. grandis*. Z. Bot. 17, 129–177.

Bauer, R., and F. Oberwinkler. 1990a. Direct connections from cytoplasm to cytoplasm; an unusual host–parasite interaction of the tremelloid mycoparasite *Tetragoniomyces uliginosus*. Protoplasma 154, 157–160.

Bauer, R., and F. Oberwinkler. 1990b. Haustoria of the mycoparasitic Heterobasidiomycete *Christiansenia pallida*. Cytologia 55, 419–424.

Bauer, R., and F. Oberwinkler. 1991a. The symplechosome: a unique organelle of some basidiomycetes. Bot. Acta 104, 93–97.

Bauer, R., and F. Oberwinkler. 1991b. The colacosomes: new structures at the host–parasite interface of a mycoparasitic basidiomycete. Bot. Acta 104, 53–57.

Bauer, R., F. Oberwinkler and G. Deml. 1989. Ultrastruktur der Basidiensepten phragmobasidialer Brandpilz. Z. Mykol. 55, 163–168.

Bauer, R., F. Oberwinkler and D. McLaughlin. 1992. Meiosis, spindle pole body cycle, and basidium ontogeny in the Heterobasidiomycete *Agaricostilbum pulcherrimum*. Syst. Appl. Microbiol. 15, 259–274.

Bauer, R., F. Oberwinkler and K. Vánky. 1997. Ultrastructural markers and systematics in smut fungi and allied taxa. Can. J. Bot. 75, 1273–1314.

Bauer, R., F. Oberwinkler, M. Piepenbring and M.L. Berbee. 2001a. Ustilaginomycetes. In: D.J. McLaughlin, E.G. McLaughlin and P.A. Lemke (Eds), Systematics and Evolution. The Mycota XII Part B. Springer-Verlag, Berlin, pp. 57–83.

Bauer, R., D. Begerow, A. Nagler and F. Oberwinkler. 2001b. The Georgefischeriales: a phylogenetic hypothesis. Mycol. Res. 105, 416–424.

Bauer, R., M. Lutz and F. Oberwinkler. 2005. *Gjaerumia*, a new genus in the Georgefischeriales (Ustilaginomyctes). Mycol. Res. 109, 1250–1258.

Bauer, R., D. Begerow, J.P. Sampaio, M. Weiß and F. Oberwinkler. 2006. The simple-septate basidiomycetes: a synopsis. Mycol. Prog. 5, 41–66.

Baum, B.R. 1992. Combining trees as a way of combining data sets for phylogenetic inference, and the desirability of combining gene trees. Taxon 41, 3–10.

Baumann, P., C.-Y. Lai, L. Baumann, D. Rouhbakhsh, N.A. Moran and M.A. Clark. 1995. Mutualistic associations of aphids and prokaryotes: biology of the genus *Buchnera*. Appl. Environ. Microbiol. 61, 1–7.

Baumberger, J.D. 1917. The food of *Drosophila melanogaster* Meigen. Proc. Natl. Acad. Sci. Wash. 3, 122–126.

Baumberger, J.D. 1919. A nutritional study of insects, with special reference to microorganisms and their substrata. J. Esp. Zool. 28, 1–81.

Baur, J.A., and D.A. Sinclair. 2006. Therapeutic use of resveratrol: the *in vivo* evidence. Nat. Rev. Drug Discov. 5, 493–506.

Baurain, D., H. Brinkmann and H. Philippe. 2007. Lack of resolution in the animal phylogeny: closely spaced cladogeneses or undetected systematic errors? Mol. Biol. Evol. 24, 6–9.

Bauters, T.G.M., D. Swinne, T. Boekhout, L. Noens and H.J. Nelis. 2001. Repeated isolation of *Cryptococcus laurentii* from the oropharynx of an immunocompromised patient. Mycopathologia 153, 133–135.

Bauwens, L., Ch. de Vroey and W. de Meurichy. 1996. A case of exfoliative dermatitis in a captive southern white rhinoceros (*Ceratotherium simum simum*). J. Zool. Wildl. Med. 27, 271–274.

Bazaz, G.R., O.L. Manfredi, R.G. Howard and A.A. Claps. 1970. *Pneumocystis carinii* pneumonia in three full-term siblings. J. Pediatr. 76, 767–769.

Beauverie, J. 1929. Sur un *Zygosaccharomyces* de la datte isohétérogame. Bull. Soc. Mycol. Fr. 45, 153–170.

Beauverie, J., and C. Lesieur. 1912. Etude de quelques levures rencontrées chez l'homme dans certains exsudats pathologiques. J. Physiol. Pathol. Gen. 14, 983–1008.

Beck, H., D. Dobritzsch and J. Piškur. 2008. *Saccharomyces kluyveri* as a model organism to study pyrimidine degradation. FEMS Yeast Res. 8, 1209–1213.

Beck, O. 1922. Eine neue *Endomyces*-Art, *Endomyces bisporus*. Ann. Mycol. 20, 219–227.

Beckett, A., I.B. Heath and D.J. McLaughlin. 1974. An Atlas of Fungal Ultrastructure. Longman Group, London.

Bedford, C.L. 1942. A taxonomic study of the genus *Hansenula*. Mycologia 34, 628–649.

Beech, F.W. 1965. *Pichia delftensis* sp. n. Antonie van Leeuwenhoek 31, 81–83.

Beech, F.W., and J.G. Carr. 1977. Cider and sherry. In: A.H. Rose (Ed.), Alcoholic Beverages, Economic Microbiology. Academic Press, London.

Beech, F.W., and R.R. Davenport. 1969. The isolation of non-pathogenic yeasts. In: D.A. Shapton and G.W. Gould (Eds), Isolation Methods for Microbiologists. Academic Press, New York, pp. 71–88.

Beech, F.W., and R.R. Davenport. 1970. The role of yeasts in cider-making. In: A.H. Rose and J.S. Harrison (Eds), The Yeasts, Vol. 3, Yeast Technology. Academic Press, London, pp. 73–146.

Beech, F.W., and R.R. Davenport. 1971. Isolation, purification and maintenance of yeasts. In: J.R. Morris and D.W. Ribbons (Eds), Methods in Microbiology, Vol. 4. Academic Press, New York, pp. 153–182.

Beech, F.W., J.G. Carr and R.C. Codner. 1955. A multipoint inoculator for plating bacteria or yeasts. J. Gen. Microbiol. 13, 408–410.

Beech, F.W., R.R. Davenport, D.A.A. Mossel, K.E. Dijkmann, M. Koopmans, J. de Jong, M.C. Put and R.H. Tilbury. 1980. Media and methods for growing yeasts: proceedings of a discussion meeting. In: F.A. Skinner, S.M. Passmore and R. R. Davenport (Eds), Biology and Activities of Yeasts. Academic Press, London, pp. 259–293.

Beech, R.W. 1993. Yeasts in cider-making. In: A.H. Rose and J.S. Harrison (Eds), The Yeasts, 2nd edn. Vol. 5. Yeast Technology. Academic Press, London, pp. 169–213.

Beek, I.C., R. Bruhn and J. Gandrass. 2006. Analysis of estrogenic activity in coastal surface waters of the Baltic Sea using the yeast estrogen screen. Chemosphere 63, 1870–1878.

Begerow, D., R. Bauer and F. Oberwinkler. 1997. Phylogenetic studies on nuclear large subunit ribosomal DNA sequences of smut fungi and related taxa. Can. J. Bot. 75, 2045–2056.

Begerow, D., R. Bauer and T. Boekhout. 2000. Phylogenetic placements of ustilaginomycetous anamorphs as deduced from nuclear LSU rDNA sequences. Mycol. Res. 104, 53–60.

Begerow, D., R. Bauer and F. Oberwinkler. 2001. *Muribasidiospora*: Microstromatales or Exobasidiales? Mycol. Res. 105, 798–810.

Begerow, D., M. Lutz and F. Oberwinkler. 2002. Implications of molecular characters for the phylogeny of the genus *Entyloma*. Mycol. Res. 106, 1392–1399.

Begerow, D., B. John and F. Oberwinkler. 2004. Evolutionary relationships among β-tubulin gene sequences of basidiomycetous fungi. Mycol. Res. 108, 1257–1263.

Begerow, D., M. Stoll and R. Bauer. 2006. A phylogenetic hypothesis of Ustilaginomycotina based on multiple gene analyses and morphological data. Mycologia 98, 906–916.

Begon, M. 1982. Yeasts and *Drosophila*. In: M. Ashburner, H.L. Carson and J.N. Thompson, Jr. (Eds), The Genetics and Biology of *Drosophila*, Vol. 3B. Academic Press, New York, pp. 345–384.

Beh, A.L., G.H. Fleet, C. Prakitchaiwattana and G.M. Heard. 2006. Evaluation of molecular methods for the analysis of yeasts in foods and beverages. In: A.D. Hocking, J.I. Pitt, R.A. Samson and U. Thrane (Eds), Advances in Food Mycology. Springer Science, New York, pp. 69–106.

Behrend, G. 1890. Über *Trichomycosis nodosa* (Juhel-Rénoy): piedra (Osorio). Berl. Klin. Wochenschr. 27, 464–467.

Beijerinck, M.W. 1889a. L'auxanographie, ou la méthode de l'hydrodiffusion dans la gélatine appliquée aux recherches microbiologiques. Arch. Néerl. Sci. Exactes Nat. 23, 367–372.

Beijerinck, M.W. 1889b. Sur le Kéfir. Arch. Néerl. Sci. Exactes Nat. 23, 428–444.

Beijerinck, M.W. 1892. Zur Ernährungs-Physiologie des Kahmpilzes. Zentralbl. Bakteriol. Parasitenkd. 11, 68–75.

Beijerinck, M.W. 1894. *Schizosaccharomyces octosporus,* eine achtsporige Alkoholhefe. Zentralbl. Bakteriol. Parasitenkd. 16, 49–58.

Beijerinck, M.W. 1895. Uber Nachweis und Verbreitung der Glukase, das Enzym der Maltose. Zentralbl. Bakteriol. Parasitenkd., Abt. II, 1, 221–229, 265, 329.

Beijerinck, M.W. 1898. Über Regeneration der Sporenbildung bei Alkoholhefen wo diese Funktion im Verschwinden begriffen ist. Zentralbl. Bakteriol. Parasitenkd., Abt. II, 4, 657–663, 721–730.

Beijerinck, M.W. 1904. *Chorella variegata*, ein bunter Mikrobe. Rec. Trav. Bot. Neerl. 1, 14–27.

Beijerinck, M.W. 1908. Die Erscheinung der Flockenbildung oder Agglutination bei Alkoholhefen. Zentralbl. Bakteriol. Parasitenkd., Abt. II, 20, 137–157, 641–650.

Beijerinck, M.W. 1912. Mutation bei Mikroben. Folia Microbiol. 1, 1–97, also in Verzamelde Geschriften V, 25, 25–88.

Bekatorou, A., C. Psarianos and A.A. Koutinas. 2006. Production of food grade yeasts. Food Technol. Biotechnol. 44, 407–415.

Bélanger, R.R., A.J. Dik and J.G. Menzies. 1998. Powdery mildews: recent advances towards integrated control. In: G.J. Boland and L.D. Kuykendall (Eds), Plant–microbe Interactions and Biological Control. Marcel Dekker, New York, pp. 89–109.

Bélanger, R.R., W.R. Jarvis and J.A. Traquair. 2002. *Sphaerotheca* and *Erysiphe* spp. powdery mildews (Erysiphaceae). In: P.G. Mason and J.T. Huber (Eds), Biological Control Programmes in Canada, 1981–2000. CAB International, Wallingford, pp. 501–505.

Belem, M.A., and B.H. Lee. 1998. Production of bioingredients from *Kluyveromyces lactis* grown on whey; an alternative. Crit. Rev. Food Sci. Nutr. 38, 565–598.

Belet, N., E. Ciftçi, E. Ince, N. Dalgiç, S. Oncel, H. Güriz, A. Yagmurlu, H. Dindar and U. Doğru. 2006. Caspofungin treatment in two infants with persistent fungaemia due to *Candida lipolytica*. Scand. J. Infect. Dis. 38, 559–562.

Belloch, C., E. Barrio, F. Uruburu, M.D. Garcia and A. Querol. 1997. Characterisation of four species of the genus *Kluyveromyces* by mitochondrial DNA restriction analysis. Syst. Appl. Microbiol. 20, 397–408.

Belloch, C., A. Querol, M.D. Garcia and E. Barrio. 2000. Phylogeny of the genus *Kluyveromyces* inferred from the mitochondrial cytochrome c oxidase II gene. Int. J. Syst. Evol. Microbiol. 50, 405–416.

Belloch, C., T. Fernández-Espinar, A. Querol, M.D. García and E. Barrio. 2002. An analysis of inter and intraspecific genetic variabilities in the *Kluyveromyces marxianus* group of yeast species for the reconsideration of the *K. lactis* taxon. Yeast 19, 257–268.

Belloch, C., M. Villa-Carvajal, M.L. Alvarez-Rodriguez and J.J.R. Coque. 2007. *Rhodotorula subericola* sp. nov., an anamorphic basidiomycetous yeast species isolated from bark of *Quercus suber* (cork oak). Int. J. Syst. Evol. Microbiol. 57, 1668–1671.

Beltran, G., M.J. Torija, M. Novo, N. Ferrer, M. Poblet, J.M. Guillamón, N. Rozes and A. Mas. 2002. Analysis of yeast populations during alcoholic fermentation, a six year follow-up study. Syst. Appl. Microbiol. 25, 287–293.

Bely, M., P. Stoeckle, I. Masneuf-Pomarède and D. Dubourdieu. 2008. Impact of mixed *Torulaspora delbrueckii–Saccharomyces cerevisiae* culture on high-sugar fermentation. Int. J. Food Microbiol. 122, 312–320.

Benbow, J.M., and D. Sugar. 1999. Fruit surface colonization and biological control of postharvest diseases of pear by pre-harvest yeast applications. Plant Dis. 83, 839–844.

Bencini, A., and E. Federici. 1928. Su due nuove specie di miceti rinvenuti nella cornea. Atti R. Accad. Fisiocrit. Siena, Ser. X, 3, 743–766.

Benda, I. 1962. *Torulopsis burgeffiana* nov. spec., eine von Weinbeeren isolierte, neue Hefeart. Antonie van Leeuwenhoek 28, 208–214.

Benda, N.D., D. Boucias, B. Torto and P.E. Teal. 2008. Detection and characterization of *Kodamaea ohmeri* associated with small hive beetle *Aethina tumida* infesting honeybee hives. J. Apicult. Res. 47, 194–201.

Bendel, C.M. 2003. Colonization and epithelial adhesion in the pathogenesis of neonatal candidiasis. Semin. Perinatol. 27, 357–364.

Benham, R.W. 1935. The terminology of the Cryptococci with a note on *Cryptococcus mollis*. Mycologia 27, 496–502.

Benitez, T., J.M. Gasent-Ramirea, F. Casterjon and A.C. Codon. 1996. Development of new strains for the food industry. Biotechnol. Prog. 12, 149–163.

Benítez Ahrendts, M.R., and L. Carrillo. 2004. *Penicillium*-inhibiting yeasts. Rev. Argent. Microbiol. 36, 182–186.

Benjamin, S., and A. Pandey. 1998. *Candida rugosa* lipases, molecular biology and versatility in biotechnology. Yeast 14, 1069–1087.

Bennett, J.W., and J. Arnold. 2001. Genomics for fungi. In: R.J. Howard and N.A.R. Gow (Volume, Eds). Biology of the Fungal Cell. In: K. Esser (Ed.). The Mycota. A Comprehensive Treatise on Fungi as Experimental Systems for Basic and Applied Research. Springer-Verlag, Berlin, pp. 267–295.

Bennett, J.W., and H.J. Phaff. 1995. Early biotechnology: the Delft connection. ASM News 59, 401–404.

Bennett, R.J., and A.D. Johnson. 2005. Mating in *Candida albicans* and the search for a sexual cycle. Annu. Rev. Microbiol. 59, 233–255.

Benny, G.L., and J.W. Kimbrough. 1980. A synopsis of the orders and families of Plectomycetes with keys to genera. Mycotaxon 12, 1–91.

Berbee, M.L. 2001. The phylogeny of plant and animal pathogens in the Ascomycota. Physiol. Mol. Plant Pathol. 59, 165–187.

Berbee, M.L., and J.W. Taylor. 1993a. Ascomycete relationships: dating the origin of asexual lineages with 18S ribosomal RNA gene sequence data. In: D.R. Reynolds and J.W. Taylor (Eds), The Fungal Holomorph: Mitotic, Meiotic and Pleomorphic Speciation in Fungal Systematics. CAB International, Wallingford, pp. 67–78.

Berbee, M.L., and J.W. Taylor. 1993b. Dating the evolutionary radiations of the true fungi. Can. J. Bot. 71, 1114–1127.

Berbee, M.L., and K. Wells. 1988b. Ultrastructural studies of mitosis and the septal pore apparatus in *Tremella globosa*. Mycologia 80, 479–492.

Bergauer, P., P.-A. Fonteyne, N. Nolard, F. Schinner and R. Margesin. 2005. Biodegradation of phenol and phenol-related compounds by psychrophilic and cold-tolerant alpine yeasts. Chemosphere 59, 909–918.

Bergman, A.G., and C.A. Kauffman. 1984. Dermatitis due to *Sporobolomyces* infection. Arch. Dermatol. 120, 1059–1060.

Bergman, A., V. Fernandez, K.O. Holmström, B.E. Claesson and H. Enroth. 2007. Rapid identification of pathogenic yeast isolates by real-time PCR and two-dimensional melting-point analysis. Eur. J. Clin. Microbiol. Infect. Dis. 26, 813–818.

Bergsten, J. 2005. A review of long-branch attraction. Cladistics 21, 163–193.

Berkeley, M.J. 1856. Decades of fungi. J. Bot. Kew Misc. 8, 272–280.

Berkeley, M.J. 1860. Outlines of British Fungology. L. Reeve, London.

Berkeley, M.J., and C.E. Broome. 1871. Notices of British fungi. Ann. Mag. Nat. Hist. IV. 7, 425–436.

Berkeley, M.J., and C.E. Broome. 1873. Enumeration of the fungi of Ceylon. Part 2. J. Linn. Soc. 14, 96.

Berkhout, C.M. 1923. De schimmelgeslachten *Monilia*, *Oidium*, *Oospora* en *Torula*. Thesis, University of Utrecht, The Netherlands.

Berlese, A.N. 1895. I funghi diversi dai *Saccaromiceti* e capaci di determinare la fermentazione alcoolica. G. Viticolt. Enol. 3, 52–55.

Bernhardt, R. 2006. Cytochromes P450 as versatile biocatalysts. J. Biotechnol. 124, 128–145.

Berry, D.R., and J.C. Slaughter. 2003. Alcoholic beverage fermentations. In: A.G.H. Lea and J.R. Piggot (Eds), Fermented Beverage Production. Kluwer Academic/Plenum Publisher, New York, pp. 25–40.

Bertram, J.S., and A.L. Vine. 2005. Cancer prevention by retinoids and carotenoids: independent action on a common target. Biochim. Biophys. Acta 1740, 170–178.

Besirbellioglu, B.A., A. Ulcay, M. Can, H. Erdem, M. Tanyuksel, I. Y. Avci, E. Araz and A. Pahsa. 2006. *Saccharomyces boulardii* and infection due to *Giardia lamblia*. Scand. J. Infect. Dis. 38, 479–481.

Bessey, E.A. 1950. Morphology and Taxonomy of Fungi. Blakiston Co., Philadelphia, PA.

Betts, G.D., P. Linton and R.J. Betteridge. 1999. Food spoilage yeasts: effects of pH, NaCl and temperature on growth. Food Control 10, 27–34.

Betts, G.D., P. Linton and R.J. Betteridge. 2000. Synergistic effect of sodium chloride, temperature and pH on growth of a cocktail of spoilage yeasts: a research note. Food Microbiol. 17, 47–52.

Beuchat, L.R. 1993. Selective media for detecting and enumerating foodborne yeasts. Int. J. Food Microbiol. 19, 1–14.

Beuchat, L.R. 1995. Indigenous fermented foods. In: H.-J. Rehm and G. Reed (Eds), Biotechnology. A Multi-Volume Comprehensive Treatise. Second, Completely Revised Edition. VCH Publishers, New York, pp. 504–559.

Bevan, E.A., and M. Makower. 1963. The physiological basis of the killer character in yeast. Proc. XIth Int. Congr. Genet. 1, 202–203.

Bezerra, J.L., and J.W. Kimbrough. 1978. A new species of *Tremella* parasitic on *Rhytidhysterium rufulum*. Can. J. Bot. 56, 3021–3033.

Bhadra, B., R. Sreenivas Rao, N. Naveen Kumar, P. Chaturvedi and P.K. Shivaji. 2007. *Pichia cecembensis* sp. nov. isolated from papaya fruit (*Carica papaya* L., Caricaceae). FEMS Yeast Res. 7, 579–584.

Bhadra, B., R.S. Rao, P.K. Singh, P.K. Sarkar and S. Shivaji. 2008a. Yeasts and yeast-like fungi associated with tree bark; diversity and identification of yeasts producing extracellular endoxylanases. Curr. Microbiol. 56, 484–489.

Bhadra, B., P.K. Singh, R.S. Rao and S. Shivaji. 2008b. *Blastobotrys serpentis* sp. nov., isolated from the intestine of a trinket snake (*Elaphe* sp., Colubridae). FEMS Yeast Res. 8, 492–498.

Bhally, H.S., S. Jain, C. Shields, N. Halsey, E. Cristofalo and W.G. Merz. 2006. Infection in a neonate caused by *Pichia fabianii*: importance of molecular identification. Med. Mycol. 44, 185–187.

Bhattacharjee, A.K., J.E. Bennett and C.P.J. Glaudemans. 1984. Capsular polysaccharides of *Cryptococcus neoformans*. Rev. Infect. Dis. 6, 619–624.

Bhosale, P., and P.S. Bernstein. 2005. Microbial xanthophylls. Appl. Microbiol. Biotechnol. 68, 445–455.

Bialkova, A., and J. Subik. 2006. Biology of the pathogenic yeast *Candida glabrata*. Folia Microbiol. (Praha) 51, 3–20.

Bicknell, J.N., and H.C. Douglas. 1970. Nucleic acid homologies among species of *Saccharomyces*. J. Bacteriol. 101, 505–512.

Biely, P., and M. Vrsanska. 1986. Xylanase of *Cryptococcus albidus*. Methods Enzymol. 160, 638–648.

Biely, P., M. Vrsanska and Z. Kratky. 1980. Xylan-degrading enzymes of the yeast *Cryptococcus albidus*, identification and cellular localization. Eur. J. Biochem. 108, 313–321.

Bigey, F., K. Tuery, D. Bougard, J.M. Nicaud and G. Moulin. 2003. Identification of a triacylglycerol lipase gene family in *Candida deformans*: molecular cloning and functional expression. Yeast 20, 233–248.

Biggs, R. 1937. *Dipodascus uninucleatus*. Mycologia 29, 34–44.

Billon-Grand, G. 1981. Contribution à la systématique du genre *Pichia*. Mycopathologia 75, 9–21.

Billon-Grand, G. 1985. Coenzyme Q de quelques espèces du genre *Pichia*. Détermination qualitative et quantitative. Mycopathologia 90, 101–106.

Billon-Grand, G. 1987. Minor ubiquinones of the yeast coenzyme Q system: importance in the taxonomy of the yeasts. J. Gen. Appl. Microbiol. 33, 381–390.

Billon-Grand, G. 1989. A new ascosporogenous yeast genus: *Yamadazyma* gen. nov. Mycotaxon 35, 201–204.

Bills, G.F., and M.S. Foster. 2004. Formulae for selected materials used to isolate and study fungi and fungal alles. In: G.M. Mueller, G.F. Bills and M.S. Fostser (Eds), Biodiversity of Fungi. Inventory and Monitoring Methods. Elsevier, Amsterdam, pp. 595–618.

Binder, L., A. Csillag and G. Tóth. 1956. Diffuse infiltration of the lungs associated with *Cryptococcus luteolus*. Lancet 260, 1043–1045.

Binder, M., D.S. Hibbett, K.-H. Larsson, E. Larsson, E. Langer and G. Langer. 2005. The phylogenetic distribution of resupinate forms across the major clades of mushroom-forming fungi (Homobasidiomycetes). Syst. Biodivers. 3, 113–157.

Bininda-Emonds, O.R.P. 2004. The evolution of supertrees. Trends Ecol. Evol. 19, 315–322.

Birgisson, H., O. Delgado, L. Garcia Arroyo, R. Hatti-Kaul and B. Mattiasson. 2003. Cold-adapted yeasts as producers of cold-active polygalacturonases. Extremophiles 7, 185–193.

Birt, D.F., S. Hendrich and W.Q. Wang. 2001. Dietary agents in cancer prevention: flavonoids and isoflavonoids. Pharmacol. Ther. 90, 157–177.

Bisby, G.R., A.H.R. Buller and J. Dearness. 1929. The Fungi of Manitoba. Longmans Green, London.

Bishop, J.A., N. Chase, S.S. Magill, C.P. Kurtzman, M.J. Fiandaca and W.G. Merz. 2008. *Candida bracarensis* detected among isolates of *Candida glabrata* by peptide nucleic acid fluorescence *in situ* hybridization: susceptibility data and documentation of presumed infection. J. Clin. Microbiol. 46, 443–446.

Bishop, N.A., and L. Guarente. 2007. Genetic links between diet and lifespan: shared mechanisms from yeast to humans. Nat. Rev. Genet. 11, 835–844.

Bisson, L.F. 1991. Microbial interactions during wine production. In: G. Zeikus and E.A. Johnson (Eds), Mixed Cultures in Biotechnology. McGraw Hill, New York, pp. 37–68.

Bisson, L.F. 1999. Stuck and sluggish fermentations. Am. J. Enol. Viticult. 50, 107–119.

Bisson, L.F. 2004. Biotechnology of wine yeast. Food Biotechnol. 18, 63–96.

Bisson, L.F., A.L. Waterhouse, S.E. Ebeler, M.A. Walker and J.T. Lapsley. 2002. The present and future of the international wine industry. Nature 418, 696–699.

Biswas, S.K., L. Wang, K. Yokoyama and K. Nishimura. 2003. Molecular analysis of *Cryptococcus neoformans* mitochondrial cytochrome b gene sequences. J. Clin. Microbiol. 41, 5572–5576.

Bjerkeng, B., M. Peisker, K. von Schwartzenberg, T. Ytrestoyl and T. Asgard. 2007. Digestibility and muscle retention of astaxanthin in Atlantic salmon, *Salmo salar*, fed diets with the red yeast *Phaffia rhodozyma* in comparison with synthetic formulated astaxanthin. Aquaculture 269, 476–489.

Björkling, F.S., E. Godtfredsen and O. Kirk. 1991. The future inpact of industrial lipases. Tibtech 9, 360–363.

Blackwell, M., D.S. Hibbett, J.W. Taylor and J.W. Spatafora. 2006. Research coordination networks: a phylogeny for kingdom Fungi (Deep Hypha). Mycologia 98, 829–837.

Blackwell, M., S.-O. Suh and J.B. Nardi. 2007. Fungi in the hidden environment: the gut of beetles. In: G. Gadd (Ed.), British Mycological Symposia: Fungi in the Environment. Cambridge University Press, Cambridge, pp. 665–693.

Blagodatskaya, V.M. 1979. *Saccharomycopsis pseudolipolytica* sp. nov., the perfect stage of *Candida pseudolipolytica*. Mikrobiologiia 48, 106–108.

Blagodatskaya, V.M., and A. Kocková-Kratochvílová. 1973. The heterogeneity of the species *Candida lipolytica, Candida pseudolipolytica* n. sp. and *Candida lipolytica* var. *thermotolerans* n. var. Biológia (Bratislava) 28, 709–716.

Blaich, R., and K. Esser. 1975. Function of enzymes in wood destroying fungi. II. Multiple forms of laccase in white rot fungi. Arch. Microbiol. 103, 271–277.

Blakely, J.A., and S.L. MacKenzie. 1969. Purification and properties of a beta-hexosidase from *Sporobolomyces singularis*. Can. J. Biochem. 47, 1021–1025.

Blakeman, J.P., and N.J. Fokkema. 1982. Potential for biological control of plant diseases on the phylloplane. Annu. Rev. Phytopathol. 20, 167–192.

Blanchette, M., G. Bourque and D. Sankhoff. 1997. Breakpoint phylogenies. In: S. Miyano and T. Takagi (Eds), Genome Informatics. Universal Academy Press, Tokyo, pp. 25–34.

Blandin, G., B. Llorente, A. Malpertuy, P. Wincker, F. Artiguenave and B. Dujon. 2000. Genomic exploration of the hemiascomycetous yeasts: 13. *Pichia angusta*. FEBS Lett. 487, 76–81.

Blandino, A., M.E. Al-Aseeri, S.S. Pandiella, D. Cantero and C. Webb. 2003. Cereal-based fermented foods and beverages. Food Res. Int. 36, 527–543.

Blanquet, S., S. Marol-Bonnin, E. Beyssac, D. Pompon, M. Renaud and M. Alric. 2001. The biodrug concept: an innovative approach to therapy. Trends Biotechnol. 19, 393–400.

Blanquet, S., J.P. Meunier, M. Minekus, S. Marol-Bonin and M. Alric. 2003. Recombinant *Saccharomyces cerevisiae* expressing P450 in artificial digestive systems: a model for biodetoxification in the human digestive environment. Appl. Environ. Microbiol. 69, 2884–2992.

Blanz, P.A., and M. Gottschalk. 1984. A comparison of 5S ribosomal RNA nucleotide sequences from smut fungi. Syst. Appl. Microbiol. 5, 518–526.

Blaschke-Hellmessen, R., H. Schuster and V. Bergmann. 1985. Differenzierung von Varianten bei *Prototheca zopfii* Krüger 1894. Arch. Exp. Vet. Med. Leipzig 39, 387–397.

Blaser, H.-U. 2003. Enantioselective catalysis in fine chemicals production. Chem. Commun. 3, 293–296.

Blaser, H.-U., B. Pugin and F. Spindler. 2005. Progress in enantioselective catalysis assessed from an industrial point of view. J. Mol. Catalysis A: Chemical 231, 1–20.

Blieck, L., G. Toye, F. Dumortier, K.J. Verstrepen, F.R. Delvaux, J.M. Thevelein and P. van Dijck. 2007. Isolation and characterization of brewer's yeast variants with improved fermentation performance under high-gravity conditions. Appl. Environ. Microbiol. 73, 815–824.

Blignaut, E., R. Senekal, J.L.F. Kock, A. Botha and J.P. van der Westhuizen. 1996. The value of cellular fatty acid analysis in the identification of oral yeasts. Syst. Appl. Microbiol. 19, 381–387.

Bloom, J.D., M.M. Meyer, P. Meinhold, C.R. Otey, D. MacMillan and F.H. Arnold. 2005. Evolving strategies for enzyme engineering. Curr. Opin. Struct. Biol. 15, 447–452.

Bloom, J.D., D.A. Drummond, F.H. Arnold and C.O. Wilke. 2006. Structural determinants of the rate of protein evolution in yeast. Soc. Mol. Biol. Evol. 23, 1751–1761.

Bodenhoff, J., P. Geertinger and J. Prause. 1979. Isolation of *Sporothrix fungorum* from a 500-year old mummy found in Greenland. Acta Pathol. Microbiol. Scand. Sect. B 87, 201–203.

Bodey, G.P. 1993. Candidiasis: Pathogenesis, Diagnosis, and Treatment, 2nd edn. Raven Press, New York.

Boedijn, K.B. 1934. The genus *Sirobasidium* in the Netherlands Indies. Bull. Jard. Bot. Buitenz., Ser. III, 13, 266–268.

Boedijn, K.B. 1960. On a new genus of the Endomycetaceae. Mycopathol. Mycol. Appl. 12, 163–167.

Boehm, D.F. 1984. Hexadecane utilization by *Prototheca zopfii*, Dissertation. West Virginia University, Morgantown, WV, 65pp.

Boekhout, T. 1987. Systematics of anamorphs of Ustilaginales (smut fungi): a preliminary survey. In: G.S. de Hoog, M.Th. Smith and A.C.M. Weijman (Eds), The Expanding Realm of Yeast-like Fungi. Elsevier, Amsterdam, pp. 137–149. (Stud. Mycol. 30, 137–149).

Boekhout, T. 1991a. A revision of ballistoconidia-forming yeasts and fungi. Stud. Mycol. 33, 1–194.

Boekhout, T. 1991b. Systematics of the genus *Itersonilia* Derx, a comparative phenetic study. Mycol. Res. 95, 135–146.

Boekhout, T. 1994. Classification of heterobasidiomycetous yeasts and fungi. Abstracts Fifth Int. Mycol. Congr., Vancouver, B.C., Canada, p. 18.

Boekhout, T. 1995. *Pseudozyma* Bandoni emend. Boekhout, a genus for yeast-like anamorphs of Ustilaginales. J. Gen. Appl. Microbiol. 41, 359–366.

Boekhout, T. 1998a. Diagnostic descriptions and key to presently accepted heterobasidiomycetous genera. In: C.P. Kurtzman and J.W. Fell (Eds), The Yeasts, A Taxonomic Study, 4th edn. Elsevier, Amsterdam, pp. 627–634.

Boekhout, T. 1998b. *Tilletiopsis* Derx ex Derx. In: C.P. Kurtzman and J.W. Fell (Eds), The Yeasts, A Taxonomic Study, 4th edn. Elsevier, Amsterdam, pp. 848–853.

Boekhout, T., and R.W. Bosboom. 1994. Karyotyping of *Malassezia* yeasts: taxonomic and epidemiological implications. Syst. Appl. Microbiol. 17, 146–153.

Boekhout, T., and J.W. Fell. 1995. Heterobasidiomycetes: systematics and applications. Stud. Mycol. 38, 5–11.

Boekhout, T., and E. Guého. 2003. Basidiomycetous yeasts. In: D.H. Howard (Ed.), Pathogenic Fungi in Humans and Animals, 2nd edn. Vol. 16. Marcel Dekker, New York, pp. 535–564.

Boekhout, T., E. Guého, P. Mayser and A. Velegraki (Eds). 2010. *Malassezia* and the skin. Science and clinical practice. Springer, Berlin. pp. 1–139.

Boekhout, T., and T. Jille. 1979. Mitosis and DNA content in yeast cells of *Itersonilia perplexans* Derx. Syst. Appl. Microbiol. 14, 117–123.

Boekhout, T., and C.P. Kurtzman. 1996. Principles and methods used in yeast classification, and an overview of currently accepted yeast genera. In: K. Wolf (Ed.), Nonconventional Yeasts in Biotechnology. A Handbook. Springer-Verlag, Berlin, pp. 1–99.

Boekhout, T., and W.A.M. Linnemans. 1982. Ultrastructure of mitosis in *Rhodosporidium toruloides*. Stud. Mycol. 22, 23–38.

Boekhout, T., and T. Nakase. 1998a. *Bensingtonia* Ingold emend. Nakase & Boekhout. In: C.P. Kurtzman and J.W. Fell (Eds), The Yeasts, A Taxonomic Study. Elsevier, Amsterdam, pp. 723–730.

Boekhout, T., and T. Nakase. 1998b. *Bullera* Derx. In: C.P. Kurtzman and J.W. Fell (Eds), The Yeasts, A Taxonomic Study, 4th edn. Elsevier, Amsterdam, pp. 731–741.

Boekhout, T., and T. Nakase. 1998c. *Sporobolomyces* Kluyver and van Niel. In: C.P. Kurtzman and J.W. Fell (Eds), The Yeasts, A Taxonomic Study, 4th edn. Elsevier, Amsterdam, pp. 828–843.

Boekhout, T., and V. Robert. 2003. Yeasts in Food: Beneficial and Detrimental Aspects. Behrs Verlag, Hamburg, pp. 1–488.

Boekhout, T., and R. Samson. 2005. Fungal biodiversity and food. In: R.M.J. Nout, W.M. de Vos and M.H. Zwietering (Eds), Food Fermentation. Wageningen Academic Publishers, The Netherlands, pp. 29–41.

Boekhout, T., and G. Scorzetti. 1997. Differential killer toxin sensitivity patterns of varieties of *Cryptococcus neoformans*. J. Med. Vet. Mycol. 35, 147–149.

Boekhout, T., and A. van Belkum. 1997. Variability of karyotypes and RAPD types in genetically related strains of *Cryptococcus neoformans*. Curr. Genet. 32, 203–208.

Boekhout, T., A. Fonseca and W.H. Batenburg-van der Vegte. 1991a. *Bulleromyces* genus novum (Tremellales), a teleomorph for *Bullera alba*, and the occurrence of mating in *Bullera variabilis*. Antonie van Leeuwenhoek 59, 81–93.

Boekhout, T., G. Poot, P. Hackmann and H.Y. Steensma. 1991b. Genomic characteristics of strains of *Itersonilia*: taxonomic consequences and life cycle. Can. J. Microbiol. 37, 188–194.

Boekhout, T., J. van Gool, H. van den Boogert and T. Jille. 1992a. Karyotyping and G+C composition as taxonomic criteria applied to the systematics of *Tilletiopsis* and related taxa. Mycol. Res. 96, 331–342.

Boekhout, T., Y. Yamada, A.C.M. Weijman, H.J. Roeijmans and W.H. Batenburg-van der Vegte. 1992b. The significance of coenzyme Q, carbohydrate composition and septal ultrastructure for the taxonomy of ballistoconidia-forming yeasts and fungi. Syst. Appl. Microbiol. 15, 1–10.

Boekhout, T., A. Fonseca, J.-P. Sampaio and W.I. Golubev. 1993. Classification of heterobasidiomycetous yeasts: characteristics and affiliation of genera to higher taxa of Heterobasidiomycetes. Can. J. Microbiol. 39, 276–290.

Boekhout, T., C.P. Kurtzman, K. O'Donnell and M.Th. Smith. 1994. Phylogeny of the yeast genera *Hanseniaspora* (anamorph *Kloeckera*), *Dekkera* (anamorph *Brettanomyces*), and *Eeniella* as inferred from partial 26S ribosomal DNA nucleotide sequences. Int. J. Syst. Bacteriol. 44, 781–786.

Boekhout, T., J.W. Fell and K. O'Donnell. 1995. Molecular systematics of some yeast-like anamorphs belonging to the Ustilaginales and Tilletiales. Stud. Mycol. 38, 175–183.

Boekhout, T., A. van Belkum, A.C. Leenders, H.A. Verbrugh, P. Mukamurangwa, D. Swinne and W.A. Scheffers. 1997. Molecular typing of *Cryptococcus neoformans*: taxonomic and epidemiological aspects. Int. J. Syst. Bacteriol. 47, 432–442.

Boekhout, T., M. Kamp and E. Guého. 1998a. Molecular typing of *Malassezia* species with PFGE and RAPD. Med. Mycol. 36, 365–372.

Boekhout, T., R.J. Bandoni, J.W. Fell and K.J. Kwon-Chung. 1998b. Discussion of teleomorphic and anamorphic genera of heterobasidiomycetous yeasts. In: C.P. Kurtzman and J.W. Fell (Eds), The Yeasts, A Taxonomic Study, 4th edn. Elsevier, Amsterdam, pp. 609–625.

Boekhout, T., G. Scorzetti and J.W. Fell. 1999a. Phenotypic characteristics of *Cryptococcus neoformans* are present in the *Cryptococcus laurentii* species complex. 4th Int. Conf. *Cryptococcus* and Cryptococcosis, September 12–16, Royal Society London, p. 193.

Boekhout, T., J.W. Fell, C.P. Kurtzman and E.A. Johnson. 1999b. Proposal to reject the name *Rhodomyces dendrorhous* (Fungi, Basidiomycota). Taxon 48, 147–148.

Boekhout, T., J.W. Fell, A. Fonseca, H.J. Prillinger, K. Lopandic and H. Roeijmans. 2000. The basidiomycetous yeast *Rhodotorula yarrowii* comb. nov. Antonie van Leeuwenhoek 77, 355–358.

Boekhout, T., B. Theelen, M. Diaz, J.W. Fell, W.C. Hop, E.C. Abeln, F. Dromer and W. Meyer. 2001. Hybrid genotypes

in the pathogenic yeast *Cryptococcus neoformans*. Microbiology (UK) 147, 891–907.
Boekhout, T., V. Robert, M.Th. Smith, J. Stalpers, D. Yarrow, F. Boer, G. Gijswijt, C.P. Kurtzman, J.W. Fell, E. Guého, J. Guillot and I. Roberts. 2002. Yeasts of the World. ETI, Amsterdam. CD-ROM.
Boekhout, T., B. Theelen, J. Houbraken, V. Robert, G. Scorzetti, A. Gafni, U. Gerson and A. Sztejnberg. 2003. Novel anamorphic mite-associated fungi belonging to the Ustilaginomycetes: *Meira geulakonigii* gen. nov., sp. nov., *Meira argovae* sp. nov. and *Acaromyces ingoldii* gen. nov., sp. nov. Int. J. Syst. Evol. Microbiol. 53, 1655–1664.
Boekhout, T., M. Bovers, J.W. Fell, M.R. Diaz, F. Hagen, B. Theelen and E.E. Kuramae. 2005. *Cryptococcus neoformans*: how many species? Proc. 6th Int. Conf. on *Cryptococcus* and Cryptococcosis. Boston, Massachusetts, p. 44.
Boekhout, T., P. Gildemacher, B. Theelen, W.H. Müller, B. Heijne and M. Lutz. 2006. Extensive colonization of apples by smut anamorphs causes a new postharvest disorder. FEMS Yeast Res. 6, 63–76.
Boekhout, T., C. Gueidan, S. de Hoog, R. Samson, J. Varga and G. Walther. 2009. Fungal taxonomy: new developments in medically important fungi. Curr. Fungal Infect. Rep. 3, 170–178.
Böer, E., G. Gellissen and G. Kunze. 2005. *Arxula adeninovorans*. In: G. Gellissen (Ed.), Production of Recombinant Proteins. Wiley-VCH Verlag, Weinheim, pp. 89–110.
Böer, E., G. Steinborn, G. Kunze and G. Gellisen. 2007. Yeast expression platforms. Appl. Microbiol. Biotechnol. 77, 513–523.
Boerema, G.H., and A.A. Verhoeven. 1972. Check-list for scientific names of common parasitic fungi. Series 1a: Fungi on trees and shrubs. Neth. J. Plant Pathol. 78 (Suppl. 1), 1–63.
Boersman, Y.L., M.J. Droge and W.J. Quax. 2007. Selection strategies for improved biocatalysts. FEBS J. 274, 2181–2195.
Boettner, M., C. Steffens, C. von Mering, P. Bork, U. Stahl and C. Lang. 2007. Sequence-based factors influencing the expression of heterologous genes in the yeast *Pichia pastoris* – comparative view of 79 human genes. J. Biotechnol. 130, 1–10.
Bogle, G.T. 1989. The isolation and characterization of an extra-chromosomal element in the yeast *Candida oleophila*. MSc Thesis, University of Western Ontario, London, Canada, 106pp.
Boidin, J., and F. Abadie. 1954. Les levures des liqueurs tannantes végétales; leur action sur les tanins pyrogalliques. Bull. Soc. Mycol. Fr. 70, 353–383.
Boidin, J., and J.-M. Adzet. 1957. Deux curieuses levures isolées d'extraits tannants d'origine végétale: *Pachysolen* (nov. gen.) *tannophilus* nov. sp. et *P. pelliculatus* nov. sp. Bull. Soc. Mycol. Fr. 73, 331–342.
Boidin, J., F. Abadie, F.L. Jacob and M.-C. Pignal. 1962. Les levures á spores réniformes. Bull. Soc. Mycol. Fr. 78, 155–203.
Boidin, J., M.-C. Pignal, G. Mermier and M. Arpin. 1963. Quelques levures camerounaises. Cah. Maboké 1, 86–100.
Boidin, J., M.-C. Pignal, Y. Lehodey, A. Vey and F. Abadie. 1964. Le genre *Pichia sensu lato* (Première Contribution). Bull. Soc. Mycol. Fr. 80, 396–438.
Boidin, J., F. Abadie and Y. Lehodey. 1965a. Le genre *Pichia sensu lato* (Deuxième Contribution). Bull. Soc. Mycol. Fr. 81, 5–23.
Boidin, J., M.-C. Pignal and M. Besson. 1965b. Le genre *Pichia sensu lato* (Quatrième Contribution). Bull. Soc. Mycol. Fr. 81, 566–606.
Boldo, X.M., L. Villa-Tanaca, G. Zuniga and C. Hernandez-Rodriguez. 2003. Genetic diversity among clinical isolates of *Candida glabrata* analyzed by randomly amplified polymorphic DNA and multilocus enzyme electrophoresis analyses. J. Clin. Microbiol. 41, 4799–4804.
Bolen, P.L., C.P. Kurtzman, J.M. Ligon, B.M. Mannarelli and R.J. Bothast. 1992. Physical and genetic characterization of linear DNA plasmids from the heterothallic yeast *Saccharomycopsis crataegensis*. Antonie van Leeuwenhoek 61, 195–205.
Bolen, P.L., E.M. Eastman, P.L. Cihak and G.T. Hayman. 1994. Isolation and sequence analysis of a gene from the linear DNA plasmid pPacl-2 of *Pichia acaciae* that shows similarity to a killer toxin gene of *Kluyveromyces lactis*. Yeast 10, 403–414.
Bölker, M., and R. Kahmann. 1993. Sexual pheromones and mating responses in fungi. Plant Cell 5, 1461–1469.
Bolotin-Fukuhara, M., C. Toffano-Nioche, F. Artiguenave, G. Duchateau-Nguyen, M. Lemaire, R. Marmeisse, R. Montrocher, C. Robert, M. Termier, P. Wincker and M. Wesolowski-Louvel. 2000. Genomic exploration of the hemiascomycetous yeasts: 11. *Kluyveromyces lactis*. FEBS Lett. 487, 66–70.
Bon, E., C. Neuveglise, A. Lepingle, P. Wincker, F. Artiguenave, C. Gaillardin and S. Casaregola. 2000. Genomic exploration of the hemiascomycetous yeasts: 6. *Saccharomyces exiguus*. FEBS Lett. 487, 42–46.
Bond, R., and R.M. Anthony. 1995. Characterization of markedly lipid-dependent *Malassezia pachydermatis* isolates from dogs. J. Appl. Microbiol. 78, 537–542.
Bond, R., S.A. Howell, P.J. Haywood and D.H. Lloyd. 1997. Isolation of *Malassezia sympodialis* and *Malassezia globosa* from healthy pet cats. Vet. Rec. 141, 200–201.
Bond, U., and A. Blomberg. 2006. Principles and applications of genomics and proteomics in the analysis of industrial yeast strains. In: A. Querol and G.H. Fleet (Eds), Yeasts in Food and Beverages. Springer-Verlag, Berlin, pp. 175–214.
Bonekamp, F.J., and J. Oosterom. 1994. On the safety of *Kluyveromyces lactis*: a review. Appl. Microbiol. Biotechnol. 41, 13.
Bonestroo, M.H., J.C. de Wit, B.J. Kusters and F.M. Rombouts. 1993. Inhibition of the growth of yeasts in fermented salads. Int. J. Food Microbiol. 17, 311–320.
Bonjean, B., and L.-D. Guillaume. 2003. Yeasts in bread and baking products. In: T. Boekhout and V. Robert (Eds), Yeasts in Food, Beneficial and Detrimental Aspects. B. Behr's Verlag, Hamburg, pp. 289–307.
Bonner, T.I., D.J. Brenner, B.R. Neufeld and R.J. Britten. 1973. Reduction in the rate of DNA reassociation by sequence divergence. J. Mol. Biol. 81, 123–135.
Bonorden, H.F. 1851. Handbuch der allgemeinen Mykologie als Anleitung zum Studium derselben, nebst speziellen Beiträgen zur Vervollkommnung dieses Zweiges der Naturkunde. Schweizerbart, Stuttgart, 336pp.
Bonrath, W., and T. Netscher. 2005. Catalytic processes in vitamins synthesis and production. Appl. Catal. A: General 280, 55–73.
Boone, C., S.S. Sommer, A. Hensel and H. Bussey. 1990. Yeast KRE genes provide evidence for a pathway of cell wall β-glucan assembly. J. Cell. Biol. 110, 1833–1843.
Boone, C.K., D.L. Six, Y. Zheng and K.F. Raffa. 2008. Parasitoids and dipteran predators exploit volatiles from microbial

symbionts to locate bark beetles. Environ. Entomol. 37, 150–161.
Boore, J.L. 2006. The use of genome-level characters for phylogenetic reconstruction. Trends Ecol. Evol. 21, 439–446.
Boore, J.L., D.V. Lavrov and W.M. Brown. 1998. Gene translocation links insects and crustaceans. Nature 392, 667–668.
Boorsma, A., H. de Nobel, B. Ter Riet, B. Bargmann, S. Brul, K.J. Hellingwerf and F.M. Klis. 2004. Characterization of the transcriptional response to cell wall stress in *Saccharomyces cerevisiae*. Yeast 21, 413–427.
Booth, C. 1981a. *Taphrina deformans*. C.M.I. Descript. Pathog. Fungi Bact. 711, 1–2.
Booth, C. 1981b. *Taphrina wiesneri*. C.M.I. Descript. Pathog. Fungi Bact. 712, 1–2.
Booth, C. 1981c. *Taphrina pruni*. C.M.I. Descript. Pathog. Fungi Bact. 713, 1–2.
Booth, J.L., and H.S. Vishniac. 1987. Urease testing and yeast taxonomy. Can. J. Microbiol. 33, 396–404.
Boretsky, Y.R., O.V. Protchenko, T.M. Prokopiv, I.O. Mukalov, D.V. Fedorovych and A.A. Sibirny. 2007. Mutations and environmental factors affecting regulation of riboflavin synthesis and iron assimilation also cause oxidative stress in the yeast *Pichia guilliermondii*. J. Basic Microbiol. 47, 371–377.
Borman, A.M., R. Petch, C.J. Linton, M.D. Palmer, P.D. Bridge and E.M. Johnson. 2008. *Candida nivariensis*, an emerging pathogenic fungus with multidrug resistance to antifungal agents. J. Clin. Microbiol. 46, 933–938.
Borman, A.M., C.J. Linton, D. Oliver, M.D. Palmer, A. Szekely, F. C. Odds and E.M. Johnson. 2009. Pyrosequencing analysis of 20 nucleotides of internal transcribed spacer 2 discriminates *Candida parapsilosis*, *Candida metapsilosis*, and *Candida orthopsilosis*. J. Clin. Microbiol. 47, 2307–2310.
Bormann, C., and H. Sahm. 1978. Degradation of microbodies in relation to activities of alcohol oxidase and catalase in *Candida boidinii*. Arch. Microbiol. 117, 67–72.
Borneman, A.R., P.J. Chambers and I.S. Pretorius. 2007. Yeast systems biology: modeling the winemaker's art. Trends Biotechnol. 25, 349–355.
Borneman, J., and R.J. Hartin. 2000. PCR primers that amplify fungal rRNA genes from environmental samples. Appl. Environ. Microbiol. 66, 4356–4360.
Borner, G.V., N. Kleckner and N. Hunter. 2004. Crossover/noncrossover differentiation, synaptonemal complex formation, and regulatory surveillance at the leptotene/zygotene transition of meiosis. Cell 117, 29–45.
Borst, A., B. Theelen, E. Reinders, T. Boekhout, A.C. Fluit and P.H.M. Savelkoul. 2003. AFLP as an identification method for medically important *Candida* spp., including *C. dubliniensis*. J. Clin. Microbiol. 41, 1357–1362.
Bortiri, E., S.-H. Oh, J. Jiang, S. Baggett, A. Granger, C. Weeks, M. Buckingham, D. Potter and D.E. Parfitt. 2001. Phylogeny and systematics of *Prunus* (Rosaceae) as determined by sequence analysis of ITS and the chloroplast trnL-trnF spacer DNA. Syst. Bot. 26, 797–807.
Borza, T., C.E. Popescu and R.W. Lee. 2005. Multiple metabolic roles for the nonphotosynthetic plastid of the green alga *Prototheca wickerhamii*. Eukarot Cell 4, 253–261.
Borzi, A. 1888. *Eremothecium cymbalariae*, nuovo ascomicete. Nuovo Giorn. Bot. Ital. 20, 452–456.
Bose, I., A.J. Reese, J.J. Ory, G. Janbon and T.L. Doering. 2003. A yeast under cover: the capsule of *Cryptococcus neoformans*. Eukaryot. Cell 2, 655–663.
Botes, A.L., J. Lotter, O.H. Rhode and A. Botha. 2005. Interspecies differences in the enantioselectivity of epoxide hydrolases in *Cryptococcus laurentii* (Kufferath) C.E. Skinner and *Cryptococcus podzolicus* (Bab'jeva & Reshetova) Golubev. Syst. Appl. Microbiol. 28, 27–33.
Botha, A. 2006. Yeasts in soil. In: G. Peter and C.A. Rosa (Eds), Biodiversity and Ecophysiology of Yeasts. Springer, Berlin, pp. 221–240.
Botha, A., and J.L.F. Kock. 1993a. Application of the fatty acid profiles in the identification of yeast. Int. J. Food Microbiol. 19, 39–51.
Botha, A., and L.F. Kock. 1993b. The distribution and taxonomic value of fatty acids and eisosanoids in the Lipomycetaceae and Dipodascaceae. Antonie van Leeuwenhoek 63, 111–123.
Botha, A., J.L.F. Kock, D.J. Coetzee, M.S. van Dijk, L. van der Berg and P.J. Botes. 1992a. Yeast eicosanoids. I. The distribution and taxonomic value of cellular fatty acids and arachidonic acid metabolites in the Dipodascaceae and related taxa. Syst. Appl. Microbiol. 15, 148–154.
Botha, A., J.L.F. Kock, D.J. Coetzee, N.A. Linde and M.S. van Dijk. 1992b. Yeast eicosanoids. II. The influence of non-steroidal antiinflammatory drugs on the life cycle of *Dipodascopsis*. Syst. Appl. Microbiol. 15, 155–160.
Botha, A., J.L.F. Kock, M.S. van Dijk, D.J. Coetzee, O.P.H. Augustyn and P.J. Botes. 1993. Yeast eicosanoids IV. Evidence for prostaglandine production during ascosporogenesis by *Dipodascopsis tothii*. Syst. Appl. Microbiol. 16, 159–163.
Botstein, D. 2003. Genomic perspective and cancer. Cold Spring Harbor Symp. Quant. Biol. 68, 417–424.
Botterel, F., C. Desterke, C. Costa and S. Bretagne. 2001. Analysis of microsatellite markers of *Candida albicans* used for rapid typing. J. Clin. Microbiol. 39, 4076–4081.
Bouchara, J.P., P. Declerck, B. Cimon, C. Planchenault, L. de Gentile and D. Chabasse. 1996. Routine use of CHROMagar *Candida* medium for presumptive identification of *Candida* yeast species and detection of mixed fungal populations. Clin. Microbiol. Infect. 2, 202–208.
Boucher, F., R. Morosoli and S. Durand. 1988. Complete nucleotide sequence of the xylanase gene from the yeast *Cryptococcus albidus*. Nucleic Acids Res. 16, 9874.
Boudier, M.E. 1887. Note sur le *Tremella fimetaria* Shum. Journal de Botanique 1, 330–333.
Bougnoux, M.E., A. Tavanti, C. Bouchier, N.A. Gow, A. Magnier, A.D. Davidson, M.C. Maiden, C. D'Enfert and F.C. Odds. 2003. Collaborative consensus for optimized multilocus sequence typing of *Candida albicans*. J. Clin. Microbiol. 41, 5265–5266.
Boulton, C.A., and C. Ratledge. 1984. *Cryptococcus terricolus*, an oleaginous yeast re-appraised. Appl. Microbiol. Biotechnol. 20, 72–76.
Bourcier, T., O. Touzeau, F. Thomas, C. Chaumeil, M. Baudrimont, V. Borderie and L. Laroche. 2003. *Candida parapsilosis* keratitis. Cornea 22, 51–55.
Bourdot, H., and L. Galzin. 1909. Hyménomycètes de France (I. Héterobasidiés). Bull. Soc. Mycol. Fr. 25, 15–36.
Bourdot, H., and L. Galzin. 1928. Hyménomycètes de France. Marcel Bry, Sceaux.
Bourgeois, M. 1915. Über Onychomykosis saccharomycetica. Dermatol. Z. 22, 411–420.
Boutrou, R., and M. Guéguen. 2005. Interests in *Geotrichum candidum* for cheese technology. Int. J. Food Microbiol. 102, 120.

Boutroux, L. 1884. Sur la conservation des ferments alcooliques dans la nature. Ann. Sci. Nat. Sér. VI 17, 144–209.

Bouza, E., and P. Muñoz. 2004. Invasive infections caused by *Blastoschizomyces capitatus* and *Scedosporium* spp. Clin. Microbiol. Infect. 10 (Suppl. 1), 76–85.

Bovee, T.F.H., G. Bor, H.H. Heskamp, R.L.A.P. Hoogenboom and M. W.F. Nielen. 2006. Validation and application of a robust yeast estrogen assay for the screening of estrogen activity in animal feed. Food Add. Contam. 23, 556–558.

Bovers, M., F. Hagen, E.E. Kuramae, M.R. Diaz, L. Spanjaard and F. Dromer. 2006. Unique hybrids between the fungal pathogens *Cryptococcus neoformans* and *Cryptococcus gattii*. FEMS Yeast Res. 6, 599–607.

Bovers, M., M.R. Diaz, F. Hagen, L. Spanjaard, B. Duim, C.E. Visser, H.L. Hoogveld, J. Scharringa, I.M. Hoepelman, J.W. Fell and T. Boekhout. 2007. Identification of genotypically diverse *Cryptococcus neoformans* and *Cryptococcus gattii* isolates using Luminex xMAP technology. J. Clin. Microbiol. 45, 1874–1883.

Bovers, M., F. Hagen, E.E. Kuramae and T. Boekhout. 2008a. Six monophyletic lineages identified within *Cryptococcus neoformans* and *Cryptococcus gattii* by multi-locus sequence typing. Fungal Genet. Biol. 45, 400–421.

Bovers, M., F. Hagen, E.E. Kuramae, H.L. Hoogveld, F. Dromer, G. St-Germain and T. Boekhout. 2008b. AIDS patient death caused by novel *Cryptococcus neoformans*–C. *gattii* hybrid. Emerg. Infect. Dis. 14, 1105–1108.

Bovers, M., F. Hagen and T. Boekhout. 2008c. Diversity of the *Cryptococcus neoformans–Cryptococcus gattii* species complex. Rev. IberoAm. Mycol. 25, S4–S12.

Bovers, M., F. Hagen, E.E. Kuramae and T. Boekhout. 2009. Promiscuous mitochondria in *Cryptococcus gattii*. FEMS Yeast Res. 9, 489–503.

Bovill, R., J. Bew and S. Robinson. 2001. Comparison of selective media for the recovery and enumeration of probiotic yeasts from animal feed. Int. J. Food Microbiol. 67, 55–61.

Bowles, J.M., and M.A. Lachance. 1983. Patterns of variation in the yeast florae of exudates in an oak community. Can. J. Bot. 61, 2984–2995.

Bowman, J.P., J.J. Gosink, S.A. McCammon, T.L. Lewis, D.S. Nicols, P.D. Nichols, J.H. Skerrat, J.T. Staley and T.A. McMeekin. 1998. Novel *Colwellia* species isolated from Antarctic fast ice. Int. J. Syst. Bacteriol. 48, 1171–1180.

Boze, H., G. Moulin and P. Galzy. 1995. Production of microbial biomass. In: H.-J. Rehm and G. Reed (Eds), Biotechnology, 2nd edn. VCH Publishers, New York.

Bracker, C.E., and E.E. Butler. 1963. The ultrastructure and development of septa in hyphae of *Rhizoctonia solani*. Mycologia 55, 35–58.

Bracker, C.E., and E.A. Butler. 1964. Function of the septal pore apparatus in *Rhizoctonia solani* during protoplasmic streaming. J. Cell Biol. 21, 152–157.

Bradsher, R.W., S.W. Chapman and P.G. Pappas. 2003. Blastomycosis. Infect. Dis. Clin. North Am. 17, 21–40. vii.

Brady, B.L., B.C. Sutton and R.A. Samson. 1984. *Agaricostilbum pulcherrimum* (Berk. & Broome) comb. nov. Trans. Br. Mycol. Soc. 83, 540–541.

Brady, L. 1960. Occurrence of *Itersonilia* and *Tilletiopsis* on lesions caused by *Entyloma*. Trans. Br. Mycol. Soc. 43, 31–50.

Braendlin, N. 1996. Enumeration of xerophilic yeasts in the presence of xerophilic moulds, a collaborative study. Int. J. Food Microbiol. 29, 185–192.

Braga, A.A., P.B. de Morais and V.R. Linardi. 1998. Screening of yeasts from Brazilian Amazon rain forest for extracellular proteinases production. Syst. Appl. Microbiol. 21, 353–359.

Brand, J.M., J. Schultz, S.J. Barras, L.J. Edson, T.L. Payne and R. L. Hedden. 1977. Bark beetle pheromones: enhancement of *Dendroctonus frontalis* (Coleoptera: Scolytidae) aggregation pheromone by yeast metabolism in laboratory bioassays. J. Chem. Ecol. 3, 657–666.

Brandt, M.E., L.C. Hutwagner, R.J. Kuykendall and R.W. Pinner. 1995. Comparison of multilocus enzyme electrophoresis and random amplified polymorphic DNA analysis for molecular subtyping of *Cryptococcus neoformans*. The Cryptococcal Disease Active Surveillance Group. J. Clin. Microbiol. 33, 1890–1895.

Brandt, M.E., C.A. Kauffman, P.G. Pappas, N. Iqbal, B.A. Arthington-Skaggs, W. Lee-Yang and M.Th. Smith. 2004. Fungemia caused by *Zygoascus hellenicus* in an allogeneic stem cell transplant recipient. J. Clin. Microbiol. 42, 3363–3365.

Branduardi, P., M. Valli, L. Brambilla, M. Sauer, L. Alberghina and D. Porro. 2004. The yeast *Zygosaccharomyces bailii*: a new host for heterologous protein production, secretion and for metabolic engineering applications. FEMS Yeast Res. 4, 493–504.

Branduardi, P., C. Smeraldi and D. Porro. 2008. Metabolically engineered yeasts: "potential" industrial applications. J. Mol. Microbiol. Biotechnol. 15, 31–40.

Brault, J., and L. Masselot. 1911. Étude sur une nouvelle mycose. Ann. Dermatol. Syph. 2, 592–602.

Braun, B.R., M. van het Hoog, C. d'Enfert, M. Martchenko, J. Dungan, A. Kuo, D.O. Inglis, M.A. Uhl, H. Hogues, M. Berriman, M. Lorenz, A. Levitin, U. Oberholzer, C. Bachewich, D. Harcus, A. Marcil, D. Dignard, T. Iouk, R. Zito, L. Frangeul, F. Tekaia, K. Rutherford, E. Wang, C.A. Munro, S. Bates, N.A. Gow, L.L. Hoyer, G. Kohler, J. Morschhauser, G. Newport, S. Znaidi, M. Raymond, B. Turcotte, G. Sherlock, M. Costanzo, J. Ihmels, J. Berman, D. Sanglard, N. Agabian, A.P. Mitchell, A.D. Johnson, M. Whiteway and A. Nantel. 2005. A human-curated annotation of the *Candida albicans* genome. PLoS Genet. 1, e1.

Breathnach, A.S., M. Gross and B. Martin. 1976. Freeze-fracture replication of cultured *Pityrosporum orbiculare*. Sabouraudia 14, 105–113.

Breeze, E.M., and N.J. Dix. 1981. Seasonal analysis of the fungal community on *Acer platanoides* leaves. Trans. Br. Mycol. Soc. 77, 321–328.

Brefeld, O. 1881. Die Brandpilze I. In: Botanische Untersuchungen über Hefenpilze. Fortsetzung der Schimmelpilze, Heft 4. Arthur Felix, Leipzig, pp. 1–191.

Brefeld, O. 1888. Basidiomyceten II. Protobasidiomyceten. Untersuchungen aus dem Gesamtgebiete der Mykologie, VII. Arthur Felix, Leipzig, pp. 1–178, Plates I–II.

Brefeld, O. 1895a. Die Brandpilze II. In: Untersuchungen aus dem Gesamtgebiete der Mykologie, Heft 11. Heinrich Schönigh, Münster i. W., pp. 1–98; Plates 1–5.

Brefeld, O. 1895b. Die Brandpilze III. Hemibasidii. In: Untersuchungen aus dem Gesamtgebiete der Mykologie, Heft 12. Heinrich Schönigh, Münster i. W., pp. 99–236; Plates 6–12.

Brefeld, O., and G. Lindau. 1891. Die Formen der Hemiasci und ihre Kultur in Nährlösungen. Unters. Gesammtgeb. Mykol. 9, 91–118.

Breierová, E. 1997. Yeast exo-glycoproteins produced under NaCl-stress conditions as efficient cryoprotective agents. Lett. Appl. Microbiol. 25, 254–256.
Breinig, F., D.J. Tipper and M.J. Schmitt. 2002. Kre1p, the plasma membrane receptor for the yeast K1 viral toxin. Cell 108, 395–405.
Breitenbach, M. 2008. The spectrum of fungal allergy. Int. J. Allergy Immunol. 145, 58–86.
Brejning, J., N. Arneborg and L. Jespersen. 2005. Identification of genes and proteins induced during the lag and early exponential phase of lager brewing yeasts. J. Appl. Microbiol. 98, 261–268.
Bremer, K. 1988. The limits of amino-acid sequence data in angiosperm phylogenetic reconstruction. Evolution 42, 795–803.
Bresadola, G. 1891. Sur un nouveau genre de Tubercullariée. Rev. Mycol. Toulouse 13, 14–15.
Bresadola, J. 1903. Fungi polonici. Ann. Mycol. 1, 65–131.
Breuer, M., K. Ditrich, T. Habicher, B. Hauer, M. Kesseler, R. Stuermer and T. Zelinski. 2004. Industrial methods for the production of optically active intermediates. Angew. Chem. Int. Ed. 43, 788–824.
Breuer, U., and H. Harms. 2006. *Debaryomyces hansenii* – an extremophilic yeast with biotechnological potential. Yeast 23, 415–437.
Brinkmann, H., M. van der Giezen, Y. Zhou, G. Poncelin de Raucourt and H. Philippe. 2005. An empirical assessment of long-branch attraction artefacts in deep eukaryotic phylogenomics. Syst. Biol. 54, 743–757.
Britten, R.J., D.E. Graham and B.R. Neufeld. 1974. Analysis of repeating DNA sequences by reassociation. In: L. Grossman and K. Moldave (Eds), Methods in Enzymology, Vol. 29. Academic Press, New York, pp. 363–418.
Brizzio, S., B. Turchetti, V. de García, D. Libkind, P. Buzzini, C. Gasparetti and M. van Broock. 2007. Extracellular enzymatic activities (EEA) in basidiomycetous yeasts isolated from glacial and subglacial waters of northwest Patagonia (Argentina). Can. J. Microbiol. 53, 519–525.
Brock, T.D. 1959. Mating reaction in *Hansenula wingei*. Relation of cell surface properties to agglutination. J. Bacteriol. 78, 59–68.
Brock, T.D. 1965. Biochemical and cellular changes occurring during conjugation in *Hansenula wingei*. J. Bacteriol. 90, 1019–1025.
Brockert, P.J., S.A. Lachke, T. Srikantha, C. Pujol, R. Galask and D.R. Soll. 2003. Phenotypic switching and mating type switching of *Candida glabrata* at sites of colonization. Infect. Immun. 71, 7109–7118.
Bromel, C., and J.E. Sykes. 2005. Epidemiology, diagnosis, and treatment of blastomycosis in dogs and cats. Clin. Tech. Small Anim. Pract. 20, 233–239.
Brooks, D.R. 1985. Historical ecology: a new approach to studying the evolution of ecological associations. Ann. Mo. Bot. Gard. 72, 660–680.
Brooks, S., and L. Brown. 1987. Systemic infection with *Malassezia furfur* in an adult receiving long-term hyperalimentation therapy. J. Infect. Dis. 156, 410–411.
Brough, S. 1974. *Tremella globospora*, in the field and in culture. Can. J. Bot. 52, 1853–1859.
Brown, C.E., and M. Chambers. 1996. Evaluation of biological products for the control of postharvest diseases of Florida citrus. Proc. Fla. State Hort. Soc. 109, 278–282.
Brown, J.L., Z. Kossaczka, B. Jiang and H. Bussey. 1993. A mutational analysis of killer toxin resistance in *Saccharomyces cerevisiae* identifies new genes involved in cell wall (1→6)-β-glucan synthesis. Genetics 133, 837–849.
Bruch, C.W. 1967. Microbes in the upper atmosphere and beyond. In: P.H. Gregory and J.L. Monteith (Eds), Airborne Microbes. Cambridge University Press, London, pp. 345–374.
Brumpt, E. 1913. Précis de Parasitologie, 2me éd., Paris.
Brumpt, E. 1922. Précis de Parasitologie, 3me éd., Paris.
Brumpt, E. 1927. Précis de Parasitologie, 4me éd. Paris.
Brumpt, E. 1936. Précis de Parasitologie, 5me éd. Paris.
Bryant, D. 2003. A classification of consensus methods for phylogenetics. In: M.F. Janowitz, F.-J. Lapointe, F.R. McMorris, B. Mirkin and F.S. Roberts (Eds), Bioconsensus. DIMACS Series in Discrete Mathematics and Theoretical Computer Science, Vol. 61. American Mathematical Society, Rhode Island, pp. 163–183.
Bryant, D., and V. Moulton. 2004. Neighbor-Net: an agglomerative method for the construction of phylogenetic networks. Mol. Biol. Evol. 21, 255–265.
Bryden, W.L. 2007. Mycotoxins in the food chain: human health implications. Asia Pac. J. Clin. Nutr. 16 (Suppl. 1), 95–101.
Brysch-Herzberg, M. 2004a. *Metschnikowia kunwiensis* comb. nov., the teleomorph of *Candida kunwiensis*. FEMS Yeast Res. 4, 605–607.
Brysch-Herzberg, M. 2004b. Ecology of yeasts in plant–bumblebee mutualism in Central Europe. FEMS Microbiol. Ecol. 50, 87–100.
Brysch-Herzberg, M., and M.A. Lachance. 2004. *Candida bombiphila* sp. nov., a new asexual yeast species in the *Wickerhamiella* clade. Int. J. Syst. Evol. Microbiol. 54, 1857–1859.
Buchanan, K.L., and J.W. Murphy. 1998. What makes *Cryptococcus neoformans* a pathogen? Emerg. Infect. Dis. 4, 71–83.
Buchner, P. 1965. Endosymbiosis of Animals with Plant Microorganisms. Interscience, New York.
Buchwald, N.F. 1939. Fungi Imperfecti (Deuteromycetes). Kongelige Veterinaer- og Landbohojskole, Copenhagen.
Buck, J.W. 2002. *In vitro* antagonism of *Botrytis cinerea* by phylloplane yeasts. Can. J. Bot. 80, 885–891.
Buck, J.W. 2004. Combinations of fungicides with phylloplane yeasts for improved control of *Botrytis cinerea* on geranium seedlings. Phytopathology 94, 196–202.
Buck, J.W., and J.H. Andrews. 1999. Attachment of the yeast *Rhodosporidium toruloides* is mediated by adhesives localized at sites of bud cell development. Appl. Environ. Microbiol. 65, 465–471.
Buck, J.W., and S.N. Jeffers. 2004. Effect of pathogen aggressiveness and vinclozolin on efficacy of *Rhodotorula glutinis* PM4 against *Botrytis cinerea* on geranium leaf disks and seedlings. Plant Dis. 88, 1262–1268.
Buck, L.B. 2006. Unraveling the sense of smell (Nobel lecture). Angew. Chem. Int. Ed. 44, 6128–6140.
Buck, L.B., and R. Axel. 1991. A novel multigene family may encode odorant receptors – a molecular basis for odor recognition. Cell 65, 175–187.
Buckholz, R.G., and M.A.G. Gleeson. 1991. Yeast systems for the commercial production of heterologous proteins. Nat. Biotechnol. 9, 1067–1072.

Buckley, H.R. 1971. Fungi pathogenic for man and animals: 2 The subcutaneous and deep-seated mycoses. In: J.R. Norris and D.W. Ribbons (Eds), Methods in Microbiology, Vol. 4. Academic Press, New York, pp. 461–478.

Buckley, H.R., and N. van Uden. 1967. *Candida shehatae* sp. n., a yeast associated with wood-destroying insects. Mycopathol. Mycol. Appl. 32, 297–301.

Buckley, H.R., and N. van Uden. 1968. Five new *Candida* species. Mycopathol. Mycol. Appl. 36, 257–266.

Buecher, E.J., and H.J. Phaff. 1972. Dimorphism in a new isolate of *Saccharomycopsis* Schiönning. Can. J. Microbiol. 18, 901–907.

Buhagiar, R.W.M. 1975. *Torulopsis bacarum*, *Torulopsis pustula* and *Torulopsis multis-gemmis* sp. nov., three new yeasts from soft fruit. J. Gen. Microbiol. 86, 1–11.

Buhagiar, R.W.M. 1979. *Candida fusiformata* sp. nov., a new yeast from cabbages and cauliflowers. J. Gen. Microbiol. 110, 91–97.

Buhagiar, R.W.M., and J.A. Barnett. 1971. The yeast of strawberries. J. Appl. Bact. 34, 727–739.

Buhagiar, R.W.M., and J.A. Barnett. 1973. *Sterigmatomyces acheniorum* species nova, a yeast from strawberries. J. Gen. Microbiol. 77, 71–78.

Buhagiar, R.W.M., D. Yarrow and J.A. Barnett. 1983. *Bullera crocea* and *Bullera armeniacea*, two new yeasts from fruit and vegetables. J. Gen. Microbiol. 129, 3149–3155.

Bujdoso, G., A. Ittzes and T. Henick-Kling. 2002. Assessment of fermentation results of *Hanseniaspora* (*Kloeckera*) strains isolated in Finger Lakes' wineries. Acta Aliment. 31, 265–278.

Bulder, C.J.E.A. 1955. Some observations on the lipolytic activity of micro-organisms and a new method for its detection. Antonie van Leeuwenhoek 21, 433–445.

Buller, A.H.R. 1993a. The translocation of protoplasm through septate mycelium of certain Pyrenomycetes, Discomycetes, and Hymenomycetes. In: Researches on Fungi, Vol. 5. Longmans, Green & Co., London, pp. 75–167.

Buller, A.H.R. 1993b. *Sporobolomyces*, a basidiomycetous yeast-genus. In: A.H.R. Buller (Ed.), Researches on Fungi, Vol. V. Longmans, Green & Co., London, pp. 171–206.

Bunting, L.A., J.B. Neilson and G.S. Bulmer. 1979. *Cryptococcus neoformans*: gastronomic delight of a soil ameba. Sabouraudia 17, 225–232.

Bureik, M., B. Schiffler, Y. Hiraoka, F. Vogel and R. Bernhardt. 2002. Functional expression of mitochondrial CYP11B2 in fission yeast and identification of a new internal electron transport protein, etp 1. Biochemistry 41, 2311–2321.

Burns, W.E. 1933. The taxonomic position of an aroma-producing mold. Iowa State Coll. J. Sci. 7, 433–437.

Burr, T.J., M.C. Matteson, C.A. Smith, M.R. Corral-Garcia and T.-C. Huang. 1996. Effectiveness of bacteria and yeasts from apple orchards as biological control agents of apple scab. Biol. Control 6, 151–157.

Burri, R., and W. Staub. 1909. *Monilia nigra* als Ursache eines Falles von Schwarzfleckigkeit bei Emmentalerkäse. Landw. Jahrb. Schweiz 23, 479–513.

Burschäpers, J., D. Schustolla, K. Schugerl, H. Roper and J.C. de Troostembergh. 2002. Engineering aspects of the production of sugar alcohols with the osmophilic yeast *Moniliella tomentosa* var. *pollinis*. Part I. Batch and fed-batch operation in stirred tank. Process Biochem. 38, 497–506.

Buscalioni, L., and O. Cassagrandi. 1898. Sul *Saccharomyces guttulatus* (Rob.). Malphigia 12, 59–75.

Buschke, A. 1895. Über eine durch Coccidien hervorgerugene Krankheit des Menschen. Dtsch. Med. Wochenschr. 21, 14.

Busse, O. 1894. Über parasitäre Zelleninschüsse und ihre Züchtung. Zentralbl. Bakteriol. Parasitenkd. Infektionskr. Hyg. Abt. 1, Orig. Reihe A 16, 175–180.

Bustamante, B., and P.E. Campos. 2001. Endemic sporotrichosis. Curr. Opin. Infect. Dis. 14, 145–149.

Buth, D.G. 1984. The application of electrophoretic data in systemic studies. Annu. Rev. Ecol. Syst. 15, 501–522.

Butinar, L., S. Santos, I. Spencer-Martins, A. Oren and N. Gunde-Cimerman. 2005. Yeast diversity in hypersaline habitats. FEMS Microbiol. Lett. 244, 229–234.

Butinar, L., I. Spencer-Martins and N. Gunde-Cimerman. 2007. Yeasts in high Arctic glaciers: the discovery of a new habitat for eukaryotic microorganisms. Antonie van Leeuwenhoek 97, 277–289.

Butler, A.R., M. Porter and M.J.R. Stark. 1991. Intracellular expression of *Kluyveromyces lactis* toxin g subunit mimics treatment with exogenous toxin and distinguishes two classes of toxin-resistant mutant. Yeast 7, 617–625.

Butler, E.E. 1954. Radiation-induced chlorophyll-less mutants of *Chlorella*. Science 120, 274–275.

Butler, E.E., and L.J. Petersen. 1970. Sexual reproduction in *Geotrichum candidum*. Science 169, 481–482.

Butler, E.E., and L.J. Petersen. 1972. *Endomyces geotrichum*, a perfect state of *Geotrichum candidum*. Mycologia 64, 365–374.

Butler, E.E., R.K. Webster and J.W. Eckert. 1965. Taxonomy, pathogenicity and physiological properties of the fungus causing sour rot of citrus. Phytopathology 55, 1262–1268.

Butler, E.E., D. Fogle and M. Miranda. 1988. *Galactomyces citri-aurantii*, a newly found teleomorph of *Geotrichum citri-aurantii*, the cause of sour rot of citrus fruit. Mycotaxon 33, 197–212.

Butler, G., C. Kenny, A. Fagan, C. Kurischko, C. Gaillardin and K.H. Wolfe. 2004. Evolution of the MAT locus and its Ho endonuclease in yeast species. Proc. Natl. Acad. Sci. USA 101, 1632–1637.

Butler, G., M.D. Rasmussen, M.F. Lin, M.A. Santos, S. Sakthikumar, C.A. Munro, E. Rheinbay, M. Grabherr, A. Forche, J.L. Reedy, I. Agrafioti, M.B. Arnaud, S. Bates, A.J. Brown, S. Brunke, M.C. Costanzo, D.A. Fitzpatrick, P.W. de Groot, D. Harris, L.L. Hoyer, B. Hube, F.M. Klis, C. Kodira, N. Lennard, M.E. Logue, R. Martin, A.M. Neiman, E. Nikolaou, M.A. Quail, J. Quinn, M.C. Santos, F.F. Schmitzberger, G. Sherlock, P. Shah, K.A. Silverstein, M.S. Skrzypek, D. Soll, R. Staggs, I. Stansfield, M.P. Stumpf, P.E. Sudbery, T. Srikantha, Q. Zeng, J. Berman, M. Berriman, J. Heitman, N.A. Gow, M.C. Lorenz, B.W. Birren, M. Kellis and C.A. Cuomo. 2009. Evolution of pathogenicity and sexual reproduction in eight *Candida* genomes. Nature 459, 657–662.

Butler, J., I. Maccallum, M. Kleber, I.A. Shlyakhter, M.K. Belmonte, E.S. Lander, C. Nusbaum and D.B. Jaffe. 2008. ALLPATHS: *de novo* assembly of whole-genome shotgun microreads. Genome Res. 18, 810–820.

Butler, M.I., and R.T.M. Poulter. 2005. The PRP8 inteins in *Cryptococcus* are a source of phylogenetic and epidemiological information. Fungal Genet. Biol. 42, 452–463.

Buts, J.-P., and P. Bernasconi. 2005. *Saccharomyces boulardii*: basic science and clinical applications in gastroenterology. Gastroenterol. Clin. North Am. 34, 515–532.

Buzzini, P., and A. Martini. 2000a. Differential growth inhibition as a tool to increase the discriminating power of killer toxin sensitivity in fingerprinting of yeasts. FEMS Microbiol. Lett. 193, 31–36.

Buzzini, P., and A. Martini. 2000b. Utilization of differential killer toxin sensitivity patterns for fingerprinting and clustering yeast strains belonging to different genera. Syst. Appl. Microbiol. 23, 450–457.

Buzzini, P., and A. Martini. 2000c. Biodiversity of killer activity in yeasts isolated from the Brazilian rain forest. Can. J. Microbiol. 46, 607–611.

Buzzini, P., and A. Martini. 2001a. Discrimination between *Candida albicans* and other pathogenic species of the genus *Candida* by their differential sensitivities to toxins of a panel of killer yeasts. J. Clin. Microbiol. 39, 3362–3364.

Buzzini, P., and A. Martini. 2001b. Large-scale screening of selected *Candida maltosa*, *Debaryomyces hansenii* and *Pichia anomala* killer toxin activity against pathogenic yeasts. Med. Mycol. 39, 479–482.

Buzzini, P., and A. Martini. 2002. Extracellular enzymatic activity profiles in yeast and yeast-like strains isolated from tropical environments. J. Appl. Microbiol. 93, 1020–1025.

Buzzini, P., S. Berardinelli, B. Turchetti, G. Cardinali and A. Martini. 2003. Fingerprinting of yeasts at the strain level by differential sensitivity responses to a panel of selected killer toxins. Syst. Appl. Microbiol. 26, 466–470.

Buzzini, P., S. Romano, B. Turchetti, A. Vaughan, U.M. Pagnoni and P. Davoli. 2005a. Production of volatile organic sulfur compounds (VOSCs) by basidiomycetous yeasts. FEMS Yeast Res. 5, 379–385.

Buzzini, P., C. Gasparetti, B. Turchetti, M.R. Cramarossa, A. Vaughan-Martini, A. Martini, U.M. Pagnoni and L. Forti. 2005b. Production of volatile organic compounds (VOCs) by yeasts isolated from the ascocarps of black (*Tuber melanosporum* Vitt.) and white (*Tuber magnatum Pico*) truffles. Arch. Microbiol. 184, 187–193.

Byrne, K.P., and K.H. Wolfe. 2005. The Yeast Gene Order Browser: combining curated homology and syntenic context reveals gene fate in polyploid species. Genome Res. 15, 1456–1461.

Byrne, K.P., and K.H. Wolfe. 2007. Consistent patterns of rate asymmetry and gene loss indicate widespread neofunctionalization of yeast genes after whole-genome duplication. Genetics 175, 1341–1350.

Byzov, B.A., V.N. Thanh and I.P. Babjeva. 1993. Interrelationships between yeasts and soil diplopods. Soil Biol. Biochem. 25, 1119–1126.

Cabañes, F.J., J.J. Hernández and G. Castellá. 2005. Molecular analysis of *Malassezia sympodialis*-related strains from domestic animals. J. Clin. Microbiol. 43, 277–283.

Cabañes, F.J., B. Theelen, G. Castellá and T. Boekhout. 2007. Two new lipid-dependent *Malassezia* species from domestic animals. FEMS Yeast Res. 7, 1064–1076.

Cabib, E., and A. Duran. 2005. Synthase III-dependent chitin is bound to different acceptors depending on location on the cell wall of budding yeast. J. Biol. Chem. 280, 9170–9179.

Cabranes, C., J. Moreno and J.J. Mangas. 1990. Dynamics of yeast populations during cider fermentation in Asturian region of Spain. Appl. Environ. Microbiol. 56, 3881–3884.

Cadete, R.M., R.O. Santos, M.A. Melo, A. Mouro, D.L. Gonçalves, B.U. Stambuk, F.C.O. Gomes, M.A. Lachance and C.A. Rosa. 2009. *Spathaspora arborariae* sp. nov., a D-xylose-fermenting yeast species isolated from rotting wood in Brazil. FEMS Yeast Res. 9, 1338–1342.

Cadez, N., P. Raspor, A.W.A.M. de Cock, T. Boekhout and M.Th. Smith. 2002. Molecular identification and genetic diversity within species of the genera *Hanseniaspora* and *Kloeckera*. FEMS Yeast Res. 1, 279–289.

Cadez, N., G.A. Poot, P. Raspor and M.Th. Smith. 2003. *Hanseniaspora meyeri* sp. nov., *Hanseniaspora clermontiae* sp. nov., *Hanseniaspora lachancei* sp. nov. and *Hanseniaspora opuntiae* sp. nov., novel apiculate yeast species. Int. J. Syst. Evol. Microbiol. 53, 1671–1680.

Cadez, N., P. Raspor and M.Th. Smith. 2006. Phylogenetic placement of *Hanseniaspora-Kloeckera* species using multigene sequence analysis with taxonomic implications: descriptions of *Hanseniaspora pseudoguilliermondii* sp. nov. and *Hanseniaspora occidentalis* var. *citrica* var. nov. Int. J. Syst. Evol. Microbiol. 56, 1157–1165.

Cadmus, M.C., A.A. Lagoda and R.F. Anderson. 1962. Production of a new polysaccharide with *Cryptococcus laurentii* var. *flavescens*. Appl. Microbiol. 10, 153–156.

Cafarchia, C., A. Camarda, D. Romito, M. Campolo, N.C. Quaglia, D. Tullio and D. Otranto. 2006. Occurrence of yeasts in cloacae of migratory birds. Mycopathologia 161, 229–234.

Cafarchia, C., D. Otranto, B.E. Campbell, M.S. Latrofa, J. Guillot and R.B. Gasser. 2007. Multilocus mutation scanning for the analysis of genetic variation within *Malassezia* (Basidiomycota: Malasseziales). Electrophoresis 28, 1176–1180.

Caggia, C., C. Restuccia, A. Pulvirenti and P. Giudici. 2001. Identification of *Pichia anomala* isolated from yogurt by RFLP of the ITS region. Int. J. Food Microbiol. 71, 71–73.

Cai, J., I.N. Roberts and M.D. Collins. 1996. Phylogenetic relationships among members of the ascomycetous yeast genera *Brettanomyces*, *Debaryomyces*, *Dekkera*, and *Kluyveromyces* deduced by small-subunit rRNA gene sequences. Int. J. Syst. Bacteriol. 46, 542–549.

Cailliez, J.C., C. Cantelli, N. Seguy, S. Conti, M. Gerloni, G. Morace and L. Polonelli. 1994. Killer toxin secretion through the cell wall of the yeast *Pichia anomala*. Mycopathologia 126, 173–177.

Cain, R.F. 1948. *Myriogonium*, a new genus among simplified ascomycetes. Mycologia 40, 158–167.

Cain, R.F. 1972. Evolution of the fungi. Mycologia 64, 1–14.

Calderone, R.A. (Ed.) 2002. *Candida* and Candidiasis. ASM Press, Washington, DC, 451pp.

Caldwell, G.A., F. Naider and J.M. Becker. 1995. Fungal lipopeptide mating pheromones: a model system for the study of protein prenylation. Microbiol. Rev. 59, 406–422.

Callejas, A., N. Ordonez, M.C. Rodriguez and E. Castaneda. 1998. First isolation of *C. neoformans* var. *gattii* serotype C, from the environment in Colombia. Med. Mycol. 36, 341–344.

Callon, C., C. Delbès, F. Duthoit and M.C. Montel. 2006. Application of SSCP-PCR fingerprinting to profile the yeast community in raw milk Salers cheeses. Syst. Appl. Microbiol. 29, 172–180.

Calvente, V., D. Benuzzi and M.I. Sanz de Tosetti. 1999. Antagonistic action of siderophores from *Rhodotorula glutinis* upon the postharvest pathogen *Penicillium expansum*. Int. Biodeterior. Biodegrad. 43, 167–172.

Calvo, J., V. Calvente, M.E. de Orellano, D. Benuzzi and M.I.S. de Tosetti. 2003. Improvement in the biocontrol of post-harvest diseases of apples with the use of yeast mixtures. BioControl 48, 579–593.

Cameotra, S.S., and R.S. Makkar. 2004. Recent application of biosurfactants as biological and immunological molecules. Curr. Opin. Microbiol. 7, 262–266.

Camin, J.H., and R.R. Sokal. 1965. A method for deducing branching sequences in phylogeny. Evolution 19, 311–326.

Camougrand, N., G. Velours and M. Guerin. 1991. Biochemical studies carried out on different groups of *Candida parapsilosis* and *Candida rhagii* strains by comparing some cellular and mitochondrial activities. Antonie van Leeuwenhoek 59, 235–241.

Campbell, I. 1972. Numerical analysis of the genera *Saccharomyces* and *Kluyveromyces*. J. Gen. Microbiol. 73, 279–301.

Campbell, I. 1973. Numerical analysis of *Hansenula*, *Pichia* and related yeast genera. J. Gen. Microbiol. 77, 427–441.

Campbell, L.T., and D.A. Carter. 2006. Looking for sex in the fungal pathogens *Cryptococcus neoformans* and *Cryptococcus gattii*. FEMS Yeast Res. 6, 588–598.

Campbell, L.T., B.J. Currie, M. Krockenberger, R. Malik, W. Meyer, J. Heitman and D. Carter. 2005. Clonality and recombination in genetically differentiated subgroups of *Cryptococcus gattii*. Eukaryot. Cell 4, 1403–1409.

Campbell, W.G. Jr. 1972. Ultrastructure of *Pneumocystis* in human lung. Life cycle in human pneumocystosis. Arch. Pathol. 93, 312–324.

Cañamás, T.P., I. Viñas, J. Usall, N. Magan, C. Solsona and N. Teixidó. 2008. Impact of mild heat treatments on induction of thermotolerance in the biocontrol yeast *Candida sake* CPA-1 and viability after spray-drying. J. Appl. Microbiol. 104, 767–775.

Cabañes, F.J., S. Vega and G. Castellá. 2010. *Malassezia cuniculi* sp. nov., a novel yeast isolated from rabbit skin. Med. Mycol. [epub ahead of print]

Cañete-Gibas, C.F., M. Takashima, T. Sugita and T. Nakase. 1998. Three new species of *Kockovaella* isolated from plants collected in the Ogasawara Islands. J. Gen. Appl. Microbiol. 44, 11–18.

Cannizzo, F.T., E. Eraso, P.A. Ezkurra, M. Villar-Vidal, E. Bollo, G. Castella, F.J. Cabañes, V. Vidotto and G. Quindos. 2007. Biofilm development by clinical isolates of *Malassezia pachydermatis*. Med. Mycol. 45, 357–361.

Capece, A., C. Fiore, A. Maraz and P. Romano. 2005. Molecular and technological approaches to evaluate strain biodiversity in *Hanseniaspora uvarum* of wine origin. J. Appl. Microbiol. 98, 136–144.

Caporali, L. 1971. Recherches sur le mode de conservation du *Taphrina deformans*. (Berk.) Tul. Rev. Cytol. Biol. Vég 34, 327–382.

Caprilli, F., G. Prignano, C. Latella and S. Tavarozzi. 1985. Amplification of the killer system for differentiation of *Candida albicans* strains. Mykosen 28, 569–573.

Capriotti, A. 1954. Recherches sur les levures de la fermentation vinaire en Italie. Antonie van Leeuwenhoek 20, 374–384.

Capriotti, A. 1957. New blastomycetes isolated from soils of Spain I: *Schwanniomyces castellii* nov. spec. Arch. Mikrobiol. 26, 434–438.

Capriotti, A. 1958a. Neue Hefen, isoliert aus Böden Spaniens II: *Torulaspora franciscae* nov. spec. Arch. Mikrobiol. 28, 238–243.

Capriotti, A. 1958b. *Torulaspora nilssoni* nov. spec. A new yeast from Swedish soil. Arch. Mikrobiol 28, 247–254.

Capriotti, A. 1958c. *Zygosaccharomyces mrakii* nova species. A new yeast from silage. Arch. Mikrobiol. 30, 387–392.

Capriotti, A. 1958d. *Saccharomyces smittii* nov. spec. A new yeast isolated from Dutch, Italian and Swedish soils. Antonie van Leeuwenhoek 24, 215–220.

Capriotti, A. 1958e. *Debaryomyces castellii* nov. spec. (Eine neue Hefe aus Böden Schwedens). Arch. Mikrobiol. 28, 344–348.

Capriotti, A. 1958f. *Candida vanriji* nova species, a new yeast from Swedish soils. Arch. Mikrobiol. 30, 226–230.

Capriotti, A. 1958g. *Torulopsis wickerhamii* nova species. A new yeast from silage. Arch. Mikrobiol. 30, 383–384.

Capriotti, A. 1961a. *Debaryomyces cantarellii* nova species, a new yeast from Finnish soil. Arch. Mikrobiol. 39, 123–129.

Capriotti, A. 1961b. *Debaryomyces phaffii* sp. n., a new yeast isolated from Finnish soil. J. Bacteriol. 82, 326–330.

Capriotti, A. 1961c. *Hansenula wickerhamii* sp. n., a new yeast from Finnish soil. J. Bacteriol. 82, 359–360.

Capriotti, A. 1961d. *Torulopsis castellii* sp. nov., a yeast isolated from Finnish soil. J. Gen. Microbiol. 26, 41–43.

Capriotti, A. 1961e. *Torulopsis vartiovaarai* sp. nov. A new yeast isolated from Finnish soil. Can. J. Microbiol. 7, 681–684.

Capriotti, A. 1966. *Saccharomyces castellii* n. sp. Una nuova specie die lievito isolata da un terreno della Finlandia. Ann. Fac. Agric. Sassar. 14, 453–459.

Capriotti, A. 1967. *Saccharomyces* servazii n. sp. A new yeast from Finland soil. Ann. Microbiol. Enzimol. 17, 79–84.

Capriotti, A. 1969. *Torulaspora benedictae* sp. n. A new yeast from sheep's milk in Sardinia, Italy. Ann. Microbiol. Enzimol. 19, 107–114.

Capriotti, A., and F. Fatichenti. 1969. *Torulopsis arnaudii* sp. n. A new yeast from Sardinian grapemust. Ann. Microbiol. Enzimol. 19, 115–119.

Carballeira Rodríguez, J.D., C. García-Burgos, M.A. Quezada Alavarez, E. Alvarez Ruiz and J.V. Sinisterra Gago. 2004. *Williopsis californica*, *Williopsis saturnus*, and *Pachysolen tannophilus*: novel microorganisms for stereoselective oxidation of secondary alcohols. Biotechnol. Bioeng. 87, 632–640.

Carnevale-Ricci, F. 1926. Fermenti e pseudofermenti parassiti e commensali delle cripte tonsillari. Colluna di Memorie di Otologia ecc. diretta dal Prof. Calamida. No. 3, pp. 1–80, tav. I–V. Soc. Albrighi e Segati, Milano (cited by Ciferri and Redaelli 1929).

Caro, L.H.P., G.J. Smits, P. van Egmond, J.W. Chapman and F.M. Klis. 1998. Transcription of multiple cell wall protein–encoding genes in *Saccharomyces cerevisiae* is differentially regulated during the cell cycle. FEMS Microbiol. Lett. 161, 345–349.

Caron, S.J., T.J. Avis, T. Boekhout, R.C. Hamelin and R.R. Belanger. 2005. Fingerprinting techniques as tools towards molecular quality control of *Pseudozyma flocculosa*. Mycol. Res. 109, 335–431.

Carotti, C., E.E. Ragni, O. Palomares, T. Fontaine, G. Tedeschi, R. Rodriguez, J.P. Latge, M. Vai and L. Popolo. 2004. Characterization of recombinant forms of the yeast Gas1 protein and identification of residues essential for

glucanosyltransferase activity and folding. Eur. J. Biochem. 271, 3635–3645.
Carpenter, S.E. 1981. Monograph of *Crocicreas* (Leotiaceae). Mem. New York Bot. Gard. 33, 1290.
Carr, R.J., R.F. Bilton and T. Atkinson. 1985. Mechanism of biodegradation of paraquat by *Lipomyces starkeyi*. Appl. Environ. Microbiol. 49, 1290–1294.
Carrau, F.M., E. Neirotti and O. Gioia. 1993. Stuck wine fermentations: effect of killer/sensitive yeast interactions. J. Ferment. Bioeng. 76, 67–69.
Carreira, A.L., Paloma and V. Louriero. 1998. Pigment producing yeasts involved in the brown, surface discoloration of ewe's cheese. Int. J. Food Microbiol. 41, 223–230.
Carreiro, S.C., F.C. Pagnocca, M. Bacci, M.-A. Lachance, C.O. Bueno, M.J.A. Hebling, C.C.C. Ruivo and C.A. Rosa. 2004. *Sympodiomyces attinorum* sp. nov., a yeast species associated with nests of leaf-cutting ant *Atta sexdens*. Int. J. Syst. Evol. Microbiol. 54, 1891–1894.
Carroll, G.C. 1987. Fungi isolated from gypsy moth egg-masses. Mycotaxon 29, 299–305.
Carroll, G.C. 1992. Fungal mutualism. In: G.C. Carroll and D.T. Wicklow (Eds), The Fungal Community: Its Organization and Role in the Ecosystem, 2nd edn. Marcel Dekker, New York, pp. 327–354.
Carroll, G.C., and D.T. Wicklow. 1992. The Fungal Community: Its Organization and Role in the Ecosystem, 2nd edn. Marcel Dekker, New York.
Carson, H.L., E.P. Knapp and H.J. Phaff. 1956. Studies on the ecology of *Drosophila* in the Yosemite Region of California. III. The yeast flora of the natural breeding sites of some species of *Drosophila*. Ecology 37, 538–544.
Cartwright, R.D., and G.E. Templeton. 1988. Biological limitations of *Protomyces gravidus* as a mycoherbicide for giant ragweed, *Ambrosia trifida*. Plant Dis. 72, 580–582.
Casadevall, A., and J.R. Perfect. 1998. *Cryptococcus neoformans*. ASM Press, Washington, DC.
Casal, M., M.J. Linares, F. Solís and F.C. Rodríguez. 1997. Appearance of colonies of *Prototheca* on CHROMagar *Candida* medium. Mycopathologia. 137, 79–82.
Casaregola, S., A. Lepingle, E. Bon, C. Neuveglise, H. Nguyen, F. Artiguenave, P. Wincker and C. Gaillardin. 2000. Genomic exploration of the hemiascomycetous yeasts: 7. *Saccharomyces servazzii*. FEBS Lett. 487, 47–51.
Casaregola, S., H.V. Nguyen, G. Lapathitis, A. Kotyk and C. Gaillardin. 2001. Analysis of the constitution of the beer yeast genome by PCR, sequencing and subtelomeric sequence hybridization. Int. J. Syst. Evol. Microbiol. 51, 1607–1618.
Casey, G.C., and D.W. Dobson. 2004. Potential of using real-time PCR-based detection of spoilage yeast in fruit juice – a preliminary study. Int. J. Food Microbiol. 91, 327–335.
Casolari, C., A. Nanetti, G.M. Cavallini, F. Rivasi, U. Fabio and A. Mazzoni. 1992. Keratomycosis with an unusual aetiology (*Rhodotorula glutinis*): a case report. Microbiologica 15, 83–87.
Cassar, S., and M. Blackwell. 1996. Convergent origins of ambrosia fungi. Mycologia 88, 596–601.
Casselton, L.A., and M.P. Challen. 2006. The mating type genes of the basidiomycetes. In: U. Kües and R. Fischer (Eds), The Mycota, Vol. I. Growth, Differentiation and Sexuality, 2nd edn. Springer, Berlin, pp. 357–374.
Cassidy, J.R., D. Moore, B.C. Lu and P.J. Pukkila. 1984. Unusual organization and lack of recombination in the ribosomal RNA genes of *Coprinus cinereus*. Curr. Genet. 8, 607–613.
Castellani, A. 1910. Observations on "tropical bronchooidiosis". Br. Med. J. ii, 868–869.
Castellani, A. 1911. Observations on fungi of the genus *Endomyces* affecting man in the tropics. Zentralbl. Bakteriol. Parasitenkd., Abt. I, 58, 236–238.
Castellani, A. 1912a. Observations on the fungi found in tropical bronchomycosis. Lancet i, 13–15.
Castellani, A. 1912b. Note on the importance of hyphomycetes and other fungi in tropical pathology. Br. Med. J. ii, 1208–1212.
Castellani, A. 1913. Further observations on the fungi of the genus *Endomyces* found in man. Arch. Parasitol. 16, 184–186.
Castellani, A. 1914. Notes on the Hyphomycetes found in sprue, with remarks on the classification of fungi of the genus *Monilia* Gmelin. J. Trop. Med. Hyg. 17, 305–310.
Castellani, A. 1915. Lectures on the higher fungi in relation to human pathology. R. Coll. Phys. London.
Castellani, A. 1916. The plurality of species of the so-called "thrush-fungus" (champignon du muguet) of temperate climates. Ann. Inst. Pasteur Paris 30, 149–154.
Castellani, A. 1920. The etiology of thrush. J. Trop. Med. Hyg. 23, 17–22.
Castellani, A. 1925. Notes on three new yeast-like organisms and a new *Bacillus* with remarks on the clinical conditions from which they have been isolated: furunculosis blastomycetica, stomatitis cryptococcobacillaris. J. Trop. Med. Hyg. 28, 217–223.
Castellani, A. 1927. Fungi and fungous diseases. Arch. Dermatol. Syph. 16, 383–425.
Castellani, A. 1928. Blastomycosis and some other conditions due to yeast-like fungi (budding fungi). Am. J. Trop. Med. 8, 379–422.
Castellani, A. 1929. A mannitol fermenting *Monilia*. Proc. Soc. Exp. Biol. Med. 26, 544–545.
Castellani, A. 1932. A new variety of *Geotrichum matalense* (*Geotrichum matalense* var. *chapmani*). J. Trop. Med. Hyg. 35, 278–279.
Castellani, A. 1933. Elastomycosis, a short general account. Med. Press Circ. 136, 438–443.
Castellani, A. 1937a. A short general account for medical men of the genus *Monilia*. Trop. Med. Hyg. 40, 293–307.
Castellani, A. 1937b. A preliminary report on two pathogenic fungi: *Trichophyton dankaliense* n. sp. and *Sporotrichum anglicum* n. sp. J. Trop. Hyg. 40, 313–318.
Castellani, A., and A.J. Chalmers. 1913. Manual of Tropical Medicine, 2nd edn. Baillière, Tindal and Cox, London.
Castellani, A., and A.J. Chalmers. 1919. Manual of Tropical Medicine, 3rd edn. Baillière, Tindal and Cox, London.
Castellani, A., and I. Jacono. 1933. Observations on fungi isolated from cases of blastomycosis cutis and blastomycosis pulmonalis in North America and Europe. Remarks on blastomycetin. J. Trop. Med. Hyg. 36, 297–321.
Castellani, A., and G.C. Low. 1913. The role played by fungi in sprue. J. Trop. Med. Hyg. 16, 33–35.
Castellani, A., and F.E. Taylor. 1925. Further observations on vaginal monilias and vaginal moniliases. J. Trop. Med. Hyg. 28, 242–249.

Castelli, T. 1932. Due nuove Torulopsidacee a pigmento rosso rosa. G. Biol. Appl. Ind. Chim. Alim. 2, 1–13.
Castelli, T. 1933. Su alcune *Hansenula* della fermentazione panaria. Arch. Mikrobiol. 4, 514–529.
Castelli, T. 1935. Su alcuni blastomiceti dei mosti umbri. Boll. Ist. Sieroter. Milan. 9, 911–916.
Castelli, T. 1938. Nuovi blastomiceti isolati da mosti del chianti e zone limitrofe. Arch. Mikrobiol. 9, 449–468.
Castelli, T. 1940. Considerazioni sulla *Torulopsis pulcherrima*. Arch. Mikrobiol. 11, 127–136.
Castelli, T. 1942. Una nuova specie di *Saccharomycodes*: *Saccharomycodes bisporus*. Arch. Mikrobiol. 12, 260–265.
Castelli, T. 1948. I lieviti della fermentazione vinaria nella regione Pugliese. Ric. Sci. 18, 3–31.
Castelli, T. 1967. Sistematica ed ecologia dei lieviti del vino. *Vini* d'Italia 9, 245–246. In Italian.
Castillo, A., and V. Cifuentes. 1994. Presence of double-stranded RNA and virus-like particles in *Phaffia rhodozyma*. Curr. Genet. 26, 364–368.
Castoria, R., F. de Curtis, G. Lima and V. de Cicco. 1997. β-1,3-glucanase activity of two saprophytic yeasts and possible mode of action as biocontrol agents against postharvest diseases. Postharvest Biol. Technol. 12, 293–300.
Castoria, R., L. Caputo, F. de Curtis and V. de Cicco. 2003. Resistance of postharvest biocontrol yeasts to oxidative stress: a possible new mechanism of action. Phytopathology 93, 564–572.
Castresana, J. 2000. Selecion of conserved blocks from mutliple alignments for their use in phylogenetic analysis. Mol. Biol. Evol. 17, 540–552.
Cavalieri, D., P.E. McGovern, D.L. Hartl, R. Mortimer and M. Posinelli. 2003. Evidence for *S. cerevisiae* fermentation in ancient wine. J. Mol. Evol. 57, S226–S232.
Cavalitto, S.F., R.A. Hours and C.F. Mignone. 2000. Growth and protopectinase production of *Geotrichum klebahnii* in batch and continuous cultures with synthetic media. J. Ind. Microbiol. Biotechnol. 25, 260–265.
Cavalli-Sforza, L.L., and A.W.F. Edwards. 1967. Phylogenetic analysis: models and estimation procedures. Evolution 21, 550–570.
Cebollero, E., D. Gonzalez-Ramos, L. Tabera and R. Gonzalez. 2007. Transgenic wine yeast technology: is it time for transgenic wine? J. Mol. Med. 85, 191–200.
Celio, G.J., M. Padamsee, B.T. Dentinger, R. Bauer and D.J. McLaughlin. 2006. Assembling the Fungal Tree of Life: constructing the structural and biochemical database. Mycologia 98, 850–859.
Cellerino, G.P. 1999. Review of poplar diseases: 3. Diseases caused by fungi. International Poplar Commission: online publications. Retrieved January 2007 from http://www.efor.ucl.ac.be/ipc/pub/celle01/celle01.htm
Centraalbureau voor Schimmelcultures. 2001. List of Cultures, 35th edn. Utrecht.
Certik, M., and S. Shimizu. 1999. Biosynthesis and regulation of microbial fatty acid production. J. Biosci. Bioeng. 87, 1–14.
Chagas, C. 1909. Trabalho do Instituto Manguinhos sobre uma nova trypanosomiase humana, pelo Dr. Carlos Chagas, assistente do Instituto. Ann. Acad. Med. Rio de Janeiro 75, 188–190.
Chakrabarti, A., M. Jatana, P. Chatha, L. Kaushal and A.A. Padhye. 1997. Isolation of *Cryptococcus neoformans* var. *gattii* from *Eucalyptus camaldulensis* in India. J. Clin. Microbiol. 35, 3340–3342.
Chalutz, E., and C.L. Wilson. 1990. Postharvest biocontrol of green and blue mold and sour rot of citrus fruit by *Debaryomyces hansenii*. Plant Dis. 74, 134–137.
Chalutz, E., L. Cohen, B. Weiss and C.L. Wilson. 1988. Biocontrol of postharvest diseases of citrus fruit by microbial antagonists. In: R. Goren and K. Mendel (Eds), Int. Citrus Conf., 6th edn. Margraf Science, Weikersheim, pp. 1–4.
Chalutz, E., S. Droby, L. Cohen, B. Weiss, R. Barkai-Golan, A. Daus, Y. Fuchs and C.L. Wilson. 1991. Biological control of Botrytis, Rhizopus, and Alternaria rots of tomato fruit by Pichia guilliermondii. In: C.L. Wilson and E. Chalutz (Eds). 1991, Biological control of Postharvest Disease of Fruits and Vegetables, Workshop Proc. Washington, DC: US GPO pp. 71–85.
Chan, Z., and S.P. Tian. 2005. Interaction of antagonistic yeasts against postharvest pathogens of apple fruit and possible mode of action. Postharvest Biol. Technol. 36, 215–223.
Chan, Z., G. Qui, X. Xu, B. Li and S. Tian. 2007. Proteome approach to characterize proteins induced by antagonist yeast and salicylic acid in peach fruit. J. Proteom. Res. 6, 1677–1688.
Chand-Goyal, T., and R.A. Spotts. 1996a. Control of postharvest pear diseases using natural saprophytic yeast colonists and their combination with a low dosage of thiabendazole. Postharvest Biol. Technol. 7, 51–64.
Chand-Goyal, T., and R.A. Spotts. 1996b. Postharvest biological control of blue mold of apple and brown rot of sweet cherry by natural saprophytic yeast alone or in combination with low doses of fungicides. Biol. Control 6, 253–259.
Chand-Goyal, T., and R.A. Spotts. 1997. Biological control of postharvest diseases of apple and pear under semi-commercial and commercial conditions using three saprophytic yeasts. Biol. Control 10, 199–206.
Chang, C.-F., C.-F. Lee and S.-M. Liu. 2008. *Cryptococcus keelungensis* sp. nov., an anamorphic basidiomycetous yeast isolated from the sea-surface microlayer of the northeast coast of Taiwan. Int. J. Syst. Evol. Microbiol. 58, 2973–2976.
Chang, H.J., H.L. Miller, N. Watkins, M.J. Arduino, D.A. Ashford, G. Midgley, S.M. Aguero, R. Pinto-Powell, C.F. von Reyn, W. Edwards, M.M. McNeil, R. Pruitt and W.R. Jarvis. 1998. An epidemic of *Malassezia pachydermatis* in an intensive care nursery associated with colonization of health care workers' pet dogs. N. Engl. J. Med. 338, 706–711.
Chang, S., L. Yang and H. Wang. 1963. Studies on the production of glycerol and arabitol by osmophilic yeasts. II. Arabitol production by *Hansenula arabitogenes* Fang. Acta Microbiol. Sin. 9, 134–139.
Chang, Y.C., and K.J. Kwon-Chung. 1994. Complementation of a capsule-deficient mutation of *Cryptococcus neoformans* restores its virulence. Mol. Cell Biol. 14, 4912–4919.
Channon, A.G. 1956. Association of a species of *Itersonilia* with parsnip canker in Great Britain. Nature (London) 178, 217.
Channon, A.G. 1963. Studies on parsnip canker I. The cause of the diseases. Ann. Appl. Biol. 51, 1–15.
Chapman, R.L. 2003. *Candida* infections in the neonate. Curr. Opin. Pediatr. 15, 97–102.

Chapman, D.D., D.L. Abercrombie, C.J. Douady, E.K. Pikitch, M.J. Stanhopen and M.S. Shivji. 2003. A streamlined, bi-organelle, multiplex PCR approach to species identification: application to global conservation and trade monitoring of the great white shark. Conserv. Genet. 4, 415–425.

Charoenchai, C., G.H. Fleet, P.A. Henschke and B.E.N. Todd. 1997. Screening of non-*Saccharomyces* wine yeasts for the presence of extracellular enzymes. Aust. J. Grape Wine Res. 3, 2–8.

Chartrain, M., P.M. Salmon, D.K. Robinson and B.C. Buckland. 2000. Metabolic engineering and directed evolution for the production of pharmaceuticals. Curr. Opin. Biotechnol. 11, 209–214.

Chaskes, S., and R.L. Tyndall. 1975. Pigment production by *Cryptococcus neoformans* from para- and ortho-diphenols: effect of the nitrogen source. J. Clin. Microbiol. 1, 509–514.

Chaskes, S., and R.L. Tyndall. 1978. Pigment production by *Cryptococcus neoformans* and other *Cryptococcus* species from aminophenols and diaminobenzenes. J. Clin. Microbiol. 7, 146–152.

Chaskes, S., S. Frases, M. Cammer, G. Gerfen and A. Casadevall. 2008. Growth and pigment production on D-tryptophan medium by *Cryptococcus gattii*, *Cryptococcus neoformans*, and *Candida albicans*. J. Clin. Microbiol. 46, 255–264.

Chatonnet, P., D. Dubourdieu and J.N. Boidron. 1995. Influence of *Brettanomyces*/*Dekkera* spp. yeasts and lactic acid bacteria on the ethylphenol content of red wines. Am. J. Enol. Vitic. 46, 463–468.

Chatton, E.R. 1913. *Coccidiascus legeri* n.g., n. sp. levure ascosporée parasite des cellules intestinales de *Drosophila funebris*. Fabr. C.R. Soc. Biol. 75, 117–120.

Chaturvedi, V., J. Fan, B. Stein, M.J. Behr, W.A. Samsonoff, B.L. Wickes and S. Chaturvedi. 2002. Molecular genetic analyses of mating pheromones reveal intervariety mating or hybridization in *Cryptococcus neoformans*. Infect. Immun. 70, 5225–5235.

Chaumentin, G., A. Boibieux, M.A. Piens, C. Douchet, P. Buttard, J.L. Bertrand and D. Peyramond. 1996. *Trichosporon inkin* endocarditis: short-term evolution and clinical report. Clin. Infect. Dis. 23, 396–397.

Chayakulkeeree, M., and J.R. Perfect. 2006. Cryptococcosis. Infect. Dis. Clin. North Am. 20, 507–544, v–vi.

Cheetham, P.S.J. 2004. Bioprocesses for the manufacture of ingredients for foods and cosmetics. Adv. Biochem. Eng. Biotechnol. 86, 83–158.

Chefson, A., and K. Auclair. 2006. Progress towards easier use of P450 enzymes. Mol. Biosyst. 2, 462–469.

Chemler, J.A., Y. Yan and M.A.G. Koffas. 2006. Biosynthesis of isoprenoids, polyunsaturated fatty acids, and flavonoids in *Saccharomyces cerevisiae*. Microb. Cell Fact. 5, 20–28.

Chen, C., and R. Contreras. 2007. Identifying genes that extend life span using a high-throughput screening system. Methods Mol. Biol. 371, 237–248.

Chen, C.-J. 1998. Morphological and molecular studies in the genus *Tremella*. Bibl. Mycol. 174, 1–225.

Chen, C.-J., F. Oberwinkler and Z.-C. Chen. 1998. *Syzygospora nivalis* sp. nov. from Taiwan. Mycotaxon 67, 217–226.

Chen, J., S. Shimura, K. Kirimura and S. Usami. 1994. Purification of extracellular lipases from *Trichosporon fermentans* WU-C12. J. Ferment. Bioeng. 77, 548–550.

Chen, J., X. Song, H. Zhang, Y. Qu and J. Miao. 2006. Sophorolipid produced from the new yeast strain *Wickerhamiella domercqiae* induces apoptosis in H7402 human liver cancer cells. Appl. Microbiol. Biotechnol. 39, 501–506.

Chen, R., S.-C. Wei, Y.-M. Jiang, Q.-M. Wang and F.-Y. Bai. 2010. *Kazachstania taianensis* sp. nov., a novel ascomycetous yeast species from orchard soil. Int. J. Syst. Evol. Microbiol. 60, 1430–1476.

Chen, S., T. Sorrell, G. Nimmo, B. Speed, B. Currie, D. Ellis, D. Marriott, T. Pfeiffer, D. Parr, K. Byth and the Australasian Cryptococcal Study Group. 2000. Epidemiology and host- and variety-dependent characteristics of infection due to *Cryptococcus neoformans* in Australia and New Zealand. Clin. Infect. Dis. 31, 499–508.

Chen, S.-C., T.-H. Chen, P.-C. Wang, Y.-C. Chen, J.-P. Huang, Y.-D. Lin, H.-C. Chaung and L.-L. Liaw. 2003. *Metschnikowia bicuspidata* and *Enterococcus faecium* co-infection in the giant freshwater prawn *Macrobrachium rosenbergii*. Dis. Aquat. Organ. 55, 161–167.

Chen, T.A., and P.B. Hill. 2005. The biology of *Malassezia* organisms and their ability to induce immune responses and skin disease. Vet. Dermatol. 16, 4–26.

Chen, W.-B., Y.-F. Han, S.-C. Yong and S.-C. Chang. 2000. Isolation, purification, and characterization of a killer protein from *Schwanniomyces occidentalis*. Appl. Environ. Microbiol. 66, 5348–5352.

Chen, Y.-C., J.D. Eisner, M.M. Kattar, S.L. Rassoulian-Barret, K. LaFe, S.L. Yarfitz, A.P. Limaye and B.T. Cookson. 2001. Polymorphic internal transcribed spacer region 1 DNA sequences identify medically important yeasts. J. Clin. Microbiol. 39, 4042–4051.

Chenevert, R., N. Pelchat and F. Jacques. 2006. Stereoselective enzymatic acylations. Curr. Organ. Chem. 10, 1067–1094.

Cheng, M.F., C.C. Chiou, Y.C. Liu, H.Z. Wang and K.S. Hsieh. 2001. *Cryptococcus laurentii* fungemia in a premature neonate. J. Clin. Microbiol. 39, 1608–1611.

Cheng, M.F., K.W. Yu, R.B. Tang, Y.H. Fan, Y.L. Yang, K.S. Hsieh, M. Ho and H.J. Lo. 2004. Distribution and antifungal susceptibility of *Candida* species causing candidemia from 1996–1999. Diagn. Microbiol. Infect. Dis. 48, 33–37.

Cheng, Y., D.J. McNally, C. Labbé, N. Voyer, F. Belzille and R.R. Bélanger. 2003. Insertional mutagenesis of a fungal biocontrol agent led to discovery of a rare cellobiose lipid with antifungal activity. Appl. Environ. Microbiol. 69, 2595–2602.

Cherniak, R., and J.B. Sundstrom. 1994. Polysaccharide antigens of the capsule of *Cryptococcus neoformans*. Infect. Immun. 62, 1507–1512.

Cherniak, R., E. Reiss, M.E. Slodki, R.D. Plattner and S.O. Blumer. 1980. Structure and antigenic activity of the capsular polysaccharide of *Cryptococcus neoformans* serotype A. Mol. Immunol. 17, 1025–1032.

Chernov, I. Yu., and I.P. Bab'eva. 1988. A new species of *Cryptococcus* yeast from tundra soil. Mikrobiologiia 57, 1031–1034.

Cherry, J.R., and A.L. Fidanstef. 2003. Directed evolution of industrial enzymes: an update. Curr. Opin. Biotechnol. 14, 438–443.

Cheung, P.C.K. 1996. The hypercholesterolemic effect of two edible mushrooms: *Auricularia auricula-judea* (tree-ear) and *Tremella fuciformis* (white jelly-leaf) in hypercholesterolemic rats. Nutr. Res. 16, 1721–1725.

Chi, Z., Z. Chi, G. Liu, F. Wang, L. Ju and T. Zhang. 2009. *Saccharomycopsis fibuligera* and its applications in biotechnology. Biotechnol. Adv. 27, 423–431.
Chida, S., and T. Ochiai. 2000a. Method of producing erythritol. US Patent 6074857.
Chida, S., and T. Ochiai. 2000b. Method for producing erythritol using a microorganism. US Patent 6110715.
Cho, H., K. Yamagishi, S. Abe and S. Morioka. 1998. Method of producing erythritol. US Patent 5981241.
Choi, I.-G., and S.H. Kim. 2007. Global extent of horizontal gene transfer. Proc. Natl. Acad. Sci. USA 104, 4489–4494.
Chotani, G., T. Dodge, A. Hsu, M. Kumar, R. DeLuca, D. Trimbur, W. Weyler and K. Sanford. 2000. The commercial production of chemicals using pathway engineering. Biochim. Biophys. Acta 1543, 434–455.
Chou, H., M.F. Tam, S.S. Lee, H.Y. Tai, C.Y. Chang, C.T. Chou and H.D. Shen. 2005. A vacuolar serine protease (Rho m 2) is a major allergen of *Rhodotorula mucilaginosa* and belongs to a class of highly conserved pan-fungal allergens. Int. Arch. Allergy Immunol. 138, 134–141.
Chowdhary, A., S. Ahmad, Z.U. Khan, D.C. Doval and H.S. Randhawa. 2004. *Trichosporon asahii* as an emerging etiologic agent of disseminated trichosporonosis: a case report and an update. Indian J. Med. Microbiol. 22, 16–22.
Christakis, G., S. Perlorentzou, M. Aslanidou, A. Megalakaki and A. Velegraki. 2005. Fatal *Blastoschizomyces capitatus* sepsis in a neutropenic patient with acute myeloid leukemia: first documented case from Greece. Mycoses 48, 216–220.
Christensen, W.B. 1946. Urea decomposition as a means of differentiating *Proteus* and *Paracolon* cultures from each other and from *Salmonella* and *Shigella* type. J. Bacteriol. 52, 461–466.
Chryssanthou, E., U. Broberger and B. Petrini. 2001. *Malassezia pachydermatis* fungaemia in a neonatal intensive care unit. Acta Paediatr. 90, 323–327.
Chu, A.M., and R.W. Davis. 2007. High-throughput creation of a whole-genome collection of yeast knockout strains. Methods. Mol. Biol. 416, 205–220.
Chu, B.C., and H. Lee. 2007. Genetic improvement of *Saccharomyces cerevisiae* for xylose fermentation. Biotechnol. Adv. 25, 425–441.
Chuck, S.L., and M.A. Sande. 1989. Infections with *Cryptococcus neoformans* in the acquired immunodeficiency syndrome. N. Engl. J. Med. 321, 794–799.
Chung, H. Jr., S.L. Lee and C.C. Chou. 2000. Production and molar yield of 2-phenylethanol by *Pichia fermentans* L-5 as affected by some medium components. J. Biosci. Bioeng. 90, 142–147.
Ciafardini, G., and B.A. Zullo. 2002. Microbiological activity in stored olive oil. Int. J. Food Microbiol. 75, 111–188.
Ciafardini, G., B.A. Zullo, G. Cioccia and A. Iride. 2006. Lipolytic activity of *Williopsis californica* and *Saccharomyces cerevisiae* in extra virgin olive oil. Int. J. Food Microbiol. 107, 27–32.
Ciani, M., and F. Fatichenti. 2001. Killer toxin of *Kluyveromyces phaffii* DBVPG 6076 as a biopreservative agent to control apiculate wine yeasts. Appl. Environ. Microbiol. 67, 3058–3063.
Ciani, M., and F. Maccarelli. 1998. Oenological properties of non-*Saccharomyces* yeasts associated with winemaking. World J. Microbiol. Biotechnol. 14, 199–203.
Ciani, M., L. Ferraro and F. Fatichenti. 2000. Influence of glycerol production on the aerobic and anaerobic growth of the wine yeast *Candida stellata*. Enzyme Microb. Technol. 27, 698–703.
Ciani, M., I. Mannazzu, P. Marinangeli, F. Clementi and A. Martini. 2004. Contribution of winery-resident *Saccharomyces cerevisiae* strains to spontaneous grape must fermentation. Antonie van Leeuwenhoek 85, 159–164.
Ciardo, D.E., G. Schar, E.C. Bottger, M. Altwegg and P.P. Bosshard. 2006. Internal transcribed spacer sequencing versus biochemical profiling for identification of medically important yeasts. J. Clin. Microbiol. 44, 77–84.
Ciccarelli, F.D., T. Doerks, C. von Mering, C.J. Creevey, B. Snel and P. Bork. 2006. Toward automatic reconstruction of a highly resolved tree of life. Science 311, 1283–1287.
Ciferri, R. 1930a. Contribuzioni alla sistematica delle Torulopsidaceae II–XIV. Arch. Protistenkd. 71, 405–452.
Ciferri, R. 1930b. Contribuzioni alla sistematica dell'*Oidium matalense* Castellani. Arch. Protistenkd. 71, 436–443.
Ciferri, R. 1931a. Contributions to the classification of Torulopsidaceae – I. An American variety of the *Torulopsis minuta*. Mycologia 23, 140–146.
Ciferri, R. 1931b. Studies on cacao. I. Actinomycetes on cacao beans. J. Dep. Agric. P. R. 15, 223–286.
Ciferri, R. 1955a. Tassonomia e nomenclatura dell'agente del "Marciume acido" dei frutti di agrume. Ann. Sper. Agrar. Roma, N.S. 9, 5–10.
Ciferri, R. 1955b. A provisional key to the genera of anascosporogenous yeasts and allied fungi. An. Soc. Biol. Pernambuco 13, 130–142.
Ciferri, R. 1960. Manuale di Micologie Medica, 2nd edn. Vol. 2, Renzo Cortina, Pavia, Italy.
Ciferri, R., and J.D. Alfonseca. 1931. A new variety of *Blastodendrion intestinale* Mattl. Zentralbl. Bakteriol. Parasitenkd., Abt. II, 83, 273–276.
Ciferri, R., and B.K. Ashford. 1929. A new species of *Blastodendrion*. Porto Rico J. Publ. Health Trop. Med. 5, 91–105.
Ciferri, R., and P. Redaelli. 1925. Monografia delle Torulopsidaceae a pigmento rosso. Atti Ist. Bot. R. Univ. Pavia, Ser. III, 2, 147–303.
Ciferri, R., and P. Redaelli. 1929. Studies on the Torulopsidaceae, a trial general systematic classification of the asporogenous ferments. Ann. Mycol. 27, 243–295.
Ciferri, R., and P. Redaelli. 1935. Contribuzione alla sistematica delle Torulopsidaceae. XV–XXXIII. Arch. Mikrobiol. 6, 9–72.
Ciferri, R., and P. Redaelli. 1947. Reisolamento del *Mycoderma glutinis-farinulae* Desm., e proposta del cambiamento del nome generico di *Mycoderma* Leberle in *Mycokluyveria nobis*. Mycopathologia 4, 54–59.
Ciferri, R., A. Montemartini and O. Ciferri. 1957. Caratteristiche morfologiche e assimilative e speciologia della Protothecae. Nuovi Ann. Ig. Microbiol. 8, 554–563.
Clare, J., K. Sreekrishna and M. Romanos. 1998. Expression of tetanus toxin fragment C. Methods. Mol. Biol. 103, 193–208.
Clark-Walker, G.D., P. Hoeben, A. Plazinska, D.K. Smith and E.H. Wimme. 1987. Application of mitochondrial DNA analysis to yeast systematics. In: G.S. de Hoog, M.Th. Smith and A.C.M. Weijman (Eds), The Expanding Realm of Yeast-like Fungi. Elsevier, Amsterdam, pp. 259–266 (Stud. Mycol. 30, 259–266).

Clement, M., D. Posada and K. Crandall. 2000. TCS: a computer program to estimate gene genealogies. Mol. Ecol. 9, 1657–1660.

Clements, F.E., and C.L. Shear. 1931. The Genera of Fungi. W.H. Wilson, New York.

Cliften, P., P. Sudarsanam, A. Desikan, L. Fulton, B. Fulton, J. Majors, R. Waterston, B.A. Cohen and M. Johnston. 2003. Finding functional features in *Saccharomyces* genomes by phylogenetic footprinting. Science 301, 71–76.

Cliften, P.F., R.S. Fulton, R.K. Wilson and M. Johnston. 2006. After the duplication: gene loss and adaptation in *Saccharomyces* genomes. Genetics 172, 863–872.

Coble, C.R., E.G. Murray and D.R. Rice. 1987. Earth Science. Prentice-Hall, Englewood Cliffs, NJ.

Cochet, G. 1940. Recherches sur la flore mycologique de l'intestin des rongeurs domestiques. Thesis, Poulet-Malassis, Alençon.

Cocolin, L., A. Heisey and D.A. Mills. 2001. Direct identification of the indigenous yeasts in commercial wine fermentations. Am. J. Enol. Vitic. 52, 49–53.

Cocolin, L., D. Aggio, M. Manzano, C. Cantoni and G. Comi. 2002. An application of PCR-DGGE analysis to profile the yeast populations in raw milk. Int. Dairy J. 12, 407–411.

Cocolin, L., K. Rantsiou, L. Iacumin, R. Zironi and G. Comi. 2004a. Molecular detection and identification of *Brettanomyces*/*Dekkera bruxellensis* and *Brettanomyces*/*Dekkera anomalus* in spoiled wines. Appl. Environ. Microbiol. 70, 1347–1355.

Cocolin, L., V. Pepe, F. Comitini, G. Comi and M. Ciani. 2004b. Enological and genetic traits of *Saccharomyces cerevisiae* isolated from former and modern wineries. FEMS Yeast Res. 5, 237–245.

Cocolin, L., R. Urso, K. Rantsiou, C. Cantoni and G. Comi. 2006. Dynamics and characterization of yeasts during natural fermentation of Italian sausages. FEMS Yeast Res. 6, 692–701.

Codreanu, R., and D. Codreanu-Balcescu. 1981. On two *Metschnikowia* yeast species producing hemocoelic infections in *Daphnia magna* and *Artemia salina* (Crustacea, Phyllopoda) from Rumania. J. Invert. Pathol. 37, 22–27.

Coelho, M.A., A. Rosa, N. Rodrigues, Á. Fonseca and P. Gonçalves. 2008. Identification of mating type genes in the bipolar basidiomycetous yeast *Rhodosporidium toruloides*: first insight into the MAT locus structure of the Sporidiobolales. Eukaryot. Cell 7, 1053–1061.

Coenjaerts, F.E. 2006. The Sixth International Conference on Cryptococcus and Cryptococcosis. FEMS Yeast Res. 6, 312–317.

Coetzee, D.J., J.L.F. Kock, A. Botha, M.S. van Dijk, E.J. Smit, P.J. Botes and O.P.H. Augustyn. 1992. Yeast eicosanoids. III. The distribution of arachidonic acid metabolites in the lifecycle of *Dipodascopsis uninucleata*. Syst. Appl. Microbiol. 15, 311–318.

Cogliati, M., M. Allaria, A.M. Tortorano and M.A. Viviani. 2000. Genotyping *Cryptococcus neoformans* with specific primers designed from PCR-fingerprinting bands sequenced using a modified PCR-based strategy. Med. Mycol. 38, 97–103.

Cogliati, M., M.C. Esposto, D.L. Clarke, B.L. Wickes and M.A. Viviani. 2001. Origin of *Cryptococcus neoformans* var. *neoformans* diploid strains. J. Clin. Microbiol. 39, 3889–3894.

Cogliati, M., M.C. Esposto, A.M. Tortorano and M.A. Viviani. 2006. *Cryptococcus neoformans* population includes hybrid strains homozygous at mating-type locus. FEMS Yeast Res. 6, 608–613.

Cohen, C., and C. Ratledge (Eds). 2005. Single Cell Oils. AOCS Press, Champaign, IL.

Cohn, F. 1872. Untersuchungen über Bakterien. Beitr. Biol. Pflanz., Heft 2, 127–224.

Coker, W.C., and L. Shanor. 1939. A remarkable saprophytic fungoid alga. J. Elisha Mitchell Sci. Soc. 55, 152–166.

Collinge, J., and A.R. Clarke. 2007. A general model of prion strains and their pathogenicity. Science 318, 930–936.

Collins, M.D., and D. Jones. 1981. J. Appl. Bacteriol. 51, 129–134.

Coluccio, A.E., R.K. Rodriguez, M.J. Kernan and A.M. Neiman. 2008. The yeast spore wall enables spores to survive passage through the digestive tract of *Drosophila*. PLoS ONE 3, e2873.

Comi, G., P. Romano, L. Cocolin and C. Fiore. 2001. Characterization of *Kloeckera apiculata* strains from the Friuli region in northern Italy. World J. Microbiol. Biotechnol. 17, 391–394.

Comitini, F., and M. Ciani. 2006. Survival of inoculated *Saccharomyces cerevisiae* strains on wine grapes during two vintages. Lett. Appl. Microbiol. 42, 248–253.

Comitini, F., J. De Ingeniis, L. Pepe, I. Mannazzu and M. Ciani. 2004. *Pichia anomala* and *Kluyveromyces wickerhamii* killer toxins as new tools against *Dekkera*/*Brettanomyces* spoilage yeasts. FEMS Microbiol. Lett. 238, 235–240.

Connell, L., R. Redman, S. Craig and R. Rodriguez. 2006. Distribution and abundance of fungi in the soils of Taylor Valley, Antarctica. Soil Biol. Biochem. 38, 3083–3094.

Connell, L.B., R. Redman, R. Rodriguez, A. Barrett, M. Iszard and Á. Fonseca. 2010. *Dioszegia antarctica* sp. nov. and *Dioszegia cryoxerica* sp. nov., psychrophilic basidiomycetous yeasts from polar desert soils in Antarctica. Int. J. Syst. Evol. Microbiol. 60, 1466–1472.

Conner, D.E., and L.R. Beuchat. 1984. Effects of essential oils from plants on growth of spoilage yeasts. J. Food Sci. 49, 429–434.

Conte, M.V., and R.S. Pore. 1973. Taxonomic implications of *Prototheca* and *Chlorella* cell wall polysaccharide characterization. Arch. Mikrobiol. 92, 227–233.

Conti, S.F., and T.D. Brock. 1965. Electron microscopy of cell fusion in conjugating *Hansenula wingei*. J. Bacteriol. 90, 524–533.

Converti, A., P. Perego, J.M. Dominguez and S.S. Silva. 2001. Effect of temperature on the microaerophilic metabolism of *Pachysolen tannophilus*. Enzyme Microb. Technol. 28, 339–345.

Conway, W.S., W.J. Janisiewicz, B. Leverentz, R.A. Saftner and M.J. Camp. 2007. Control of blue mold of apple by combining controlled atmosphere, antagonist mixture, and sodium bicarbonate. Postharvest Biol. Technol. 45, 326–332.

Cook, D.W.M. 2002a. Effect of formulated yeast in suppressing the liberation of *Botrytis cinerea* conidia. Plant Dis. 86, 1265–1270.

Cook, D.W.M. 2002b. A laboratory simulation for vectoring of *Trichosporon pullulans* by conidia of *Botrytis cinerea*. Phytopathology 92, 1293–1299.

Cook, R.C. 1977. The Biology of Symbiotic Fungi. John Wiley and Sons, London.

Cooke, S.W. 2000. Role of megabacteria in mammals. Vet. Rec. 147, 371–372.

Cooke, W.B. 1968a. Studies in the genus *Prototheca*. I. Literature review. J. Elisha Mitchell Sci. Soc. 84, 213–216.
Cooke, W.B. 1968b. Studies in the genus *Prototheca*. II. Taxonomy. J. Elisha Mitchell Sci. Soc. 84, 217–220.
Cooper, C.R. Jr. 1998. From bamboo rats to humans: the odyssey of *Penicillium marneffei*. ASM News 64, 390–397.
Cooper, C.R. Jr. 2002. New and emerging pathogens: what's a lab to do? In: R.A. Calderone and R.L. Cihlar (Eds), Fungal Pathogenesis. Principles and Clinical Applications. Marcel Dekker, New York, pp. 751–757.
Cooper, C.R. Jr. 2005. Deep phaeoyphomycosis. In: W.G. Merz and R.J. Hay (Eds), Medical Mycology, 10th edn. Hodder Arnold, London, pp. 739–748.
Cooper, C.R. Jr., and N.G. Haycocks. 2000. *Penicillium marneffei*: an insurgent species among the penicillia. J. Eukaryot. Microbiol. 47, 24–28.
Cooper, C.R. Jr., and N. Vanittanakom. 2008. Insights into the pathogenicity of *Penicillium marneffei*. Future Microbiol. 3, 43–55.
Cooper, C.R. Jr., D.M. Dixon and I.F. Salkin. 1992. Laboratory-acquired sporotrichosis. J. Med. Vet. Mycol. 30, 169–171.
Corbo, M.R., R. Lanciotti, M. Albenzio and M. Sinigaglia. 2001. Occurrence and characterization of yeasts isolated from milks and dairy products of Apulia region. Int. J. Food. Microbiol. 69, 147–152.
Corda, A.C.J. 1842. Icones Fungorum Hucusque Cognitorum, Vol. 3. Pragae.
Cordier, H., F. Mendes, I. Vasconcelos and J.M. Francois. 2007. A metabolic and genomic study of engineered *Saccharomyces* strains for high glycerol production. Metabol. Eng. 9, 364–378.
Cordro'ch, M. 1937. Nouvelle espèce de levure du genre *Zygosaccharomyces*: *Z. ashbyii*. Ann. Ferment. 3, 87–104.
Cornelissen, S., A. Botha, W.J. Conradie and G.M. Wolfaardt. 2003. Shifts in community composition provide a mechanism for maintenance of activity of soil yeasts in the presence of elevated copper levels. Can. J. Microbiol. 49, 425–432.
Corredor, M., A.-M. Davila, C. Gaillardin and S. Casarégola. 2000. DNA probe specific for the yeast species *Debaryomyces hansenii*: useful tools for rapid identification. FEMS Microbiol. Lett. 193, 171–177.
Corredor, M., A.-M. Davila, S. Casarégola and C. Gaillardin. 2003. Chromosomal polymorphism in the yeast species *Debaryomyces hansenii*. Antonie van Leeuwenhoek 83, 215–222.
Correia, A., P. Sampaio, S. James and C. Pais. 2006. *Candida bracarensis* sp. nov., a novel anamorphic yeast species phenotypically similar to *Candida glabrata*. Int. J. Syst. Evol. Microbiol. 56, 313–317.
Corry, J.E.L. 1976. The effect of sugars and polyols on the heat resistance and morphology of osmophilic yeasts. J. Appl. Bacteriol. 40, 269–276.
Corti, A., S. Frassinetti, G. Vallini, S. D'Antone, C. Fichi and R. Solaro. 1995. Biodegradation of nonionic surfactants. I. Biotransformation of 4-(1-nonyl)phenol by a *Candida maltosa* isolate. Environ. Pollut. 90, 83–87.
Cosentino, S., M.E. Fadda, M. Deplano, A.F. Mulargia and F. Palmas. 2001. Yeasts associated with Sardinian ewe's dairy products. Int. J. Food Microbiol. 69, 53–58.
Costamagna, L., I. Rosi, I. Garuccio and O. Arrigoni. 1986. Ascorbic acid specific utilization by some yeasts. Can. J. Microbiol. 32, 756–758.
Costantin, M.J. 1901. Sur les levures des animaux. Bull. Soc. Mycol. Fr. 17, 145–148.
Coton, E., M. Coton, D. Levert, S. Casaregola and D. Sohier. 2006. Yeast ecology in French cider and black olive natural fermentations. Int. J. Food Microbiol. 108, 130–135.
Cottini, G.B. 1939. Un caso di "Lingua nigra et pilosa" con isolamento di *Mycotorula guilliermondi* (Cast.) n. comb. Mycopathologia 2, 75–79.
Cottrell, M. 1989. Cellular longchain fatty acid composition, prostaglandins and electrophoretic karyotypes in the yeast family Lipomycetaceae. PhD Thesis, University of Orange Free State, Bloemfontein, South Africa.
Cottrell, M., and J.L.F. Kock. 1989. The yeast family Lipomycetaceae Novak et Zolt emend. van der Walt et al. and the genus *Myxozyma* van der Walt et al. 1. A historical account of its delimitation and 2. The taxonomic relevance of cellular long chain fatty acid composition and other phenotypic characters. Syst. Appl. Microbiol. 12, 291–305.
Cottrell, M., and J.L.F. Kock. 1990. An electrophoretic karyotype comparison of the yeast genera *Dipodascopsis* Batra et Millner, *Lipomyces* Lodder et Kreger-van Rij, *Myxozyma* van der Walt et von Arx 1990. Syst. Appl. Microbiol. 13, 136–141.
Cottrell, M., J.L.F. Kock, P.M. Lategan, P.J. Botes and T.J. Britz. 1985. The longchain fatty acid compositions of species representing the genus *Kluyveromyces*. FEMS Micriobiol. Lett. 30, 373–376.
Cottrell, M., B. Viljoen, J.L.F. Kock and P. Lategan. 1986. The long-chain fatty acid compositions of species representing the genera *Saccharomyces*, *Schwanniomyces* and *Lipomyces*. J. Gen. Microbiol. 132, 2401–2403.
Cottrell, M., J.L.F. Kock, P.M. Lategan, P.J. Botes and T.J. Britz. 1987. The value of long-chain fatty acid composition in the taxonomy of species representing the genus *Kluyveromyces*. Syst. Appl. Microbiol. 9, 277–279.
Couch, J.N. 1938. The Genus *Septobasidium*. University of North Carolina Press, Chapel Hill, NC.
Coughlan, C.M., and J.L. Brodsky. 2005. Use of yeast as a model system to investigate protein conformational diseases. Mol. Biotechnol. 30, 171–180.
Coulon, J., J.I. Husnik, D.L. Inglis, G.K. van der Merwe, A. Lonvaud, D.J. Erasmus and H.J.J. van Vaureen. 2006. Metabolic engineering of *Saccharomyces cerevisiae* to minimize the production of ethyl carbamate in wine. Am. J. Enol. Vitic. 57, 113–124.
Couppie, P., C. Aznar, B. Carme and M. Nacher. 2006. American histoplasmosis in developing countries with a special focus on patients with HIV: diagnosis, treatment, and prognosis. Curr. Opin. Infect. Dis. 19, 443–449.
Cousens, L.S., J.R. Shuster, C. Gallegos, L. Ku, M.M. Stempien, M.S. Urdea, R. Sanchez-Pescador, A. Taylor and P. Tekampolson. 1987. High-level expression of proinsulin in the yeast *Saccharomyces cerevisiae*. Gene 61, 265–275.
Cowan, D. 1996. Industrial enzyme technology. TIBTECH 14, 177–178.
Cox, D.E. 1976. A new homobasidiomycete with anomalous basidia. Mycologia 68, 481–510.
Craig, G.D., R.J. Newsam and K. Gull. 1977. Subhymenial branching and dolipore septation in *Agaricus bisporus*. Trans. Br. Mycol. Soc. 69, 337–344.
Crandall, M.A., and T.D. Brock. 1968. Molecular basis of mating in the yeast *Hansenula wingei*. Bacteriol. Rev. 32, 139–163.

Crane, F.L., and R. Barr. 1985. Chemical structure and properties of conenzyme Q and related compounds. In: G. Lenaz (Ed.), Coenzyme Q: Biochemistry, Bioenergetics and Clinical Applications of Ubiquinone. John Wiley, Chichester, pp. 1–37.

Cregg, J.M. (Ed.) 2007. *Pichia* Protocols, 2nd edn. Humana Press, Totowa, NJ.

Cregg, J.M., and K.R. Madden. 1988. Development of the methylotrophic yeast, *Pichia pastoris*, as a host system for the production of foreign proteins. Dev. Ind. Microbiol. 29, 33–41.

Cregg, J.M., T.S. Vedvick and W.C. Raschke. 1993. Recent advances in the expression of foreign genes in *Pichia pastoris*. Bio/Technology 11, 905–910.

Crespo, M.J., M.L. Abarca and F.J. Cabañes. 1999. Isolation of *Malassezia furfur* from a cat. J. Clin. Microbiol. 37, 1573–1574.

Crespo Erchiga, V., and V. Delgado Florencio. 2006. *Malassezia* yeasts and pityriasis versicolor. Curr. Opin. Infect. Dis. 19, 139–147.

Crespo Erchiga, V., and E. Guého. 2005. Superficial diseases caused by *Malassezia* species. In: W.G. Merz and R.J. Hay (Eds), Topley and Wilson's Microbiology and Microbial Infections, Medical Mycology, 10th edn. Vol. 5. Hodder Arnold, London, pp. 202–243.

Crespo Erchiga, V., A. Ojeda Martos, A. Vera Casaño, A. Crespo Erchiga, F. Sanchez-Fajardo and E. Guého. 1999. Mycology of pityriasis versicolor. J. Mycol. Méd. 9, 143–148.

Crespo Erchiga, V., A. Ojeda Martos, A. Vera Casaño, A. Crespo Erchiga and F. Sanchez Fajardo. 2000. *Malassezia globosa* as the causative agent of pityriasis versicolor. Br. J. Dermatol. 143, 799–803.

Crespo, M.J., M.L. Abarca and F.J. Cabañes. 2000a. Evaluation of different preservation and storage methods for *Malassezia* spp. J. Clin. Microbiol. 39, 3872–3875.

Crespo, M.J., M.L. Abarca and F.J. Cabañes. 2000b. A typical lipid-dependent *Malassezia* species isolated from dogs with otitis externa. J. Clin. Microbiol. 38, 2383–2385.

Crespo, M.J., M.L. Abarca and F.J. Cabañes. 2002. Occurrence of *Malassezia* spp. in horses and domestic ruminants. Mycoses 45, 333–337.

Crestani, J., M.F. Landell, J. Faganello, M.H. Vainstein, H.S. Vishniac and P. Valente. 2009. *Cryptococcus terrestris* sp. nov., a Tremellaceous, anamorphic yeast phylogenetically related to *Cryptococcus flavescens*. Int. J. Syst. Evol. Microbiol. 59, 631–636.

Criseo, G., M. Gallo and A. Pernice. 1999. Killer activity at different pHs against *Cryptococcus neoformans* var. *neoformans* serotype A by environmental yeast isolates. Mycoses 42, 601–608.

Crognale, S., A. D'Annibale, F. Federici, M. Fenice, D. Quaratino and M. Petruccioli. 2006. Olive oil mill wastewater valorisation by fungi. J. Chem. Technol. Biotechnol. 81, 1547–1555.

Crommelin, D.J.A., R.D. Sindelar and B. Meibohm (Eds). 2008. Pharmaceutical Biotechnology, 3rd edn. Informa Healthcare USA, New York, NY

Cronk, T.C., K.H. Steinkraus, L.R. Hackler and L.R. Mattick. 1977. Indonesian tape ketan fermentation. Appl. Environ. Microbiol. 33, 1067–1073.

Crook, E.M., and I.R. Johnston. 1962. The qualitative analysis of the cell walls of selected species of fungi. Biochem. J. 83, 325–331.

Crowther, K.S., A.T. Webb and P.H. McWhinney. 2003. *Trichosporon inkin* peritonitis in a patient on continuous ambulatory peritoneal dialysis returning from the Caribbean. Clin. Nephrol. 59, 69–70.

Cruz-López, L., E.A. Malo, J. Toledo, A. Virgen, A. Del Mazo and J.C. Rojas. 2006. A new potential attractant for *Anastrepha obliqua* from *Spondias mombin* fruits. J. Chem. Ecol. 32, 351–365.

Cuervo, A.M. 2004. Autophagy: in sickness and in health. Trends Cell Biol. 14, 70–77.

Cui, Z., D. Mochizuki, Y. Matsuno, T. Nakamura, Y. Liu, T. Hatano, S. Fukui and T. Miyakawa. 1992. Cloning and molecular analysis of cDNA encoding a carboxymethylcellulase of the yeast *Cryptococcus flavus*. Biosci. Biotechnol. Biochem. 56, 1230–1235.

Cullen, W.R., B.C. McBride and A.W. Pickett. 1979. The transformation of arsenicals by *Candida humicola*. Can. J. Microbiol. 25, 1201–1205.

Cullen, W.R., B.C. McBride and A.W. Pickett. 1990. The uptake of arsenicals by *Candida humicola*. Appl. Organomet. Chem. 4, 119–125.

Cummings, M.P., S.A. Handley, D.S. Myers, D.L. Reed, A. Rokas and K. Winka. 2003. Comparing bootstrap and posterior probability values in the four-taxon case. Syst. Biol. 52, 477–487.

Cunningham, A.C., J.P. Leeming, E. Ingham and G. Gowland. 1990. Differentiation of three serovars of *Malassezia furfur*. J. Appl. Bacteriol. 68, 439–446.

Cunnington, J.H., and R.C. Mann. 2004. The disappearance of *Taphrina bullata* from Australia. Australas. Plant Pathol. 33, 125–127.

Cuny, H. 1966. Louis Pasteur: The Man and His Theories. Paul S. Eriksson, New York.

Currah, R.S., and R. Sherburne. 1992. Septal ultrastructure of some fungal endophytes from boreal orchid mycorrhizas. Mycol. Res. 96, 583–587.

Currie, C.R., J.A. Scott, R.C. Summerbell and D. Malloch. 1999. Fungus-growing ants use antibiotic-producing bacteria to control garden parasites. Nature 398, 701–704.

Currie, R.C., B. Wong, A.E. Stuart, T.R. Schultz, S.A. Rehner, U.G. Mueller, G.H. Sung, J.W. Spatafora and N.A. Straus. 2003. Ancient tripartite coevolution in the attine ant-microbe symbiosis. Science 299, 386–388.

Curry, K.J. 1985. Ascosporogenesis in *Dipodascopsis tothii* (Hemiascomycetidae). Mycologia 77, 401–411.

Curtin, C.D., J.R. Bellon, P.A. Henschke, P.W. Godden and M.A. de Baros Lopes. 2007. Genetic diversity of *Dekkera bruxellensis* yeasts isolated from Australian wineries. FEMS Yeast Res. 7, 471–481.

Curtis, F. 1986. Contribution à l'étude de la Saccharomycose humaine. Ann. Inst. Pasteur 10, 449–468.

Curvale-Fauchet, N., F. Botterel, P. Legrand, J. Guillot and S. Bretagne. 2004. Frequency of intravascular catheter colonization by *Malassezia* spp. in adult patients. Mycoses 47, 491–494.

Cushion, M.T. 1989. *In vitro* studies of *Pneumocystis carinii*. J. Protozool. 36, 45–52.

Cushion, M.T. 1998. Taxonomy, genetic organization, and life cycle of *Pneumocystis carinii*. Semin. Respir. Infect. 13, 304–312.

Cushion, M.T. 2005. *Pneumocystis* pneunomia. In: W.G. Merz and R.J. Hay (Eds), Medical Mycology, 10th edn. Hodder Arnold, London, pp. 763–805.

Cushion, M.T. 2006. *Pneumocystis* pneumonia. In: W.G. Merz and R.J. Hay (Eds), Topley & Wilson's Medical Mycology. Edward Arnold, Washington, DC, pp. 763–806.

Cushion, M.T., and J.M. Beck. 2001. Summary of *Pneumocystis* research presented at the 7th International Workshop on Opportunistic Protists. J. Eukaryot. Microbiol. (Suppl.). 101S–105S.

Cushion, M.T., J. Zhang, M. Kaselis, D. Giuntoli, S.L. Stringer and J.R. Stringer. 1993. Evidence for two genetic variants of *Pneumocystis carinii* coinfecting laboratory rats. J. Clin. Microbiol. 31, 1217–1223.

Cushion, M.T., S.P. Keely and J.R. Stringer. 2004. Molecular and phenotypic description of *Pneumocystis wakefieldiae* sp. nov., a new species in rats. Mycologia 96, 429–438.

Cushion, M.T., S.P. Keely and J.R. Stringer. 2005. Validation of the name *Pneumocystis wakefieldiae*. Mycologia 97, 268.

Cushion, M.T., A.G. Smulian, B.E. Slaven, T. Sesterhenn, J. Arnold, C. Staben, A. Porollo, R. Adamczak and J. Meller. 2007. Transcriptome of *Pneumocystis carinii* during fulminate infection: carbohydrate metabolism and the concept of a compatible parasite. PLoS ONE 2, e423.

Custers, M.Th.J. 1940. Onderzoekingen over het gistgeslacht *Brettanomyces*. Thesis, Delft University of Technology.

Custis, P.H., J.A. Haller and E. de Juan. 1995. An unusual case of cryptococcal endophthalmitis. Retina 15, 300–304.

Cutrona, A.F., M. Shah, M.S. Himes and M.A. Miladore. 2002. *Rhodotorula minuta*: an unusual fungal infection in hip-joint prosthesis. Am. J. Orthop. 31, 137–140.

Czárán, T.L., and R.F. Hoekstra. 2003. Killer-sensitive coexistence in metapopulations of micro-organisms. Proc. R. Soc. Lond. B Biol. Sci. 270, 1373–1378.

Czárán, T.L., R.F. Hoekstra and L. Pagie. 2002. Chemical warfare between microbes promotes biodiversity. Proc. Natl. Acad. Sci. USA 99, 786–790.

da Cunha, A.B., A.M. El Tabey Shehata and W. Oliveira. 1957. A study of the diets and nutritional preferences of tropical species of *Drosophila*. Ecology 38, 98–106.

da Fonseca, O.O.R. 1922. Sobreos agentes das blastomycoses europeas. Cyclo sexuado e posicao do levedo de Hudelo. Bras. Med. 36, 101 (Rev. in: Bull. Inst. Pasteur 21, 651).

da Fonseca, O.O.R., and A.E. de Arêa Leao. 1929. Sobre o agente da proteomycose. Bras. Med. 43, 667.

da Silva, G.A. 1996. The occurrence of killer, sensitive, and neutral yeasts in Brazilian Riesling Italico grape must and the effect of neutral strains on killing behaviour. Appl. Microbiol. Biotechnol. 46, 112–121.

Da Silva Rodrigues, G., R.R. de Faria, L.S. Guazzelli, F. de Matto Oliveira and L.C. Severo. 2006. Infección nosocomial por *Trichosporon asahii*: revisión clínica de 22 casos. Rev. Iberoam. Micol. 23, 85–89. In Spanish.

Dai, C.C., J. Tao, F. Xie, Y.J. Dai and M. Zhao. 2007. Biodiesel generation from oleaginous yeast *Rhodotorula glutinis* with xylose assimilating activity. Afr. J. Biotechnol. 6, 2130–2134.

Dakin, J.C., and A.C. Stolk. 1968. *Moniliella acetoabutans*: some further characteristics and industrial significance. Int. J. Food Sci. Technol. 3, 49–53.

Dalmasso, G., F. Cottrez, V. Imbert, P. Lagadec, J.F. Peyron, P. Rampal, D. Czerucka and H. Groux. 2006. *Saccharomyces boulardii* inhibits inflammatory bowel disease by trapping T cells in mesenteric lymph nodes. Gastroenterology 131, 1812–1825.

Daly, R., and M.T.W. Hearn. 2005. Expression of heterologous proteins in *Pichia pastoris*: a useful experimental tool in protein engineering and production. J. Mol. Recog. 18, 119–138.

Danforth, B.N., and J. Ascher. 1999. Flowers and insect evolution. Science 283, 143a.

Dangeard, P.A. 1906. Les anĉestres des champignons supérieurs. Botaniste 9, 263–303.

Daniel, A.E. 1983. Comparisons of yeasts in the genus *Candida* using molecular biological technology. MSc Thesis, Georgia State University, Atlanta, GA.

Daniel, H.J., M. Reuss and C. Syldatk. 1998. Production of sophorolipids in high concentration from deproteinized whey and rapeseed oil in a two stage fed batch process using *Candida bombicola* ATCC 2214 and *Cryptococcus curvatus* ATCC 20509. Biotechnol. Lett. 20, 1153–1156.

Daniel, H.-M. 2002. Molecular phylogeny applied to *Candida* species and related ascomycetous yeasts. PhD Thesis, Verlag fuer Wissenschaft und Forschung, Berlin.

Daniel, H.-M., and W. Meyer. 2003. Evaluation of ribosomal RNA and actin gene sequences for the identification of ascomycetous yeasts. Int. J. Food Microbiol. 86, 71–78.

Daniel, H.-M., T.C. Sorrell and W. Meyer. 2001. Partial sequence analysis of the actin gene and its potential for studying the phylogeny of *Candida* species and their teleomorphs. Int. J. Syst. Evol. Microbiol. 51, 1593–1606.

Danielson, R.M., and M.F. Jurgensen. 1973. The propagule density of *Lipomyces* and other yeasts in forest soils. Mycopathol. Mycol. Appl. 51, 191–198.

Danker, W.M., S.A. Spector, J. Fierer and C.E. Davis. 1987. *Malassezia* fungemia in neonates and adults: complication of hyperalimentation. Rev. Infect. Dis. 9, 743–753.

Das, A., S.H. Yoon, S.H. Lee, J.Y. Kim, D.K. Oh and S.W. Kim. 2007. An update on microbial carotenoid production: application of recent metabolic engineering tools. Appl. Microbiol. Biotechnol. 77, 505–512.

Dastur, J.F., and J. Singh. 1930. A new *Nematospora* on cotton bolls in the Central Provinces (India). Ann. Mycol. 28, 291–296.

Daszewska, W. 1912. Étude sur la désagrégation de la cellulose dans la terre de bruyère et la tourbe. Bull. Soc. Bot. Genève, Sér. 2, 4, 255–316.

Daughtrey, M.L., K.T. Hodge and N. Shishkoff. 2003. Archiascomycete and Hemiascomycete pathogens. In: R.N. Trigiano, M.T. Windham and A.S. Windham (Eds), Plant Pathology: Concepts and Laboratory Exercises. CRC Press, Boca Raton, FL, pp. 111–116.

Davenport, R.R. 1975. The distribution of yeasts and yeast-like organisms in an English vineyard. PhD Thesis, University of Bristol.

Davenport, R.R. 1976. Distribution of yeasts and yeast-like organisms from aerial surfaces of developing apples and grapes. In: C.H. Dickinson and T.F. Preece (Eds), Microbiology of Aerial Plant Surfaces. Academic Press, London, pp. 199–215.

Davenport, R.R. 1980a. Cold-tolerant yeasts and yeast-like organisms. In: F.A. Skinner, S.M. Passmore and R.R. Davenport (Eds), Biology and Activities of Yeasts. Academic Press, London, pp. 215–230.

Davenport, R.R. 1980b. An outline guide to media and methods for studying yeasts and yeast-like organisms. In: F.A. Skinner, S.M. Passmore and R.R. Davenport (Eds), Biology and Activities of Yeasts. The Society for Applied Bacteriology Symposium Series No. 9. Academic Press, London, pp. 261–263.

Davenport, R.R. 1996. Forensic microbiology for the soft drinks business. Soft Drinks Manage. Int. April, 34–35.

David, M., M. Gabriel and M. Kopecká. 2007a. Microtubular and actin cytoskeletons and ultrastructural characteristics of the potentially pathogenic basidiomycetous yeast *Malassezia pachydermatis*. Cell. Biol. Int. 31, 16–23.

David, M., M. Gabriel and M. Kopecká. 2007b. Cytoskeletal structures, ultrastructural characteristics and the capsule of the basidiomycetous yeast *Cryptococcus laurentii*. Antonie van Leeuwenhoek 92, 29–36.

Davies, R.J. 1988. Yeast oil from cheese whey: process development. In: R.S. Moreton (Ed.), Single Cell Oil. Longman Scientific & Technical, London, pp. 99–145.

Davila, T., G. San-Blas and F. San-Blas. 1986. Effect of papulacandin B on glucan synthesis in *Paracoccidioides brasiliensis*. J. Med. Vet. Mycol. 24, 193–202.

Davis, R.P. and C. Dennis. 1977. The fungal flora of loganberries in relation to storage and spoilage Annals of Applied Biology, 85,301–304.

Davis, B.J. 1964. Disc electrophoresis. II. Method and application to human serum proteins. Ann. N. Y. Acad. Sci. 121, 404–427.

Davis, J.J. 1907. A new species of *Protomyces*. J. Mycol. 13, 188–189.

Davis, R.R., H. Spencer and P.O. Wakelin. 1964. A case of human protothecosis. Trans. R. Soc. Trop. Hyg. 58, 448–451.

Davoli, P., V. Mierau and R.W. Weber. 2004. Carotenoids and fatty acids in red yeasts *Sporobolomyces roseus* and *Rhodotorula glutinis*. Prikl. Biokhim. Mikrobiol. 40, 460–465. In Russian.

Dawes, C.J. 1969. *Saprochaete saccharophila*: ultrastructure, X-ray diffraction and chitin assay of cell wall as aids in evaluating taxonomic position. Trans. Am. Microsc. Soc. 88, 572–581.

Dayhoff, M.O., R.M. Schwartz and B.C. Orcutt. 1978. A model of evolutionary change in proteins. In: M.E. Dayhoff (Ed.), Atlas of Protein Sequence and Structure. National Biomedical Research Foundation, Silver Spring, MD, pp. 348–352.

de Almeida, F.P. 1933. As blastomycoses no Brasil. An. Fac. Med. São Paulo 9, 69–163.

de Araujo, F.V., C.A.G. Soares, A.N. Hagler and L.C. Mendonça-Hagler. 1995. Ascomycetous yeast communities of marine invertebrates in a Southeast Brazilian mangrove ecosystem. Antonie van Leeuwenhoek 68, 91–99.

de Araújo, M., L.G. Fietto, I. de Miranda Castro, A.N.G. dos Santos, M.X. Coutrim and R.L. Brandão. 2006. Isolation of *Saccharomyces* strains producing higher levels of flavoring compounds for production of "cachaça", the Brazilian sugarcane spirit. Int. J. Food Microbiol. 108, 51–59.

de Arêa Leão, A.E. 1940. Considerações sobre os Thallosporados. O gênero *Trichosporon. Trichosporon minor* n. sp. produtor da piedra axilar. Mem. Inst. Oswaldo Cruz 35, 729–745.

de Baere, T., G. Claeys, D. Swinne, C. Massonet, G. Verschraegen, A. Muylaert and M. Vaneechoutte. 2002. Identification of cultured isolates of clinically important yeast species using fluorescent fragment length analysis of the amplified internally transcribed rRNA spacer 2 region. BMC Microbiol. 2, 21–27.

De Baets, S., and E.J. Vandamme. 1998. Polymers from fungi and yeasts and their technical and medical application. Biol. Ital. 28, 13–17.

De Baets, S., and E.J. Vandamme. 1999. Yeasts as producers of polysaccharides with novel application potential. SIM-News 49, 321–328.

De Baets, S., and E.J. Vandamme. 2001. Extracellular *Tremella* polysaccharides: structure, properties and applications. Biotechnol. Lett. 23, 1361–1366.

De Baets, S., S. Du Laing, S. François, C. de Caluwé and E.J. Vandamme. 2000. Synthesis of exopolysaccharides by *Tremella mesenterica* NRRL Y–6158. Med. Fac. Landbouw. Univ. Gent 65/3a, 187–195.

De Baets, S., S. Du Laing, S. François and E.J. Vandamme. 2002a. Optimization of exopolysaccharide production by *Tremella mesenterica* NRRL Y-6158 through implementation of fed-batch fermentation. J. Ind. Microbiol. Biotechnol. 29, 181–184.

De Baets, S., S. Du Laing and E.J. Vandamme. 2002b. Yeast extracellular polysaccharides. In: S. De Baets, E.J. Vandamme and A. Steinbuchel (Eds), Biopolymers: Polysaccharides II. Polysaccharides from Eukaryotes, Vol. 6. Wiley-VCH, Weinheim, pp. 93–122.

de Barros Lopes, M., A. Soden, A.L. Martens, P.A. Henschje and P. Langridge. 1998. Differentiation and species identification of yeasts using PCR. Int. J. Syst. Bacteriol. 48, 279–286.

de Barros Lopes, M., S. Rainiere, P.A. Henschje and P. Langridge. 1999. AFLP fingerprinting for analysis of yeast genetic variation. Int. J. Syst. Bacteriol. 49, 915–924.

de Barros Lopes, M., J.R. Bellon, N.J. Shirley and P.F. Ganter. 2002. Evidence of multiple interspecific hybridization in *Saccharomyces sensu stricto* species. FEMS Yeast Res. 1, 323–331.

de Barros, J.D., S.M. do Nascimento, F.J. de Araujo, R.D. Braz, V.S. Andrade, B. Theelen, T. Boekhout, M.T. Illnait-Zaragozi, M.N. Gouveía, M.C. Fernandes, M.G. Monteiro and M.T. Barreto de Oliveíra. 2009. *Kodamaea* (*Pichia*) *ohmeri* fungemia in a pediatric patient admitted in a public hospital. Med. Mycol. 47, 775–779.

de Bary, A. 1879. Die Erscheinung der Symbiose. Verlag Von Karl J. Truber, Strassburg.

de Bary, A. 1887. Comparative Morphology and Biology of Fungi, Mycetozoa and Bacteria. Clarendon Press, Oxford, 525pp.

de Beer, Z.W., D. Begerow, R. Bauer, G.S. Pegg, P.W. Crous and M.J. Wingfield. 2006. Phylogeny of Quambalariaceae fam. nov., including important *Eucalyptus* pathogens in South Africa and Australia. Stud. Mycol. 55, 289–298.

de Beurmann, L., and H. Gougerot. 1909. Les exascoses, saccharomycoses (mycose de Busse-Buschke) et parasaccharomycoses. Zymonématoses (mycose de Gilchrist). Parendomycoses et endomycoses (muguet). Bull. Mém. Soc. Méd. Hôp. Paris 28, 250–263.

de Beurmann, L., and H. Gougerot. 1910. Les Nouvelles Mycoses. Masson, Paris.

de Capdeville, G., C.L. Wilson, S.V. Beer and J.R. Aist. 2002. Alternative disease control agents induce resistance to blue mold in harvested "Red Delicious" apple fruit. Phytopathology 92, 900–908.

de Castro, L.E.F., O.A. Sarraf, J.M. Lally, H.P. Sandoval, K.D. Solomon and D.T. Vroman. 2005. Case Report. *Cryptococcus albidus* keratitis after corneal transplantation. Cornea 24, 882–883.

de Curtis, F., S. Torriani, F. Rossi and V. de Ciccio. 1996. Selection and use of *Metschnikowia pulcherrima* as a biological control agent for postharvest rots of peaches and table grapes. Ann. Microbiol. Enzimol. 46, 45–55.

de García, V., S. Brizzio, D. Libkind, P. Buzzini and M. van Broock. 2007. Biodiversity of cold-adapted yeasts from glacial meltwater rivers in Patagonia, Argentina. FEMS Microbiol. Ecol. 59, 331–341.

de García, V., S. Brizzio, G. Russo, C.A. Rosa, T. Boekhout, B. Theelen, D. Libkind and M.R. van Broock. 2010. *Cryptococcus spencermartinsiae* sp. nov., a basidiomycetous yeast isolated from glacial waters and apple fruits. Int. J. Syst. Evol. Microbiol. 60, 707–711.

de Gentile, L., J.P. Bouchara, C. Le Clen'h, B. Cimon, F. Symoens and D. Chabasse. 1995. Prevalence of *Candida ciferrii* in elderly patients with trophic disorders of the legs. Mycopathologia 131, 99–102.

de Groot, P.W.J., C. Ruiz, C.R. Vazquez de Aldana, E. Duenas, V.J. Cid, F. Del Rey, J.M. Rodriquez-Pena, P. Perez, A. Andel, J. Caubin, J. Arroyo, J.C. Garcia, C. Gil, M. Molina, L.J. Garcia, C. Nombela and F.M. Klis. 2001. A genomic approach for the identification and classification of genes involved in cell wall formation and its regulation in *Saccharomyces cerevisiae*. Comp. Funct. Genomics 2, 124–142.

de Groot, P.W.J., K.J. Hellingwerf and F.M. Klis. 2003. Genome-wide identification of fungal GPI proteins. Yeast 20, 781–796.

de Groot, P.W.J., A.D. de Boer, J. Cunningham, H.L. Dekker, L. de Jong, K.J. Hellingwerf, C. de Koster and F.M. Klis. 2004. Proteomic analysis of *Candida albicans* cell walls reveals covalently bound carbohydrate-active enzymes and adhesins. Eukaryot. Cell 3, 955–965.

de Groot, P.W.J., A.F. Ram and F.M. Klis. 2005. Features and functions of covalently linked proteins in fungal cell walls. Fungal Genet. Biol. 42, 657–675.

de Groot, P.W.J., Q.Y. Yin, M. Weig, G.J. Sosinska, F.M. Klis and C.G. de Koster. 2007. Mass spectrometric identification of covalently-bound cell wall proteins from the fission yeast *Schizosaccharomyces pombe*. Yeast 24, 267–278.

de Hoog, G.S. 1979a. Taxonomic review of *Moniliella*, *Trichosporonoides* and *Hyalodendron*. Stud. Mycol. 19, 1–36.

de Hoog, G.S. 1979b. The taxonomic position of *Moniliella*, *Trichosporonoides* and *Hyalodendron* – an essay. Stud. Mycol. 19, 81–90.

de Hoog, G.S. 1981. CBS Progress Report 1980. In: Verhandelingen der Koninklijke Nederlandse Akademie van Wetenschappen Afdeling and Tweede Natuurkunde (Eds), Reeks, 77.

de Hoog, G.S. 1982a. CBS Progress Report 1981. In: Verhandelingen der Koninklijke Nederlandse Akademie van Wetenschappen, Afdeling Natuurkunde, Tweede Reeks, 79.

de Hoog, G.S. 1982b. Morphology of anamorphs II. *Sporidiobolus* and *Sporobolomyces*. Stud. Mycol. 22, 10–14.

de Hoog, G.S. 1992. *Sporothrix*-like anamorphs of *Ophiostoma* species and other fungi. In: M.J. Wingfield, K.A. Seifert and J.F. Webber (Eds), Ceratocystis and *Ophiostoma*: Taxonomy, Ecology and Pathology. American Pathological Society, St. Paul, MN, pp. 53–60.

de Hoog, G.S. 1993. Evolution of black yeasts: possible adaptation to the human host. Antonie van Leeuwenhoek 63, 105–109.

de Hoog, G.S. 1996. Risk assessment of fungi from humans and animals. Mycoses 39, 407–417.

de Hoog, G.S. 1998. *Ascoidea* Brefeld & Lindau. In: C.P. Kurtzman and J.W. Fell (Eds), The Yeasts, A Taxonomic study. Elsevier, Amsterdam, pp. 136–140.

de Hoog, G.S., and T. Boekhout. 1982. Teliospores, teliospore-mimics and chlamydospores. Stud. Mycol. 22, 15–22.

de Hoog, G.S., and O. Constantinescu. 1981. A new species of *Sporothrix* from calf skin. Antonie van Leeuwenhoek 47, 367–370.

de Hoog, G.S., and G.A. de Vries. 1973. Two new species of *Sporothrix* and their relation to *Blastobotrys nivea*. Antonie van Leeuwenhoek 39, 515–520.

de Hoog, G.S., and E. Guého. 1984. Deoxyribonucleic acid base composition and taxonomy of *Moniliella* and allied genera. Antonie van Leeuwenhoek 50, 135–141.

de Hoog, G.S., and E. Guého. 2005. White piedra, black piedra, and tinea nigra. In: W.G. Merz and R.J. Hay (Eds), Topley & Wilson's Microbiology and Microbial Infections. Medical Mycology, 10th edn. Hodder Arnold, London, pp. 195–201.

de Hoog, G.S., and M.Th. Smith. 1998a. *Blastobotrys* von Klopotek. In: C.P. Kurtzman and J.W. Fell (Eds), The Yeasts, A Taxonomic Study, 4th edn. Elsevier, Amsterdam, pp. 443–448.

de Hoog, G.S., and M.Th. Smith. 1998b. *Trichosporonoides* Haskins & Spencer. In: C.P. Kurtzman and J.W. Fell (Eds), The Yeasts, A Taxonomic Study, 4th edn. Elsevier, Amsterdam, pp. 873–877.

de Hoog, G.S., and M.Th. Smith. 1998c. *Moniliella* Stolk & Dakin. In: C.P. Kurtzman and J.W. Fell (Eds), The Yeasts, A Taxonomic Study, 4th edn. Elsevier, Amsterdam, pp. 785–788.

de Hoog, G.S., and M.Th. Smith. 1998d. *Hyalodendron* Diddens. In: C.P. Kurtzman and J.W. Fell (Eds), The Yeasts, A Taxonomic Study, 4th edn. Elsevier, Amsterdam, pp. 773–774.

de Hoog, G.S., and M.Th. Smith. 2004. The ribosomal gene phylogeny and species delimitation in *Geotrichum* and its teleomorphs. Stud. Mycol. 50, 489–515.

de Hoog, G.S., A.H. Rantio-Lehtimäki and M.Th. Smith. 1985. *Blastobotrys*, *Sporothrix* and *Trichosporiella*: generic delimitation, new species, and a *Stephanoascus* teleomorph. Antonie van Leeuwenhoek 51, 79–109.

de Hoog, G.S., M.Th. Smith and E. Guého. 1986. A revision of the genus *Geotrichum* and its teleomorphs. Stud. Mycol. 29, 1–131.

de Hoog, G.S., E. Guého and M.Th. Smith. 1997. Nomenclatural notes on some arthroconidial yeasts. Mycotaxon 63, 345–347.

de Hoog, G.S., M.Th. Smith and E. Guého. 1998a. *Dipodascus* de Lagerheim. In: C.P. Kurtzman and J.W. Fell (Eds), The Yeasts, A Taxonomic Study, 4th edn. Elsevier, Amsterdam, pp. 181–193.

de Hoog, G.S., M.Th. Smith and E. Guého. 1998b. *Galactomyces* Redhead & Malloch. In: C.P. Kurtzman and J.W. Fell (Eds), The Yeasts, A Taxonomic Study, 4th edn. Elsevier, Amsterdam, pp. 209–213.

de Hoog, G.S., M.Th. Smith and E. Guého. 1998c. *Geotrichum* Link: Fries. In: C.P. Kurtzman and J.W. Fell (Eds), The Yeasts, A Taxonomic Study, 4th edn. Elsevier, Amsterdam, pp. 574–579.

de Hoog, G.S., J. Guarro, M.J. Figueras and J. Gené. 2000. Atlas of Clinical Fungi, 2nd edn. Centraalbureau voor Schimmelcultures/Universitat Rovira I Virgili, Utrecht/Reus, 1126pp.

de Hoog, G.S., V. Vicente, R.B. Caligiorne, S. Kantarcioglu, K. Tintelnot, A.H. Gerrits van den Ende and G. Haase. 2003. Species diversity and polymorphism in the *Exophiala spinifera* clade containing opportunistic black yeast-like fungi. J. Clin. Microbiol. 41, 4767–4778.

de Koch, S. 1998. Control of post-harvest decay of fruit by means of antagonistic microorganisms. PhD Dissertation, University of Stellenbosch, Capetown.

de Koning, W., and W. Harder. 1992. Methanol-utilizing yeasts. In: J.C. Murell and H. Dalton (Eds), Methane and Methanol Utilizers. Plenum Press, New York, pp. 207–244.

de La Torre, M.J., M.C. Millan, P. Perez-Juan, J. Morales and J.M. Ortega. 1999. Indigenous yeasts associated with two *Vitis vinifera* grape varieties cultured in southern Spain. Microbios 100, 27–40.

de Lagerheim, G. 1892. *Dipodascus albidus*, eine neue, Geschlechtliche Hemiascee. Jahrb. Wiss. Bot. 24, 549–565.

de Lima, S.M., and L.A. Aciole de Queiroz. 1972. Uma nova espécie de *Trichosporon* Behrend. Inst. de Micologia da Univ. Fed. de Pernambuco, Publicação No. 690, 1–8.

de Maria, L., J. Vind, K.M. Oxenbøll, A. Svendsen and S. Paktar. 2007. Phospholipases and their industrial applications. Appl. Microbiol. Biotechnol. 74, 290–300.

de Meeus, T., F. Renaud, E. Mouveroux, J. Reynes, G. Galeazzi, M. Mallie and J.M. Bastide. 2002. Genetic structure of *Candida glabrata* populations in AIDS and non-AIDS patients. J. Clin. Microbiol. 40, 2199–2206.

de Montigny, J., M.-L. Straub, S. Potier, F. Tekaia, B. Dujon, P. Wincker, F. Artiguenave and J.-L. Souciet. 2000a. Genomic exploration of the hemiascomycetous yeasts: 8. *Zygosaccharomyces rouxii*. FEBS Lett. 487, 52–55.

de Montigny, J., C. Spehner, J.-L. Souciet, F. Tekaia, B. Dujon, P. Wincker, F. Artiguenave and S. Potier. 2000b. Genomic exploration of the hemiascomycetous yeasts: 15. *Pichia sorbitophila*. FEBS Lett. 487, 87–90.

de Mot, R., and H. Verachtert. 1982. Biocatalysis and biotechnology with yeasts. ASM News 50, 526–531.

de Mot, R., and H.S. Verachtert. 1985. Purification and characterization of extracellular amylolytic enzymes from the yeast *Filobasidium capsuligenum*. Appl. Environ. Microbiol. 50, 1474–1482.

de Mot, R., and H. Verachtert. 1987. Purification and characterization of extracellular alpha-amylase and glucoamylase from the yeast *Candida antarctica* CBS 6678. Eur. J. Biochem. 164, 643–654.

de Nobel, H., C. Ruiz, H. Martin, W. Morris, S. Brul, M. Molina and F.M. Klis. 2000. Cell wall perturbation in yeast results in dual phosphorylation of the Slt2/Mpk1 MAP kinase and in an Slt2-mediated increase in FKS2-lacZ expression, glucanase resistance and thermotolerance. Microbiology 146, 2121–2132.

de Nobel, J.G., C. Dijkers, E. Hooijberg and F.M. Klis. 1989. Increased cell wall porosity in *Saccharomyces cerevisiae* after treatment with dithiothreitol or EDTA. J. Gen. Microbiol. 135, 2077–2084.

de Rossi, G. 1917. I micodermi del vino. Sta. Sper. Agrar. Ital. 50, 529–562.

de Rossi, G. 1920. I lieviti apiculati nella fermentazione vinaria. Sta. Sper. Agrar. Ital. 53, 233–297.

de Schutter, K., Y.C. Lin, P. Tiels, A. van Hecke, S. Glinka, J. Weber-Lehmann, P. Rouze, Y. van de Peer and N. Callewaert. 2009. Genome sequence of the recombinant protein production host *Pichia pastoris*. Nat. Biotechnol. 27, 561–566.

de Siloniz, M.I., E.M. Payo, M.A. Callejo, D. Marquina and J.M. Peinado. 2002. Environmental adaptation factors of two yeasts isolated from the leachate of a uranium mineral heap. FEMS Microbiol. Lett. 210, 233–237.

De Vroey, C., and F. Gattii. 1989. *Cryptococcus neoformans* var. *gattii* Vanbreuseghem and Takashio.

De Vuyst, L.D., and P. Neysens. 2005. The sourdough microflora: biodiversity and metabolic interactions. Trends Food Sci. Technol. 16, 43–56.

de Winde, J.H. (Ed.) 2003. Functional Genetics of Industrial Yeasts. Springer, Berlin.

Deák, T. 1991. Foodborne yeasts. Adv. Appl. Microbiol. 36, 179–278.

Deák, T. 2001. Identification of yeasts isolated from poultry meat. Acta Biol. Hung. 52, 195–200.

Deák, T. 2003. Detection, enumeration and isolation of yeasts. In: T. Boekhout and V. Robert (Eds), Yeasts in Food: Beneficial and Detrimental Aspects. Behr's Verlag, Hamburg, pp. 39–68.

Deák, T. 2006a. *Candida* and related genera. In: C. de W. Blackburn (Ed.), Food Spoilage Microorganisms. Woodhead Publishing, Cambridge, pp. 336–353.

Deák, T. 2006b. Environmental factors influencing yeasts. In: C. A. Rosa and G. Peter (Eds), Biodiversity and Ecophysiology of Yeasts. Springer-Verlag, Berlin, pp. 155–174.

Deák, T. 2007. Handbook of Food Spoilage Yeasts, 2nd edn. Taylor and Francis.

Deák, T., and L.R. Beuchat. 1993. Yeasts associated with fruit juice concentrates. J. Food Prot. 56, 777–782.

Deák, T., and L.R. Beuchat. 1996. Handbook of Food Spoilage Yeasts. CRC Press, Boca Raton, FL, p. 210.

Deák, T., J. Chen, D.A. Golden, M.S. Tapia, J. Tornai-Lehoczki, B.C. Viljoen, M.T. Wyder and L.R. Beuchat. 2001. Comparison of dichloran 18% glycerol (DG18) agar with general purpose mycological media for enu-merating food spoilage yeasts. Int J. Food Microbiol. 67, 49–53.

Debenedetti, P.G., and H.E. Stanley. 2003. Supercooled and glassy water. Phys. Today 56, 40.

DeBry, R.W. 2001. Improving interpretation of the decay index for DNA sequence data. System. Biol. 50, 742–752.

Decostere, A., K. Hermans, T. de Baere, F. Pasmans and F. Haesebrouck. 2003. First report on *Cryptococcus laurentii* associated with feather loss in a glossy starling (*Lamprotornis chalybaeus*). Avian Pathol. 32, 309–311.

Deegenaars, M.L., and K. Watson. 1997. Stress proteins and stress tolerance in an Antarctic, psychrophilic yeast, *Candida psychrophila*. FEMS Microbiol. Lett. 151, 191–196.

Deerberg, F., G. Pohlmeyer, M. Wullenweber and H.J. Hedrich. 1993. History and pathology of an enzootic *Pneumocystis carinii* pneumonia in athymic Han:RNU and Han:NZNU rats. J. Exp. Anim. Sci. 36, 1–11.

Degenaars, M.L., and K. Watson. 1998. Heat shock response in psychrophilic and psychrotrophic yeast from Antarctica. Extremophiles 2, 41–50.

Dei-Cas, E., E. Mazars, C.O. Ferragut, I. Durand, E.M. Aliouat, M. Dridba, F. Palluault, J.C. Cailliez, N. Seguy and M. Tibayrenc. 1994. Ultrastructural, genomic, isoenzymatic and biological features make it possible to distinguish rabbit *Pneumocystis* from other mammal *Pneumocystis* strains. J. Eukaryot. Microbiol. 41, 84S.

Dei-Cas, E., M. Chabe, R. Moukhlis, I. Durand-Joly, E.M. Aliouat, J.R. Stringer, M. Cushion, C. Noel, G.S. de Hoog, J. Guillot and E. Viscogliosi. 2006. *Pneumocystis oryctolagi* sp. nov., an uncultured fungus causing pneumonia in rabbits at weaning: review of current knowledge, and description of a new taxon on genotypic, phylogenetic and phenotypic bases. FEMS Microbiol. Rev. 30, 853–871.

Deinema, M.H. 1961. Intra- and extra-cellular lipid production by yeasts. Meded. Land-bouwhogeschool, Wageningen 61, 1–54.

Dejong, J.M., Y. Liu, A.P. Bollon, R.M. Long, S. Jennewein, D. Williams and R.B. Croteau. 2006. Genetic engineering of taxol biosynthetic genes in *Saccharomyces cerevisiae*. Biotechnol. Bioeng. 93, 212–224.

Dekoster, C.G., W. Heerma, H.A.M. Pepermans, A. Groenewegen, H. Peters and J. Haverkamp. 1995. Tandem mass spectrometry and nuclear magnetic resonance spectroscopy studies of *Candida bombicola* sophorolipids and product formed on hydrolysis by cutinase. Anal. Biochem. 230, 135–148.

Delanoë, P., and M. Delanoë. 1912. Sur les rapports kystes de Carini du poumon des rats avec le *Trypanosoma lewisi*. C. R. Acad. Sci. 155, 658–660.

Delcourt, A., and E. Guyenot. 1910. De la possibilite d'etudier certain Dipteres en milien definite. C. R. Hebd. Séance. Acad. Sci., Paris 151, 255–257.

Delfini, C., P. Gaia, R. Schellino, M. Strano, A. Pagliara and S. Ambro. 2002. Fermentability of grape must after inhibition with dimethyl dicarbonate (DMDC). J. Agric. Food Chem. 50, 5605–5611.

Delitsch, H. 1943. Systematik der Schimmelpilze. In: A. Lembke (Ed.), Ergebnisse der angewandten Mikrobiologie I. J. Neumann, Neudamm, 175pp.

Delsuc, F., H. Brinkmann and H. Philippe. 2005. Phylogenomics and the reconstruction of the tree of life. Nat. Rev. Genet. 6, 361–375.

Demain, A.L., and J.E. Davies (Eds). 1999. Manual of Industrial Microbiology and Biotechnology. 2nd edn. ASM Press, Washington, DC.

Demme, R. 1889. *Saccharomyces ruber*. Ann. Micrographie 2, 555–556.

Demuyter, C., M. Collier, J.L. Legras and C. Le Jeune. 2004. Predominance of *Saccharomyces uvarum* during spontaneous alcoholic fermentation, for three consecutive years, in an Alsatian winery. J. Appl. Microbiol. 97, 1140–1148.

den Dooren de Jong, L.E. 1927. Een nieuwe, vetvormende gist. Ned. Tijdschr. Hyg. Microbiol. Serol. 1, 136–148.

d'Enfert, C., S. Goyard, S. Rodriguez-Arnaveilhe, L. Frangeul, L. Jones, F. Tekaia, O. Bader, A. Albrecht, L. Castillo, A. Dominguez, J.F. Ernst, C. Fradin, C. Gaillardin, S. Garcia-Sanchez, P. de Groot, B. Hube, F.M. Klis, S. Krishnamurthy, D. Kunze, M.C. Lopez, A. Mavor, N. Martin, I. Moszer, D. Onesime, J. Perez Martin, R. Sentandreu, E. Valentin and A.J. Brown. 2005. CandidaDB: a genome database for *Candida albicans* pathogenomics. Nucleic Acids Res. 33, D353–357.

Depree, J., G.W. Emerson and P.A. Sullivan. 1993. The cell wall of the oleaginous yeast *Trichosporon cutaneum*. J. Gen. Microbiol. 139, 2123–2133.

DePriest, P.T., N.V. Ivanova, D. Fahselt, V. Alstrup and A. Gargas. 2000. Sequences of psychrophilic fungi amplified from glacier-preserved ascolichens. Can. J. Bot. 78, 1450–1459.

Dequin, S. 2001. The potential of genetic engineering for improving brewing, wine-making, and baking yeasts. Appl. Microbiol. Biotechnol. 56, 577–588.

Dequin, S., J.-M. Salmon, H.-V. Nguyen and B. Blondin. 2003. Wine yeasts. In: T. Boekhout and V. Robert (Eds), Yeasts in Food. Beneficial and Detrimental Aspects. Behr's Verlag, Hamburg, pp. 389–412.

Derx, H.G. 1930. Étude sur les Sporobolomycètes. Ann. Mycol. 28, 1–23.

Derx, H.G. 1948. *Itersonilia* nouveau genre de Sporobolomycètes à mycelium bouclé. Bull. Bot. Gard., Buitenzorg, Ser. III, 17, 465–472.

Desmazières, J.B. 1827. Recherches microscopiques et physiologiques sur le genre *Mycoderma*. Ann. Sci. Nat. 10, 42–67.

Desper, R., and O. Gascuel. 2002. Fast and accurate phylogeny reconstruction algorithms based on the minimum-evolution principle. J. Comput. Biol. 9, 687–705.

Desper, R., and O. Gascuel. 2004. Theoretical foundation of the balanced minimum evolution method of phylogenetic inference and its relationship to weighted least-squares tree-fitting. Mol. Biol. Evol. 21, 587–598.

DeStefano, J.A., M.T. Cushion, V. Puvaanesarajah and P.D. Walzer. 1990. Analysis of *Pneumocystis carinii* cyst wall. II. Sugar composition. J. Protozool. 37, 436–441.

Deva, R., R. Ciccoli, T. Schewe, J.L.F. Kock and S. Nigram. 2000. Arachidonic acid stimulates cell growth and forms a novel oxygenated metabolite in *Candida albicans*. Biochim. Biophys. Acta 1486, 299–311.

Deva, R., R. Ciccoli, J.L.F. Kock and S. Nigram. 2001. Involvement of aspirin-sensitive oxylipins in vulvovaginal candidiasis. FEMS Microbiol. Lett. 198, 37–43.

Devlin, R.K. 2006. Invasive fungal infections caused by *Candida* and *Malassezia* species in the neonatal intensive care unit. Adv. Neonatal Care 6, 68–77.

Devos, D., S. Dokudovskaya, R. Williams, F. Alber, N. Eswar, B.T. Chait, M.P. Rout and A. Sali. 2006. Simple fold composition and modular architecture of the nuclear pore complex. Proc. Natl. Acad. Sci. USA 103, 2172–2177.

Dewick, P.M. 1997. Medicinal Natural Products. A Biosynthetic Approach. John Wiley & Sons, New York.

Dharmsthiti, S., and P. Ammaranond. 1997. Purification and characterization of lipase from a raw-milk yeast (*Trichosporon asteroides*). Biotechnol. Appl. Biochem. 2, 111–116.

di Menna, M.E. 1954. *Debaryomyces marama* n. sp., isolated from the air. J. Gen. Microbiol. 10, 65–67.

di Menna, M.E. 1957. The isolation of yeasts from soil. J. Gen. Microbiol. 17, 678–688.

di Menna, M.E. 1958a. Two new species of yeasts from New Zealand. J. Gen. Microbiol. 18, 269–272.

di Menna, M.E. 1958b. *Torulopsis ingeniosa* n. sp., from grass leaves. J. Gen. Microbiol. 19, 581–583.

di Menna, M.E. 1959. Yeasts from leaves of pasture plants. N.Z.J. Agric. Res. 2, 394–405.

di Menna, M.E. 1960. Yeasts from Antarctica. J. Gen. Micobiol. 23, 295–300.

di Menna, M.E. 1962. The antibiotic relationships of some yeasts from soil and leaves. J. Gen. Appl. Microbiol. 27, 249–257.

di Menna, M.E. 1965. *Schizoblastosporion starkeyi-henricii* Ciferri. Mycopathol. Mycol. Appl. 25, 205–212.

di Menna, M.E. 1966a. Three new yeasts from Antarctic soils: *Candida nivalis*, *Candida gelida*, and *Candida frigida* spp. n. Antonie van Leeuwenhoek 32, 25–28.

di Menna, M.E. 1966b. Yeasts in Antarctic soils. Antonie van Leeuwenhoek 32, 29–38.

Diamond, J.M. 1975. Assembly of species communities. In: M.L. Cody and J.M. Diamond (Eds), Ecology and Evolution of Communities. Harvard University Press, Cambridge, MA, pp. 342–444.

Diaz, M.R. 2007. Bead suspension arrays for identifying fungal pathogens. Microbe 2, 74–81.

Diaz, M.R., and J.W. Fell. 2000. Molecular analysis of ITS and IGS rDNA regions of the psychrophilic yeasts in the genus *Mrakia*. Antonie van Leeuwenhoek 77, 7–12.

Diaz, M.R., and J.W. Fell. 2004. High throughput detection of pathogenic yeasts in the genus *Trichosporon*. J. Clin. Microbiol. 42, 3696–3706.

Diaz, M.R., and J.W. Fell. 2005. Use of a suspension array for rapid identification of the varieties and genotypes of the *Cryptococcus neoformans* species complex. J. Clin. Microbiol. 43, 3662–3672.

Diaz, M.R., T. Boekhout, B. Theelen and J.W. Fell. 2000. Molecular sequence analyses of the intergenic spacer (IGS) associated with rDNA of the two varieties of the pathogenic yeast, *Cryptococcus neoformans*. Syst. Appl. Microbiol. 23, 535–545.

Diaz, M.R., T. Boekhout, T. Kiesling and J.W. Fell. 2005. Comparative analysis of the intergenic spacer regions and population structure of the species complex of the pathogenic yeast *Cryptococcus neoformans*. FEMS Yeast Res. 5, 1129–1140.

Diaz, M.R., T. Boekhout, B. Theelen, M. Bovers, F.J. Cabañes and J.W. Fell. 2006. Barcoding and flow cytometry as a high-throughput identification system for *Malassezia* species. J. Med. Microbiol. 55, 1197–1209.

Dib, I., and B. Nidetzky. 2008. The stabilizing effects of immobilization in D-amino acid oxidase from *Trigonopsis variabilis*. BMC Biotechnol. 8, 72–83.

Dickinson, J.R., and A.L. Kruckeberg. 2006. Carbohydrate metabolism. In: A. Querol and G.H. Fleet (Eds), Yeasts in Food and Beverages. Springer-Verlag, Berlin, pp. 215–242.

Diddens, H.A. 1934. Eine neue Pilzgattung, *Hyalodendron*. Zentralbl. Bakteriol. Parasitenkd., Abt. II, 90, 315–319.

Diddens, H.A., and J. Lodder. 1939. On some sporogenous yeasts and their imperfect stages. Mycopathologia 2, 28–36.

Diddens, H.A., and J. Lodder. 1942. Die anaskosporogenen Hefen, II. Hälfte. North-Holland, Amsterdam.

Diederich, P. 1986. Lichenicolous fungi from the Grand Duchy of Luxembourg and surrounding areas. Lejeunia 119, 1–25.

Diederich, P. 1996. The lichenicolous heterobasidiomycetes. Bibl. Lichenol. 61, 1–198.

Dien, B.S., C.P. Kurtzman, B.C. Saha and R.J. Bothast. 1996. Screening of L-arabinose fermenting yeasts. Appl. Biochem. Biotechnol. 57/58, 233–242.

Dien, B.S., M.A. Cotta and T.W. Jeffries. 2003. Bacteria engineered for fuel ethanol production, current status. Appl. Microbiol. Biotechnol. 63, 258–266.

Dietrich, F.S., S. Voegeli, S. Brachat, A. Lerch, K. Gates, S. Steiner, C. Mohr, R. Pohlmann, P. Luedi, S. Choi, R.A. Wing, A. Flavier, T.D. Gaffney and P. Philippsen. 2004. The *Ashbya gossypii* genome as a tool for mapping the ancient *Saccharomyces cerevisiae* genome. Science 304, 304–307.

Dietrichson, E. 1954. Étude d'une collection norvégienne de levures. Ann. Parasitol. Hum. Comp. 29, 271–288, 460–498.

Dik, A.J., and Y. Elad. 1999. Comparison of antagonists of *Botrytis cinerea* in greenhouse-grown cucumber and tomato under different climatic conditions. Eur. J. Plant Pathol. 105, 123–137.

Dik, A.J., and J.A. van Pelt. 1992. Interaction between phyllosphere yeasts, aphid honeydew and fungicide effectiveness in wheat under field conditions. Plant Pathol. 41, 661–675.

Dik, A.J., N.J. Fokkema and J.A. van Pelt. 1991. Consumption of aphid honeydew, a wheat yield reduction factor, by phyllosphere yeasts under field conditions. Eur. J. Plant Pathol. 97, 209–232.

Dik, A.J., G. Koning and J. Köhl. 1999. Evaluation of microbial antagonists for biological control of *Botrytis cinerea* stem infection in cucumber and tomato. Eur. J. Plant Pathol. 105, 115–122.

Dill, I., C. Ramírez and A. González. 1984. *Candida lignophila* sp. nov., a new basidiomycetous yeast anamorph from rotting wood of *Drymis winteri*. Antonie van Leeuwenhoek 50, 219–225.

Dillon, V.M., and R.G. Board. 1990. A study of sulfite-tolerant yeasts from comminuted lamb products. Biotechnol. Appl. Biochem. 12, 99–115.

Dillon, V.M., and R.G. Board. 1991. Yeasts associated with red meats. J. Appl. Bacteriol. 71, 93–108.

Ding, D.Q., Y. Tomita, A. Yamamoto, Y. Chikashige, T. Haraguchi and Y. Hiraoka. 2000. Large-scale screening of intracellular protein localization in living fission yeast cells by the use of a GFP-fusion genomic DNA library. Genes Cells 5, 169–190.

Ding, R., K.L. McDonald and J.R. McIntosh. 1993. Three-dimensional reconstruction and analysis of mitotic spindles from the yeast *Schizosaccharomyces pombe*. J. Cell Biol. 120, 141–151.

Ding, R., R.R. West, D.M. Morphew, B.R. Oakley and J.R. McIntosh. 1997. The spindle pole body of *Schizosaccharomyces pombe* enters and leaves the nuclear envelope as the cell cycle proceeds. Mol. Biol. Cell. 8, 1461–1479.

Dini, L., P.M. DU, M. Wong, A. Karstaedt, V. Fernandez and J. Frean. 2006. Prevalence of DHPS polymorphisms associated with sulfa resistance in South African *Pneumocystis jirovecii* strains. J. Eukaryot. Microbiol. 53 (Suppl. 1), S110–S111.

Dirar, H.A. 1994. Commentary – the fermented foods of the Sudan. Ecol. Food Nutr. 32, 207–218.

Dismukes, W.E., P.G. Pappas and J.D. Sobel. 2003. Clinical Mycology. Oxford University Press, Oxford.

Ditlevsen, E., and A. Hjort. 1964. *Hanseniaspora pijperi* (van der Walt et Tscheuschner) nov. comb. C.R. Trav. Lab. Carlsberg 34, 347–357.

Dittrich, H.H. 1964. Die alkoholische Vergärung der l-Apfelsäure durch *Schizosaccharomyces pombe* var. *acidodevoratus*. Zentralbl. Bakteriol. Parasitenkd., Abt. II, 118, 406–421.

Divol, B., and A. Lonvaud-Funel. 2005. Evidence for viable but nonculturable yeasts in *Botrytis*-affected wine. J. Appl. Microbiol. 99, 85–93.

Dixon, D.M., and A. Polak-Wyss. 1991. The medically important dematiaceous fungi and their identification. Mycoses 34, 1–18.

Djelal, H., F. Larher, G. Martin and A. Amrane. 2006. Effect of the dissolved oxygen on the bioproduction of glycerol and ethanol by *Hansenula anomala* growing under salt stress conditions. J. Biotechnol. 125, 95–103.

Dlauchy, D., J. Tornai-Lehoczki, L. Fülöp and G. Péter. 2003. *Pichia* (*Komagataella*) *pseudopastoris* sp. nov., a new yeast species from Hungary. Antonie van Leeuwenhoek 83, 327–332.

do Carmo-Sousa, L. 1965. *Trichosporon penicillatum* sp. n. Antonie van Leeuwenhoek 31, 153–156.

do Carmo-Sousa, L. 1969a. Distribution of yeasts in nature. In: A.H. Rose and J.S. Harrison (Eds), The Yeasts. Vol. 1. Academic Press, London, pp. 79–105.

do Carmo-Sousa, L. 1969b. Endospore formation in the genus *Trichosporon*. In: A. Kocková-Kratochvílová (Ed.), Proc. 2nd Symp. on Yeasts, 1966, Bratislava, pp. 87–92.

do Carmo-Sousa, L. 1970a. *Nematospora* Peglion. In: J. Lodder (Ed.), The Yeasts, A Taxonomic Study, 2nd edn. North-Holland, Amsterdam, pp. 441–447.

do Carmo-Sousa, L., and H.J. Phaff. 1962. An improved method for the detection of spore discharge in the Sporobolomycetaceae. J. Bacteriol. 83, 434–435.

do Carmo-Sousa, L., and N. van Uden. 1967. Reisolation of *Sarcinomyces inkin* and its transfer to the genus *Trichosporon*. Mycologia 59, 653–657.

Dobzhansky, T. 1973. Nothing in biology makes sense except in the light of evolution. Am. Biol. Teach. 35, 125–129.

Dobzhansky, T., and A.B. da Cunha. 1955. Differentiation of nutritional preferences in Brazilian species of *Drosophila*. Ecology 36, 34–39.

Dodge, C.W. 1935. Medical Mycology. Fungous Diseases of Men and Other Mammals. Mosby, St. Louis, MO.

Dodge, C.W., and M. Moore. 1936. Morphology, physiology and cytology of *Syringospora inexorabilis* (*Monilia inexorabilis*). Ann. Mo. Bot. Gard. 23, 129–150.

Dodgson, A.R., C. Pujol, D.W. Denning, D.R. Soll and A.J. Fox. 2003. Multilocus sequence typing of *Candida glabrata* reveals geographically enriched clades. J. Clin. Microbiol. 41, 5709–5717.

Dodgson, A.R., C. Pujol, M.A. Pfaller, D.W. Denning and D.R. Soll. 2005. Evidence for recombination in *Candida glabrata*. Fungal Genet. Biol. 42, 233–243.

Dolinski, K., and D. Botstein. 2005. Changing perspectives in yeast research nearly a decade after the genome sequence. Genome Res. 15, 1611–1619.

Domart-Coulon, I.J., C.S. Sinclair, R.T. Hill, S. Tambutte, S. Puverel and G.K. Ostrander. 2004. A basidiomycete isolated from the skeleton of *Pocillopora damicornis* (Scleractinia) selectively stimulates short-term survival of coral skeletogenic cells. Mar. Biol. 144, 583–592.

Dombrowski, W. 1910. Die Hefen in Milch und Milchprodukten. Zentralbl. Bakteriol. Parasitenkd., Abt. II, 28, 345–403.

Domer, J.E. 1971. Monosaccharide and chitin content of cell walls of *Histoplasma capsulatum* and *Blastomyces dermatitidis*. J. Bacteriol. 107, 870–877.

Domergue, R., I. Castano, A. de Las Penas, M. Zupancic, V. Lockatell, J.R. Hebel, D. Johnson and B.P. Cormack. 2005. Nicotinic acid limitation regulates silencing of *Candida* adhesins during UTI. Science 308, 866–870.

Dominguez-Bocanegra, A.R., T. Ponce-Noyola and J.A. Torres-Munoz. 2007. Astaxanthin production by *Phaffia rhodozyma* and *Haematococcus pluvialis*: a comparative study. Appl. Microbiol. Biotechnol. 75, 783–791.

Donachie, S.P., and M.K. Zdanowski. 1998. Potential digestive function of bacteria in krill *Euphausia superba* stomach. Aquat. Microb. Ecol. 14, 129–136.

Donk, M.A. 1960. Checklist of European Hymenomycetous Heterobasidiae. Persoonia 4, 145–335.

Donk, M.A. 1963. Proposals for conservation of some names of fungi: *Monilia* Bon. (Deuteromycetes) I. Taxon 12, 266–271.

Donnelly, S.M., D.J. Sullivan, D.B. Shanley and D.C. Coleman. 1999. Phylogenetic analysis and rapid identification of *Candida dubliniensis* based on analysis of ACT1 intron and exon sequences. Microbiology 145, 1871–1882.

Dooley, D.P., M.L. Beckius, C.K. McAllister and B.S. Jeffery. 1990. Prostatitis caused by *Hansenula fabianii*. J. Infect. Dis. 161, 1040–1041.

Dooley, D.P., M.L. Beckius and B.S. Jeffrey. 1994. Misidentification of clinical yeast isolates by using the updated Vitek Yeast Biochemical Card. J. Microbiol. 32, 2889–2892.

Dooms, L., G.L. Hennebert and H. Verachtert. 1971. Polyol synthesis and taxonomic characters in the genus *Moniliella*. Antonie van Leeuwenhoek 37, 107–118.

Doostzadeh, J., R.W. Davis, G.N. Giaever, C. Nislow and J.W. Langston. 2007. Chemical genomic profiling for identifying intracellular targets of toxicants producing Parkinson's disease. Toxicol. Sci. 95, 182–187.

Dörfler, C. 1990. Vergleichende Untersuchungen zum biochemischen Aufbau der Zellwand an Hefestadien von niederen und höheren Basidiomyceten. Bibl. Mycol. 129, 1–163.

Dorfler, J., and H.V. Amorim. 2007. Applied bioethanol technology in Brazil. Zuckerindustrie 132, 694–697.

Dorko, E., M. Kmetova, E. Pilipcinec, I. Bracokova, F. Dorko, J. Danko, E. Svicky and L. Tkacikova. 2000. Rare non-*albicans Candida* species detected in different clinical diagnoses. Fol. Microbiol. 45, 364–368.

Dorko, E., E. Pilipcinec and L. Tkacikova. 2002. Fungal diseases of the respiratory tract. Fol. Microbiol. 47, 302–304.

Dorrestein, G.M., P. Zwart and M.N. Buitellaar. 1980. Problems arising from disease during the periods of breeding and rearing canaries and other aviary birds. Tijdschr. Diergeneeskd 105, 535–543.

Doublés, J.C., and D.J. McLaughlin. 1991. A new basidiomycetous septal type: the multiperforate septum in *Kriegeria eriophori*. Am. J. Bot. 78, 1542–1548.

Doublés, J.C., and D.J. McLaughlin. 1992. Basidial development, life history and the anamorph of *Kriegeria eriophori*. Mycologia 84, 668–678.

Douglas, A.E. 1989. Mycetocyte symbiosis in insects. Biol. Rev. Cambr. Philos. Soc. 64, 409–434.

Dow, J.M., D.W. Darnall and V.D. Villa. 1983. Two distinct classes of polyuronide from the cell walls of a dimorphic fungus, *Mucor rouxii*. J. Bacteriol. 155, 1088–1093.

Dowd, P.F. 1992. Insect fungal symbionts: a promising source of detoxifying enzymes. J. Ind. Microbiol. 9, 149–161.

Dowd, P.F., and S.K. Shen. 1990. The contribution of symbiotic yeast to toxin resistance of the cigarette beetle (*Lasioderma serricorne*). Entomol. Exp. Appl. 56, 241–248.

Dragan, C.A., S. Zearo, F. Hanneman, R. Bernhardt and M. Bureik. 2005. Efficient conversion of 11-deoxycortisol to

cortisol (hydrocortisone) by recombinant fission yeast *Schizosaccharomyces pombe*. FEMS Yeast Res. 5, 621–625.

Droby, S., E. Chalutz, C. Wilson and M. Wisniewski. 1989. Characterization of the biocontrol activity of *Debaryomyces hansenii* in the control of *Penicillium digitatum* on grapefruit. Can. J. Microbiol. 35, 794–800.

Droby, S., R. Hofstein, C.L. Wilson, M. Wisniewski, B. Fridlender, L. Cohen, B. Weiss, A. Daus, D. Timar and E. Chalutz. 1993. Pilot testing of *Pichia guilliermondii*: a biocontrol agent of postharvest diseases of citrus fruit. Biol. Control 3, 4, 7–52.

Droby, S., M.E. Wisniewski, L. Cohen, B. Weiss, D. Touitou, Y. Eilam and E. Chalutz. 1997. Influence of $CaCl_2$ on *Penicillium digitatum*, grapefruit peel tissue, and biocontrol activity of *Pichia guilliermondii*. Phytopathology 87, 310–315.

Droby, S., L. Cohen, A. Daus, B. Weiss, B. Horev, E. Chalutz, H. Katz, M. Keren-Tzur and A. Shachnai. 1998. Commercial testing of Aspire: a yeast preparation for the biological control of postharvest decay of citrus. Biol. Control 12, 97–101.

Droby, S., V. Vinokur, B. Weiss, L. Cohen, A. Daus, E.E. Goldschmidt and R. Porat. 2002. Induction of resistance to *Penicillium digitatum* in grapefruit by the yeast biocontrol agent *Candida oleophila*. Phytopathology 92, 393–399.

Droby, S., M. Wisniewski, A. El-Ghaouth and C. Wilson. 2003. Influence of food additives on the control of postharvest rots of apple and peach and efficacy of the yeast-based biocontrol product Aspire. Postharvest Biol. Technol. 27, 127–135.

Dromer, F., A. Varma, O. Ronin, S. Mathoulin and B. Dupont. 1994. Molecular typing of *Cryptococcus neoformans* serotype D clinical isolates. J. Clin. Microbiol. 32, 2364–2371.

Dromer, F., A. Moulignier, B. Dupont, E. Guého, M. Baudrimont, L. Improvisi, F. Provost and G. Gonzalez-Canali. 1995. Myeloradiculitis due to *Cryptococcus curvatus* in AIDS. AIDS 9, 395–396.

Dromer, F., S. Mathoulin-Pelissier, A. Fontanet, O. Ronin, B. Dupont and O. Lortholary. French Cryptococcosis Study Group. 2004. Epidemiology of HIV-associated cryptococcosis in France (1985–2001): comparison of the pre- and post HAART eras. AIDS 18, 555–562.

Druvefors, U.A., and J. Schnürer. 2005. Mold-inhibitory activity of different yeast species during airtight storage of wheat grain. FEMS Yeast Res. 5, 373–378.

Druvefors, U., N. Jonsson, M.E. Boysen and J. Schnürer. 2002. Efficacy of the biocontrol yeast *Pichia anomala* during long-term storage of moist feed grain under different oxygen and carbon dioxide regimens. FEMS Yeast Res. 2, 389–394.

Druvefors, U.A., V. Passoth and J. Schnürer. 2005. Nutrient effect on biocontrol of *Penicillium roqueforti* by *Pichia anomala* J121 during airtight storage of wheat. Appl. Environ. Microbiol. 71, 1865–1869.

Du, Y., M. Pypaert, P. Novick and S. Ferro-Novick. 2001. Aux1p/Swa2p is required for cortical endoplasmic reticulum inheritance in *Saccharomyces cerevisiae*. Mol. Biol. Cell 12, 2614–2628.

Du, Y., S. Ferro-Novick and P. Novick. 2004. Dynamics and inheritance of the endoplasmic reticulum. J. Cell Sci. 117, 2871–2878.

du Preez, J.C., and J.P. van der Walt. 1983. Fermentation of D-xylose to ethanol by a strain of *Candida shehatae*. Biotechnol. Lett. 5, 357–362.

Du Toit, M., and I.S. Pretorius. 2000. Microbial spoilage and preservation of wine: using weapons from nature's own arsenal – a review. South Afr. J. Enol. Viticult. 21, 74–96.

Duarte, E.R., M.M. Melo, R.C. Hahn and J.S. Hamdan. 1999. Prevalence of *Malassezia* spp. in the ears of asymptomatic cattle and cattle with otitis in Brazil. Med. Mycol. 37, 159–162.

Duarte, E.R., J.C. Resende, C.A. Rosa and J.S. Hamdan. 2001. Prevalence of yeasts and mycelial fungi in bovine parasitic otitis in the State of Minas Gerais, Brazil. J. Vet. Med. B Infect. Dis. Vet. Public Health 48, 631–635.

Duarte, E.R., M.-A. Lachance and J.S. Hamdan. 2002. Identification of atypical strains of *Malassezia* spp. from cattle and dog. Can. J. Microbiol. 48, 749–752.

Dubos, R.J. 1960. Louis Pasteur, Free Lance of Science. De Capo Press, New York.

Dudley, M.W., C.Q. Sheeler, H. Wang and S. Khan. 2000. Activation of human estrogen receptor by the antiestrogens ICI 182, 780, and tamoxifen in yeast genetic systems: implications for their mechanisms of action. Proc. Natl. Acad. Sci. USA 97, 3696–3701.

Dufait, R. 1985. Présence de *Malassezia pachydermatis* (syn. *Pityrosporum canis*) sur les poils et les plumes des animaux domestiques. Bull. Soc. Fr. Mycol. Méd. 14, 19–22.

Dufait, R., R. Velho and C. de Vroey. 1987. Rapid identification of the two varieties of *Cryptococcus neoformans* by D-proline assimilation. Mykosen 30, 483.

Dufosse, L. 2006. Microbial production of food grade pigments. Food Technol. Biotechnol. 44, 313–321.

Dufour, J.-P., K. Verstrepen and G. Derdelinckx. 2003. Brewing yeasts. In: T. Boekhout and V. Robert (Eds), Yeasts in Food. Beneficial and Detrimental Aspects. Behr's Verlag, Hamburg, pp. 347–388.

Dujon, B. 2006. Yeasts illustrate the molecular mechanisms of eukaryotic genome evolution. Trends Genet. 22, 375–387.

Dujon, B., D. Sherman and G. Fisher. 2004. Genome evolution in yeasts. Nature 430, 35–44.

Duncan, C., H. Schwantje, C. Stephen, J. Cambell and K. Bartlett. 2006. *Cryptococcus gattii* in wildlife of Vancouver Island, British Columbia, Canada. J. Wildl. Dis. 42, 175–178.

Dunlap, C.A., K.O. Evans, B. Theelen, T. Boekhout and D.A. Schisler. 2007. Osmotic shock tolerance and membrane fluidity of cold-adapted *Cryptococcus flavescens* OH 182.9, previously reported as *C. nodaensis*, a biocontrol agent of fusarium head blight. FEMS Yeast Res. 7, 449–458.

Dupont, P.F., and L.R. Hedrick. 1971. Deoxyribonucleic acid base composition and numerical taxonomy of yeasts in the genus *Trichosporon*. J. Gen. Microbiol. 66, 349–359.

Duport, C., R. Sapgnoli, E. Degryse and D. Pompon. 1998. Self-sufficient biosynthesis of pregnenolone and progesterone in engineered yeast. Nat. Biotechnol. 16, 186–189.

Dutilh, B.E., V. van Noort, R.T. van der Heijden, T. Boekhout, B. Snel and M.A. Huynen. 2007. Assessment of phylogenomic and orthology approaches for phylogenetic inference. Bioinformatics 23, 815–824.

Dwidjoseputro, D., and F.T. Wolf. 1970. Microbiological studies of Indonesian fermented foodstuffs. Mycopathol. Mycol. Appl. 41, 211–222.

Dykhuizen, D.E., and L. Green. 1991. Recombination in *Escherichia coli* and the definition of biological species. J. Bacteriol. 173, 7257–7268.

Eason, R.G., N. Pourmand, W. Tongprasit, Z.S. Herman, K. Anthony, O. Jejelowo, R.W. Davis and V. Stolc. 2004. Characterization of synthetic DNA bar codes in *Saccharomyces cerevisiae* gene-deletion strains. Proc. Natl. Acad. Sci. USA 101, 11046–11051.

Ebbert, M.A., J.L. Marlowe and J.J. Burkholder. 2003. Protozoan and intracellular fungal gut endosymbionts in *Drosophila*: prevalence and fitness effects of single and dual infections. J. Invert. Pathol. 83, 37–45.

Ebert, D., M. Lipsitch and K.L. Mangin. 2000a. The effect of parasites on host population density and extinction: experimental epidemiology with *Daphnia* and six microparasites. Am. Nat. 156, 459–477.

Ebert, D., C.D. Zschokke-Rohringer and H.J. Carius. 2000b. Dose effects and density dependent regulation of two microparasites of *Daphnia magna*. Oecologia (Berlin) 122, 200–209.

Echavarri-Erasun, C. 2005. Characterization of astaxanthin biosynthesis in the yeasts *Phaffia rhodozyma* and *Xanthophyllomyces dendrorhous*. PhD Thesis, University of Wisconsin-Madison.

Echavarri-Eraun, C., and E.A. Johnson. 2004. Stimulation of astaxanthin formation in the yeast *Xanthophyllomyces dendrorhous* by the fungus *Epicoccum nigrum*. FEMS Yeast Res. 4, 511–519.

Ecker, M., R. Deutzmann, L. Lehle, V. Mrsa and W. Tanner. 2006. PIR-proteins of *Saccharomyces cerevisiae* are attached to β-1,3-glucan by a new protein–carbohydrate linkage. J. Biol. Chem. 281, 11523–11529.

Edgar, R., and K.E. Aidoo. 2001. Microflora of blanched minimally processed fresh vegetables as components of commercial chilled ready-to-use meals. Int. J. Food Sci. Technol. 36, 107–110.

Edgar, R.C. 2004. MUSCLE: multiple sequence alignment with high accuracy and high throughput. Nucleic Acids Res. 32, 1792–1797.

Edman, J.C., and K.J. Kwon-Chung. 1990. Isolation of the URA5 gene from *Cryptococcus neoformans* var. *neoformans* and its use as a selective marker for transformation. Mol. Cell. Biol. 10, 4538–4544.

Edman, J.C., J.A. Kovacs, H. Masur, D.V. Santi, H.J. Elwood and M.L. Sogin. 1988. Ribosomal RNA sequence shows *Pneumocystis carinii* to be a member of the fungi. Nature 334, 519–522.

Edwards, A.W.F., and L.L. Cavalli-Sforza. 1964. Reconstruction of evolutionary trees. In: V.H. Heywood and J. McNeill (Eds), Phenetic and Phylogenetic Classification. Systematics Association, Publ. No. 6, London, pp. 67–76.

Edwards-Ingram, L., P. Gitsham, N. Burton, G. Warhurst, I. Clarke, D. Hoyle, S.G. Oliver and L. Stateva. 2007. Genotypic and physiological characterization of *Saccharomyces boulardii*, the probiotic strain of *Saccharomyces cerevisiae*. Appl. Environ. Microbiol. 73, 2458–2467.

Efron, B. 1979. Bootstrap methods: another look at the jackknife. Ann. Stat. 7, 1–26.

Efron, B. 1985. Bootstrap confidence intervals for a class of parametric problems. Biometrika 72, 45–58.

Egli, C.M., and Th. Henick-Kling. 2001. Identification of *Brettanomyces*/*Dekkera* species based on polymorphism in the rRNA internal transcribed spacer region. Am. J. Enol. Vitic. 52, 241–247.

Eisen, J.A. 2002. Brouhaha over the other yeast. Nature 415, 845–848.

Eisenman, H.C., J.D. Nosanchuk, J.B. Webber, R.J. Emerson, T.A. Camesano and A. Casadevall. 2005. Microstructure of cell wall-associated melanin in the human pathogenic fungus *Cryptococcus neoformans*. Biochemistry 44, 3683–3693.

Eisfeld, K., F. Riffer, J. Mentges and M.J. Schmitt. 2000. Endocytotic uptake and retrograde transport of a virally encoded killer toxin in yeast. Mol. Microbiol. 37, 926–940.

Eisikowitch, D., M.A. Lachance, P.G. Kevan, S. Willis and D.L. Collins-Thompson. 1990. The role of the natural assemblage of microorganisms and selected strains of the yeast *Metschnikowia reukaufii* in controlling the germination of pollen of common milkweed, *Asclepias syriaca*. Can. J. Bot. 68, 1163–1165.

Ekendahl, S., A.H. O'Neill, E. Thomsson and K. Pedersen. 2003. Characterisation of yeasts isolated from deep igneous rock aquifers of the Fennoscandian Shield. Microb. Ecol. 46, 416–428.

Eksteen, J.M., P. van Rensburg, R.R. Cordero Otero and I.S. Pretorius. 2003. Starch fermentation by recombinant *Saccharomyces cerevisiae* strains expressing the alpha-amylase and glucoamylase genes from *Lipomyces kononenkoae* and *Saccharomycopsis fibuligera*. Biotechnol. Bioeng. 84, 639–646.

El-Batal, A.I. 2002. Continuous production of L-phenylalanine by *Rhodotorula glutinis* immobilized cells using a column reactor. Acta Microbiol. Pol. 51, 153–169.

El-Ghaouth, A., J.L. Smilanick, G.E. Brown, A. Ippolito, M. Wisniewski and C.L. Wilson. 2000a. Applications of *Candida saitoana* and glycolchitosan for the control of postharvest diseases of apple and citrus fruit under semicommercial conditions. Plant Dis. 84, 243–248.

El-Ghaouth, A., J.L. Smilanick and C.L. Wilson. 2000b. Enhancement of the performance of *Candida saitoana* by the addition of glycolchitosan for the control of postharvest decay of apple and citrus fruit. Postharvest Biol. Technol. 19, 103–110.

El-Ghaouth, A., J.L. Smilanick, M. Wisniewski and C.L. Wilson. 2000c. Improved control of apple and citrus fruit decay with a combination of *Candida saitoana* and 2-deoxy-D-glucose. Plant Dis. 84, 249–253.

El-Ghauth, A., C. Wilson and M. Wisniewski. 2001a. Evaluation of two biocontrol products, Bio-Coat and Biocure, for control of postharvest decay of pome and citrus fruit. IOBC wprs Bull. 24, 161–165.

El-Ghaouth, A., J. Smilanick, G.E. Brown, A. Ippolito and C.L. Wilson. 2001b. Control of decay of apple and citrus fruits in semicommercial tests with *Candida saitoana* and 2-deoxy-D-glucose. Biol. Control 20, 96–101.

El Ghaouth, A., C.L. Wilson and M. Wisniewski. 2003. Control of postharvest decay of apple fruit with *Candida saitoana* and induction of defense responses. Phytopathology 93, 344–348.

El Halouat, A., and J.M. Debevere. 1996. Influence of modified atmosphere and preservatives on the growth of

Zygosaccharomyces rouxii isolated from dried fruits. Int. J. Food Microbiol. 33, 219–229.

El-Masry, H.G., and J. Zsolt. 1968. *Geotrichum novakii* n. sp. Acta Univ. Szeged., Acta Biol., N.S. 12, 67–70.

El-Mehalawy, A.A. 2004. The rhizospere yeast fungi as biocontrol agents for wilt disease of kidney bean caused by *Fusarium oxysporum*. Int. J. Agric. Biol. 6, 310–316.

El-Mehalawy, A.A., N.M. Hassanein, H.M. Khater, El-Din E.A. Karam and Y.A. Youssef. 2004. Influence of maize root colonization by the rhizosphere actinomycetes and yeast fungi on plant growth and on the biological control of late wilt disease. Int. J. Agric. Biol. 6, 599–605.

El-Tarabily, K.A. 2004. Suppression of *Rhizoctonia solani* diseases of sugar beet by antagonistic and plant growth-promoting yeasts. J. Appl. Microbiol. 96, 69–75.

El-Tarabily, K.A., and K. Sivasithamparam. 2006. Potential of yeasts as biocontrol agents of soil-borne fungal plant pathogens and as plant growth promoters. Mycoscience 47, 25–35.

Elad, Y., J. Köhl and N.J. Fokkema. 1994. Control of infection and sporulation of *Botrytis cinerea* on bean and tomato by saprophytic yeasts. Phytopathology 84, 1193–1200.

Elez-Martinez, P., J. Escola-Hernandez, R.C. Solvia-Fortury and O.M. Martin-Belloso. 2004. Inactivation of *Saccharomyces cerevisiae* suspended in orange juice using high-intensity pulsed electric fields. J. Food Prot. 67, 2596–2602.

Elinov, N.P., E.P. Anan'eva and G.A. Iaskovich. 1999. Activity of exoglycans as sorbents of heavy metal ions. Prikl. Biokhim. Mikrobiol. 35, 190–193. In Russian.

Ellis, D.H., and T.J. Pfeiffer. 1990. Natural habitat of *Cryptococcus neoformans* var. *gattii*. J. Clin. Microbiol. 28, 1642–1644.

Ells, R., J.L.F. Kock and C.H. Pohl. 2009. *Candida albicans* or *Candida dubliniensis*? Mycoses. doi:10.1111/j.1439-0507.2009.01759.x.

Elmer, P.A.G., and T. Reglinski. 2006. Biosuppression of *Botrytis cinerea* in grapes. Plant Pathol. 55, 155–177.

Emmerich, W., and F. Radler. 1983. The anaerobic metabolism of glucose and fructose by *Saccharomyces bailii*. J. Gen. Microbiol. 129, 3311–3318.

Enache-Angoulvant, A., and C. Hennequin. 2005. Invasive *Saccharomyces* infection, a comprehensive review. Clin. Infect. Dis. 41, 1559–1568.

Enache-Angoulvant, A., J. Chandenier, F. Symones, P. Lacube, J. Bolognini, C. Douchet, J.L. Poirot and C. Hennequin. 2007. Molecular identification of *Cryptococcus neoformans* serotypes. J. Clin. Microbiol. 45, 1261–1265.

Enczi, K., M. Yamaguchi and M. Sipiczki. 2007. Morphology transition genes in the dimorphic fission yeast *Schizosaccharomyces japonicus*. Antonie van Leeuwenhoek 92, 143–154.

Endler, J.A. 1982. Problems in distinguishing historical from ecological factors in biogeography. Am. Zool. 22, 441–452.

Endoh, R., M. Suzuki and Y. Benno. 2008a. *Ambrosiozyma kamigamensis* sp. nov. and *Ambrosiozyma neoplatypodis* sp. nov., two new ascomycetous yeasts from ambrosia beetle galleries. Antonie van Leeuwenhoek 94, 365–376.

Endoh, R., M. Suzuki and Y. Benno. 2008b. *Pichia rarassimilans* sp. nov., a novel yeast species isolated from body surface of the ambrosia beetle *Platypus quercivorus*. J. Gen. Appl. Microbiol. 54, 181–186.

Endoh, R., M. Suzuki, Y. Benno and F. Kazuyoshi. 2008c. *Candida kashinagacola* sp. nov., *C. pseudovanderkliftii* sp. nov. and *C. vanderkliftii* sp. nov., three new yeasts from ambrosia beetle-associated sources. Antonie van Leeuwenhoek 94, 389–402.

Engel, G., and N. Rosch. 1995. Development of yeasts during production and ripening of Harzer cheese (yellow cheese type). Kieler Milchwirtsch. Forschungsber. 47, 97–112.

Engel, L. 1877. Untitled. Bull. Soc. Sci. de Nancy Sér II, 3, Fascicule VI, 20.

Erasmus, D.J., G.K. van der Merwe and H.J. van Vuren. 2003. Genomic-wide expression analysis: metabolic adaption of *Saccharomyces cerevisiae* to high sugar stress. FEMS Yeast Res. 3, 375–399.

Eriksson O.E. (Ed.) 2000. Notes on ascomycete systematics. Nos 29403127. Myconet 5, 135.

Eriksson, O.E., and K. Winka. 1997. Supraordinal taxa of the Ascomycota. Myconet 1, 1–16.

Eriksson, O.E. 1994. *Pneumocystis carinii*, a parasite in lungs of mammals, referred to a new family and order (Pneumocystidaceae, Pneumocystidales, Ascomycota). Syst. Ascomycetum 13, 165–180.

Eriksson, O.E., H.-O. Baral, R.S. Currah, K. Hansen, C.P. Kurtzman, G. Rambold and T. Læssú. 2003. Outline of Ascomycota. Myconet 9, 1–89.

Erixon, P., B. Svennblad, T. Britton and B. Oxelman. 2003. Reliability of Bayesian posterior probabilities and bootstrap frequencies in phylogenetics. Syst. Biol. 52, 665–673.

Erke, K.H. 1976. Light microscopy of basidia, basidiospores and nuclei in spores and hyphae of *Filobasidiella neoformans* (*Cryptococcus neoformans*). J. Bacteriol. 128, 445–455.

Erwin, J.A. 1973. Comparative biochemistry of fatty acids in eukaryotic microorganisms. In: J.A. Erwin (Ed.), Lipids and biomembranes of eukaryotic microorganisms. Academic Press, New York, pp. 41–142.

Escandon, P., A. Sanchez, M. Martinez, W. Meyer and E. Castaneda. 2006. Molecular epidemiology of clinical and environmental isolates of the *Cryptococcus neoformans* species complex reveals a high genetic diversity and the presence of the molecular type VGII mating type a in Colombia. FEMS Yeast Res. 6, 625–635.

Espinel-Ingroff, A., L. Stockman, G. Roberts, D. Pincus, J. Pollack and J. Marler. 1998. Comparison of RapID Yeast Plus system with API 20C system for identification of common, new and emerging yeast pathogens. J. Clin. Microbiol. 36, 883–886.

Esser, K., and J.W. Bennett (Eds). 2002. Industrial Applications, Vol. X. The Mycota. A Comprehensive Treatise on Fungi as Experimental Systems for Basic and Applied Research. Springer-Verlag, Berlin.

Esteve-Zarzoso, B., C. Belloch, F. Uruburu and A. Querol. 1999. Identification of yeasts by RFLP analysis of the 5.8S rRNA gene and the two ribosomal internal transcribed spacers. Int. J. Syst. Bacteriol. 49, 329–337.

Esteve-Zarzoso, B., M.J. Peris-Torán, D. Ramón and A. Querol. 2001a. Molecular characterisation of *Hanseniaspora* species. Antonie van Leeuwenhoek 80, 85–92.

Esteve-Zarzoso, B., M.J. Peris-Torán, E. García-Maiquez, F. Uruburu and A. Querol. 2001b. Yeast population dynamics during the fermentation and biological aging of sherry wines. Appl. Environ. Microbiol. 67, 2056–2061.

Etchells, J.L., and T.A. Bell. 1950a. Film yeasts on commercial cucumber brines. Food Technol. 4, 77–83.

Etchells, J.L., and T.A. Bell. 1950b. Classification of yeasts from the fermentation of commercially brined cucumbers. Farlowia 4, 87–112.

Ettayebi, K., F. Errachidi, L. Jamai, M.A. Tahri-Jouti, K. Sendide and M. Ettayebi. 2003. Biodegradation of polyphenols with immobilized *Candida tropicalis* under metabolic induction. FEMS Microbiol. Lett. 223, 215–219.

Evans, D., and R. Das. 2005. Monoclonal Antibody Therapies: Evolving into a $30 Billion Market. Data Monitor, London, UK.

Evans, D.G., L.K. Everis and G.P. Betts. 2004. Use of survival analysis and classification and regression trees to model the growth/no growth boundary of spoilage yeasts as affected by alcohol, pH, sucrose, sorbate and temperature. Int. J. Food Microbiol. 92, 55–67.

Evans, E.E. 1949. An immunologic comparison of twelve strains of *Cryptococcus neoformans* (*Torula histolytica*). Proc. Soc. Exp. Biol. Med. 71, 644–646.

Evans, E.E. 1950. The antigenic composition of *Cryptococcus neoformans*. I. A serologic classification by means of the capsular and agglutination reactions. J. Immunol. 64, 423–430.

Evans, R.G. 1965. *Sporobolomyces* as a cause of respiratory allergy. Acta Allergol. 20, 197–205.

Faber, K. 2004. Biotransformations in Organic Chemistry. A Textbook, 5th edn. Springer-Verlag, Heidelberg.

Fabian, F.W., and H.H. Hall. 1933. Yeasts found in fermented maple syrup. Zentralbl. Bakteriol. Parasitenkd., Abt. II, 89, 31–47.

Fabian, F.W., and R.I. Quinet. 1928. A study of the cause of honey fermentation. Tech. Bull. Agric. Exp. Stn. Michigan St. Coll. 92, 1–41.

Fadda, M.E., S. Cosentino, M. Deplano and F. Palmas. 2001. Yeast populations in Sardinian feta cheese. Int. J. Food Microbiol. 69, 153–156.

Fadda, M.E., V. Mossa, M.B. Pisano, M. Deplano and S. Cosetino. 2004. Occurrence and characterization of yeasts isolated from artisanal Fiore Sardo cheese. Int. J. Food Microbiol. 95, 51–59.

Faergemann, J. 2002. Atopic dermatitis and fungi. Clin. Microbiol. Rev. 15, 545–563.

Fairclough, O. 2002. Attempt to poison cider uncovered. The Times, 5 April 2002.

Fairweather, J.K., T. Karoli and V. Ferro. 2004. The synthesis of phosphorylated disaccharide components of the extracellular phosphomannan of *Pichia* (*Hansenula*) *holstii* NRRL Y-2448. Bioorg. Med. Chem. 12, 6063–6075.

Fairweather, J.K., E. Hammond, K.D. Johnstone and V. Ferro. 2008. Synthesis and heparanase inhibitory activity of sulfated mannooligosaccharides related to the antiangiogenic agent PI-88. Bioorg. Med. Chem. 16, 699–709.

Faizutdinova, R.N., N.E. Suzina, V.I. Duda, L.E. Petrovskaya and D.A. Gilichinsky. 2005. Yeasts isolated from ancient permafrost. In: J.D. Castello and S.O. Rogers (Eds), Life in Ancient Ice. Princeton University Press, Princeton, NJ, pp. 118–126.

Falcão de Morais, J.D., and M.H. Dália Maia. 1959. Estudos de microorganismos encontrados em leitos de despéjos de caldas de destilarias de Pernambuco, II. Una nova espécie de *Hansenula*: *H. polymorpha*. An. Esc. Super. Quim. Univ. Recife 1, 15–20.

Fall, R., P. Phelps and D. Spindler. 1984. Bioconversion of xylan to triglycerides by oil-rich yeasts. Appl. Environ. Microbiol. 47, 1130–1134.

Fan, M., L.C. Chen, M.A. Ragan, R.R. Gutell, J.R. Warner, B.P. Currie and A. Casadevall. 1995. The 5S rRNA and the rRNA intergenic spacer of the two varieties of *Cryptococcus neoformans*. J. Med. Vet. Mycol. 33, 215–221.

Fan, Q., and S. Tian. 2000. Postharvest biological control of *Rhizopus* rot of nectarine fruits by *Pichia membranefaciens*. Plant Dis. 84, 1212–1216.

Fan, Q., and S.P. Tian. 2001. Postharvest biological control of grey mold and blue mold on apple by *Cryptococcus albidus* (Saito) Skinner. Postharvest Biol. Technol. 21, 341–350.

Fan, Q., S.P. Tian, S. Liu and Y. Xu. 2002. Production of β-1,3-glucanase and chitinase of two biocontrol agents and their possible modes of action. Chin. Sci. 47, 292–296.

Fan, S.-R., F.-Y. Bai, Q.-P. Liao, Z.-H. Liu, J. Li and X.-P. Liu. 2008. Genotype distribution of *Candida albicans* strains associated with different conditions of vulvovaginal candidiasis, as revealed by microsatellite typing. Sex. Transm. Infect. 84, 103–106.

Fang, S.-F., T.-C. Yen and J.-C. Yue. 1966. Identification of some species of *Geotrichum*. Acta Microbiol. Sin. 12, 64–73.

Fares, M.A., K.P. Byrne and K.H. Wolfe. 2006. Rate asymmetry after genome duplication causes substantial long-branch attraction artifacts in the phylogeny of *Saccharomyces* species. Mol. Biol. Evol. 23, 245–253.

Farhi, M., N. Dudareva, T. Masci, D. Weiss, A. Vainstein and H. Abeliovich. 2006. Synthesis of the food flavoring methyl benzoate by genetically engineered *Saccharomyces cerevisiae*. J. Biotechnol. 122, 307–315.

Farid, S.S. 2006. Process economics of industrial monoclonal antibody manufacture. J. Chromatogr. B. 848, 8–18.

Farmer, L.J. 1965. The phloem–yeast complex during infestations of the mountainpine beetle in lodgepole pine. Diss. Abstr. 26, 1304–1305.

Farr, D.F., A.Y. Rossman, M.E. Palm and E.B. McCray. 2006. Fungal Databases. Systematic Botany and Mycology Laboratory, ARS, USDA.

Farrell, A.E., R.J. Plevin, B.T. Tuner, A.D. Jones, M. O'Hare and D.M. Kammen. 2006. Ethanol can contribute to energy and environmental goals. Science 311, 506–508.

Farrell, B.D., A.S. Sequeira, B.C. O′Meara, B.B. Normark, J.H. Chung and B.H. Jordal. 2001. The evolution of agriculture in beetles (Curculionidae: Scolytinae and Platypodinae). Evolution 55, 2011–2027.

Farris, J.S. 1969. A succesive approximations approach to character weighting. System. Zool. 18, 374–385.

Farris, J.S. 1977. Phylogenetic analysis under Dollo's law. System. Zool. 26, 77–88.

Farris, J.S. 1989a. The retention index and homoplasy excess. System. Zool. 38, 406–407.

Farris, J.S. 1989b. The retention index and the rescaled consistency index. Cladistics 5, 417–419.

Farris, J.S., V.A. Albert, M. Källersjö, D. Lipscomb and A.G. Kluge. 1996. Parsimony jackknifing outperforms neighbor-joining. Cladistics 12, 99–124.

Farris, S.H. 1965. Repositories of symbiotic fungi in ambrosia beetle *Monarthrum scutellare* Lec. (Coleoptera: Scolytidae). Proc. Entomol. Soc. B.C 62, 30–33.

Fay, J.C., and J.A. Benavides. 2005. Evidence for domesticated and wild populations of *Saccharomyces cerevisiae*. PloS Genet. 1, 0066–0071.

Fayod, V. 1885. Notes sur quelques champignons parasites nouveaux ou peu connus. Ann. Sci. Nat. Sér. 7, 2, 28–54.

Federici, F. 1985. Production, purification and partial characterization of an endo-polygalacturonase from *Cryptococcus albidus* var. *albidus*. Antonie van Leeuwenhoek 51, 139–150.

Federici, F., G.F. Montedoro, M. Servili and M. Petruccioli. 1988. Pectic enzyme production by *Cryptococcus albidus* var. *albidus* on olive oil vegetation waters enriched with sunflower calathide meal. Biol. Wastes 25, 291–301.

Fell, J.W. 1961. A new species of *Saccharomyces* isolated from a subtropical estuary. Antonie van Leeuwenhoek 27, 27–30.

Fell, J.W. 1966. *Sterigmatomyces*, a new fungal genus from marine areas. Antonie van Leeuwenhoek 32, 99–104.

Fell, J.W. 1967. Distribution of yeasts in the Indian Ocean. Bull. Mar. Sci. 17, 454–470.

Fell, J.W. 1970a. *Sterigmatomyces* Fell. In: J. Lodder (Ed.), The Yeasts, A Taxonomic Study, 2nd edn. North-Holland, Amsterdam, pp. 1229–1234.

Fell, J.W. 1970b. Yeasts with heterobasidiomycetous life cycles. In: D.G. Ahearn (Ed.), Recent Trends in Yeast Research, Spectrum, Vol. I. Georgia State University, Atlanta, GA, pp. 49–66.

Fell, J.W. 1974a. Distribution of yeasts in water masses of the Southern Ocean. In: R. Colwell and R. Morita (Eds), Effect of the Ocean Environment on Microbial Activities. University Park Press.

Fell, J.W. 1974b. Heterobasidiomycetous yeasts *Leucosporidium* and *Rhodosporidium*. Their systematics and sexual incompatibility systems. Trans. Mycol. Soc. Jpn 15, 316–323.

Fell, J.W. 1976. Yeasts in oceanic regions. In: E.B.G. Jones (Ed.), Recent Advances in Aquatic Mycology. Elek Science, London, pp. 93–124.

Fell, J.W. 1984a. Teliospore-forming yeasts. In: N.J.W. Kreger-van Rij (Ed.), The Yeasts, A Taxonomic Study, 3rd edn. Elsevier, Amsterdam, pp. 491–495.

Fell, J.W. 1984b. *Sympodiomyces* Fell et Statzell. In: N.J.W. Kreger-van Rij (Ed.), The Yeasts, A Taxonomic Study, 3rd edn. Elsevier, Amsterdam, pp. 930–932.

Fell, J.W. 1993. Rapid identification of yeast species using three primers in a polymerase chain reaction. Mol. Mar. Biol. Biotechnol. 2, 174–180.

Fell, J.W., and G.M. Blatt. 1999. Separation of strains of the yeasts *Xanthophyllomyces dendrorhous* and *Phaffia rhodozyma* based on rDNA IGS and ITS sequence analysis. J. Ind. Microbiol. Biotechnol. 23, 677–681.

Fell, J.W., and I.L. Hunter. 1968. Isolation of heterothallic yeast strains of *Metschnikowia* Kamienski and their mating reactions with *Chlamydozyma* Wickerham spp. Antonie van Leeuwenhoek 34, 365–376.

Fell, J.W., and I.L. Hunter. 1974. *Torulopsis austromarina* sp. nov. A yeast isolated from the Antarctic Ocean. Antonie van Leeuwenhoek 40, 307–310.

Fell, J.W., and S.A. Meyer. 1967. Systematics of yeast species in the *Candida parapsilosis* group. Mycopathol. Mycol. Appl. 32, 177–193.

Fell, J.W., and H.J. Phaff. 1967. Three new yeasts: *Cryptococcus dimennae, Cryptococcus kuetzingii* and *Cryptococcus lactativorus* spp. n. Antonie van Leeuwenhoek 33, 464–472.

Fell, J.W., and H.J. Phaff. 1970. *Leucosporidium* Fell, Statzell, Hunter et Phaff. In: J. Lodder (Ed.), The Yeasts, A Taxonomic Study. Elsevier, Amsterdam, pp. 776–802.

Fell, J.W., and J.I. Pitt. 1969. Taxonomy of the yeast genus *Metschnikowia*: a correction and a new variety. J. Bacteriol. 98, 853–854.

Fell, J.W., and G. Scorzetti. 2004. Reassignment of the basidiomycetous yeasts *Trichosporon pullulans* to *Guehomyces pullulans* gen. nov., comb. nov. and *Hyalodendron lignicola* to *Trichosporon lignicola* comb. nov. Int. J. Syst. Evol. Microbiol. 54, 995–998.

Fell, J.W., and A.C. Statzell. 1971. *Sympodiomyces* gen. n., a yeast-like organism from southern marine waters. Antonie van Leeuwenhoek 37, 359–367.

Fell, J.W., and A. Statzell-Tallman. 1980a. *Rhodosporidium paludigenum* sp. nov. A basidiomycetous yeast from intertidal waters of South Florida. Int. J. Syst. Bacteriol. 30, 658–659.

Fell, J.W., and A. Statzell-Tallman. 1980b. Mating between strains of the yeasts *Aessosporon salmonicolor* and *Sporobolomyces* spp. Int. J. Syst. Bacteriol. 30, 206–207.

Fell, J.W., and A. Statzell-Tallman. 1981. Heterothallism in the basidiomycetous yeast genus *Sporidiobolus* Nyland. Curr. Microbiol. 5, 77–82.

Fell, J.W., and A. Statzell-Tallman. 1982. Multiple allelic incompatibility factors among bifactorial strains of the yeast *Leucosporidium* (*Candida*) *scottii*. Curr. Microbiol. 7, 213–216.

Fell, J.W., and A. Statzell-Tallman. 1984. *Sporidiobolus* Nyland. In: N.J.W. Kreger-van Riji (Ed.), The Yeasts, A Taxonomic Study, 3rd edn. Elsevier, Amsterdam, pp. 532–540.

Fell, J.W., and A. Statzell-Tallman. 1992. Systematic placement of the basidiomycetous yeast *Cystofilobasidium lari-marini* comb. nov. as predicted by rRNA nucleotide sequence analysis. Antonie van Leeuwenhoek 62, 209–213.

Fell, J.W., and A. Statzell-Tallman. 1998a. *Cryptococcus* Vuillemin. In: C.P. Kurtzman and J.W. Fell (Eds), The Yeasts, A Taxonomic Study, 4th edn. Elsevier, Amsterdam, pp. 742–767.

Fell, J.W., and A. Statzell-Tallman. 1998b. *Rhodosporidium* Banno. In: C.P. Kurtzman and J.W. Fell (Eds), The Yeasts, A Taxonomic Study, 4th edn. Elsevier, Amsterdam, pp. 678–692.

Fell, J.W., and A. Statzell-Tallman. 1998c. *Rhodotorula* F.C. Harrison. In: C.P. Kurtzman and J.W. Fell (Eds), The Yeasts, A Taxonomic Study, 4th edn. Elsevier Science, Amsterdam, pp. 800–827.

Fell, J.W., and A. Statzell-Tallman. 1998d. The genus *Mrakia*. In: C. P. Kurtzman and J.W. Fell (Eds), The Yeasts, A Taxonomic Study, 4th edn Elsevier, Amsterdam, pp. 667–668.

Fell, J.W., A. Statzell, I.L. Hunter and H.J. Phaff. 1969. *Leucosporidium* gen. nov. The heterobasidiomycetous stage of several yeasts of the genus *Candida*. Antonie van Leeuwenhoek 35, 433–462.

Fell, J.W., I.L. Hunter and A.S. Tallman. 1973. Marine basidiomycetous yeasts (*Rhodosporidium* spp. n.) with tetrapolar and multiple allelic bipolar mating systems. Can. J. Microbiol. 19, 643–657.

Fell, J.W., A. Statzell-Tallman and C.P. Kurtzman. 1984a. *Sterigmatomyces* Fell. In: N.J.W. Kreger-van Rij (Ed.), The Yeasts, A Taxonomic Study, 3rd edn. Elsevier, Amsterdam, pp. 921–929.

Fell, J.W., A. Statzell-Tallman and D.G. Ahearn. 1984b. *Rhodotorula* Harrison. In: N.J.W. Kreger-van Rij (Ed.), The Yeasts, A Taxonomic Study, 3rd edn. Elsevier, Amsterdam, pp. 893–905.

Fell, J.W., C.P. Kurtzman, A.S. Tallman and J.D. Buck. 1988. *Rhodosporidium fluviale* sp. nov., a homokaryotic red yeast from a subtropical brackish environment. Mycologia 80, 560–564.

Fell, J.W., C.P. Kurtzman and K.J. Kwon-Chung. 1989. Proposal to conserve *Cryptococcus* (Fungi). Taxon 38, 151–152.

Fell, J.W., A. Statzell-Tallman, M.J. Lutz and C.P. Kurtzman. 1992. Partial rRNA sequences in marine yeasts: a model for identification of marine eukaryotes. Mol. Mar. Biol. Biotechnol. 1, 175–186.

Fell, J.W., T. Boekhout and D.W. Freshwater. 1995. The role of nucleotide sequence analysis in the systematics of the yeast genera *Cryptococcus* and *Rhodotorula*. Stud. Mycol. 38, 129–146.

Fell, J.W., G.M. Blatt and A. Statzell-Tallman. 1998. Validation of the basidiomycetous yeast, *Sporidiobolus microsporus* sp. nov., based on phenotypic and molecular analyses. Antonie van Leeuwenhoek 74, 265–270.

Fell, J.W., H. Roeijmans and T. Boekhout. 1999. Cystofilobasidiales, a new order of basidiomycetous yeasts. Int. J. Syst. Bacteriol. 49, 907–913.

Fell, J.W., T. Boekhout, Á. Fonseca, G. Scorzetti and A. Statzell-Tallman. 2000. Biodiversity and systematics of basidiomycetous yeasts as determined by large-subunit rDNA D1/D2 domain sequence analysis. Int. J. Syst. Evol. Microbiol. 50, 1351–1372.

Fell, J.W., T. Boekhout, Á. Fonseca and J.P. Sampaio. 2001. Basidiomycetous yeasts. In: K. Esser and P.A. Lemke (Eds), The Mycota, A Comprehensive Treatise on Fungi as Experimental Systems for Basic and Applied Research, Vol. II, systematics and Evolution, Part B. D.J. McLaughlin, E.G. McLaughlin and P.A. Lemke (Vol. Eds). Springer, Berlin, pp. 3–35.

Fell, J.W., G. Scorzetti, A. Statzell-Tallman, N. Pinel and D. Yarrow. 2002. Recognition of the basidiomycetous yeast *Sporobolomyces ruberrimus* sp. nov. as a distinct species based on molecular and morphological analyses. FEMS Yeast Res. 1, 265–270.

Fell, J.W., A. Statzell-Tallman and C.P. Kurtzman. 2004. *Lachancea meyersii* sp. nov., an ascosporogenous yeast from mangrove regions in the Bahama Islands. Stud. Mycol. 50, 359–363.

Fell, J.W., G. Scorzetti, L. Connell and S. Craig. 2006. Biodiversity of micro-eukaryotes in Antarctic Dry Valley soils with $<5\%$ soil moisture. Soil Biol. Biochem. 38, 3107–3119.

Fell, J.W., G. Scorzetti, A. Statzell-Tallman and K. Boundy-Mills. 2007. Molecular diversity and intragenomic variability in the yeast genus *Xanthophyllomyces*: the origin of *Phaffia rhodozyma*? FEMS Yeast Res. 7, 1399–1408.

Felse, P.A., V. Shah, J. Chan, K.J. Rao and R.A. Gross. 2007. Sophorolipid biosynthesis by *Candida bombicola* from industrial fatty acid residues. Enzyme Microb. Technol. 40, 316–323.

Felsenstein, J. 1973. Maximum likelihood and minimum-steps methods for estimating evolutionary trees from data on discrete characters. Syst. Zool. 22, 240–249.

Felsenstein, J. 1981. Evolutionary trees from DNA sequences: a maximum likelihood approach. J. Mol. Evol. 17, 368–376.

Felsenstein, J. 1985. Confidence limits on phylogenies: an approach using the bootstrap. Evolution 39, 783–791.

Felsenstein, J. 2004. Inferring Phylogenies. Sinauer, Sunderland, MA, 664pp.

Felsenstein, J. 1978a. The number of evolutionary trees. Syst. Zool. 27, 27–33.

Felsenstein, J. 1978b. Cases in which parsimony or compatibility methods will be positively misleading. Syst. Zool. 27, 401–410.

Fenchel, T., and B.J. Finlay. 2004. The ubiquity of small species: patterns of local and global diversity. Bioscience 54, 777–784.

Fenn, J.P. 2007. Update of medically important yeasts and a practical approach to their identification. Lab. Med. 38, 178–183.

Fernandez-Arroyo, L., D. Marin, A.G. de Segura, D. Linde, M. Alcalde, P. Gutierrez-Alonso, I. Ghazi, F.J. Plou, M. Fernandez-Lobato and A. Ballesteros. 2007. Transformation of maltose into prebiotic isomalto-oligosaccharides by a novel alpha-glucosidase from *Xanthophyllomyces dendrorhous*. Process Biochem. 42, 1530–1536.

Fernandez-Espinar, T., E. Barrio and A. Querol. 2003. Analysis of the genetic variability in the species of the *Saccharomyces sensu stricto* complex. Yeast 20, 1213–1226.

Fernandez-Espinar, M.T., P. Martorell, R. de Llanos and A. Querol. 2006. Molecular methods to identify and characterize yeasts in foods and beverages. In: A. Querol and G.H. Fleet (Eds), Yeast in Food and Beverages. Springer, Berlin, pp. 55–82.

Fernández Gonzalez, M.J., P. García García, A. Garrido Fernández and M.C. Durán Quintana. 1993. Microflora of the aerobic preservation of directly brined green olives from *Hojiblanca* cultivar. J. Appl. Bacteriol. 75, 226–233.

Ferraris, T. 1899. Contribuzione allo studio dei miceti degli agrumi. Di un nuovo ifomiceti parasitica nei fruti d'Arancio. Malpighia 13, 368–381.

Ferreira, J.D., and H.J. Phaff. 1959. Life cycle and nuclear behavior of a species of the yeast genus *Schwanniomyces*. J. Bacteriol. 78, 352–361.

Ferrer, M., A. Beloqui and P.N. Golyshin. 2007a. Microbial metagenomes: moving forward industrial biotechnology. J. Chem. Technol. Biotechnol. 82, 421–423.

Ferrer, M., O. Golyshina, A. Beloqui and P.N. Golyshin. 2007b. Mining enzymes from extreme environments. Curr. Opin. Microbiol. 10, 207–214.

Ferro, V., K. Fewings, M.C. Palermo and C. Li. 2001. Large-scale preparation of the oligosaccharide phosphate fraction of *Pichia holstii* NRRL Y-2448 phosphomannan for use in the manufacture of PI-88. Carbohydr. Res. 332, 183–189.

Ferro, V., C. Li, K. Fewings, M.C. Palermo, R.J. Linhardt and T. Toida. 2002. Determination of the composition of the oligosaccharide phosphate fraction of *Pichia* (*Hansenula*) *holstii* NRRL Y–2448 phosphomannan by capillary electrophoresis and HPLC. Carbohydr. Res. 337, 139–146.

Fiasson, J.-L. 1967. Recherche chimiotaxonomique sur les champignons. Les caroténoïdes de *Sporidiobolus johnsonii* Nyland. C.R. Acad. Sci. Paris, Ser. D, 264, 2744–2745.

Fiasson, J.-L. 1972. Recherche des caroténoïdes chez diverses levures anascosporeés. C.R. Acad. Sci. Ser. D, 247, 3465–3467.

Fiasson, J.-L., M. Trouilloud and A. Grange. 1973. Variation de contenu pigmentaire de *Sporidiobolus johnsonii* (Sporobolomycétacéae) sous l'influence de divers facteurs de milieu. Rev. Mycol. 37, 48–59.

Fickers, P., P.H. Bennett, Y. Wache, A. Marty, S. Mauersberger, M.S. Smit and J.-M. Nicaud. 2005. Hydrophobic substrate utilisation by the yeast *Yarrowia lipolytica*, and its potential applications. FEMS Yeast Res. 5, 527–543.

Fidalgo-Jiménez, A., H.-M. Daniel, P. Evrard, C. Decock and M.-A. Lachance. 2008. *Metschnikowia cubensis* sp. nov., a new yeast species isolated from flowers in Cuba. Int. J. Syst. Evol. Microbiol. 58, 2955–2961.

Fidel, P.L. Jr., J.A. Vasquez and J.D. Sobel. 1999. *Candida glabrata*: review of epidemiology, pathogenesis, and clinical disease with comparison to *C. albicans*. Clin. Microbiol. Rev. 12, 80–96.

Fields, S., and O. Song. 1989. A novel genetic system to detect protein–protein interactions. Nature 340, 245–246.

Figueroa, D.L., M.A. Resende and M.A.L. Bragança. 2006. *Candida azymoides* sp. n., a yeast species from tropical fruits and larva (Ascomycota) of *Anastrepha mucronota* (Diptera: Tephritidae). Lundiana 7, 83–86.

Filion, T., S. Kidd and K. Aguirre. 2006. Isolation of *Cryptococcus laurentii* from Canada goose guano in rural upstate New York. Mycopathologia 162, 363–368.

Filippich, L.J., and R.A. Perry. 1993. Drug trials against megabacteria in budgerigars (*Melopsittacus undulatus*). Aust. Vet. Prac. 23, 184–189.

Filippich, L.J., D.A. O'Boyle, R. Webb and J.A. Fuerst. 1993. Megabacteria in birds in Australia. Aust. Vet. Prac. 23, 72–76.

Filippov, G.S. 1932. Porča fruktovyh konservov, vyzvannaja drozzevym gribkom. Tr. Cent. Nauchno-Issled. Biohim. Inst. Pisc. Vkus. Prom. Narkomsnaba Sojuza SSR 2, 26–32.

Filonow, A.B. 1999. Yeasts reduce the stimulatory effect of acetate esters from apple on the germination of *Botrytis cinerea* conidia. J. Chem. Ecol. 25, 1555–1565.

Filonow, A.B. 2001. Butyl acetate and yeasts interact in adhesion and germination of *Botrytis cinerea* conidia *in vitro* and in fungal decay of Golden Delicious apple. J. Chem. Ecol. 4, 831–844.

Filonow, A.B., H.S. Vishniac, J.A. Anderson and W.J. Janisiewicz. 1996. Biological control of *Botrytis cinerea* in apple by yeasts from various habitats and their putative mechanisms of antagonism. Biol. Control 7, 212–220.

Findley, K., M. Rodriguez-Carres, B. Metin, J. Kroiss, A. Fonseca, R. Vilgalys and J. Heitman. 2009. Phylogeny and phenotypic characterization of pathogenic *Cryptococcus* species and closely related saprobic taxa in the *Tremellales*. Eukaryot. Cell 8, 353–361.

Finogenova, T.V., I.G. Morgunov, S.V. Kamzolova and O.G. Chernyavskaya. 2005. Organic acid production by the yeast *Yarrowia lipolytica*: a review of prospects. Appl. Biochem. Microbiol. 41, 418–425.

Fiol, J.B. 1967. Les besoins vitaminiques dans les genres *Debaryomyces* Kloecker, *Schwanniomyces* Kloecker, *Hansenula* H. et P. Sydow et *Endomycopsis* Dekker. C.R. Acad. Sci. Paris, Ser. D, 264, 1605–1607.

Fiol, J.B., and G. Billon-Grand. 1977. Nitrate réductase des *Saccharomyces* (groupe *Torulaspora*) et des *Debaryomyces*. Implications systématiques. Mycopathologia 60, 109–113.

Fiol, J.B., and G. Billon-Grand. 1978a. Osidases, nitrite et nitrate réductases dans les genres *Hanseniaspora* et *Kloeckera*. Mycopathologia 63, 47–51.

Fiol, J.B., and G. Billon-Grand. 1978b. Étude de quelques enzymes intracellulaires dans les genres *Dekkera* et *Brettanomyces*; conséquences systematiques. Mycopathologia 64, 183–186.

Fiol, J.B., and G. Billon-Grand. 1981. Bio-systématique des *Pichia*. Mycopathologia 74, 3–8.

Fiore, C., J. Arrizon, A. Gschaedler, J. Flores and P. Romano. 2005. Comparison between yeasts from grape and agave musts and traits of technological interest. World J. Microbiol. Biotechnol. 21, 1141–1147.

Fischer, B., and C. Brebeck. 1894. Zur Morphologie, Biologie, und Systematik der Kahmpilze, der *Monilia candida* Hansen und des Soorerregers. C. Fischer, Jena.

Fischer, G.W., and C.S. Holton. 1957. Biology and Control of the Smut Fungi. Ronald Press, New York.

Fisher, M.C., W.P. Hanage, S. de Hoog, E. Johnson, M.D. Smith, W.J. White and N. Vanittanakom. 2005. Low effective dispersal of asexual genotypes in heterogeneous landscapes by the endemic pathogen *Penicillium marneffei*. PLoS Pathog. 1, e20.

Fisk, D.G., C.A. Ball, K. Dolinski, S.R. Engel, E.L. Hong, L. Issel-Tarver, K. Schwartz, A. Sethuraman, D. Botstein and J.M. Cherry. 2006. *Saccharomyces cerevisiae* S288C genome annotation: a working hypothesis. Yeast 23, 857–865.

Fiss, M., O. Barckhausen, Y. Gherbawy, A. Kollar, M. Hamamoto and G. Auling. 2003. Characterization of epiphytic yeasts of apple as potential biocontrol agents against apple scab (*Venturia inaequalis*). Z. Pflanzenkr. Pflanzensch. 110, 513–523.

Fitch, W.M. 1971. Toward defining the course of evolution: minimum change for a specific tree topology. Syst. Zool. 20, 406–416.

Fitch, W.M., and E. Margoliash. 1967. Construction of phylogenetic trees. Science 155, 277–284.

Fitzgerald, D.J., M. Stratford, M. Glasson and A. Narbad. 2004. The potential application of vanillin in preventing yeast spoilage of soft drinks and fruit juices. J. Food Prot. 67, 391–395.

Fitzpatrick, D.A., M.E. Logue, J.E. Stajich and G. Butler. 2006. A fungal phylogeny based on 42 complete genomes derived from supertree and combined gene analysis. BMC Evol. Biol. 6, 99.

Fitzpatrick, R.E. 1934. The life history and parasitism of *Taphrina deformans*. Sci. Agric. 14, 305–326.

Flamm, E.L. 1991. How FDA approved chymosin: a case study. Nat. Biotechnol. 9, 349–351.

Flarer, F. 1931. Ricerche cliniche e sperimentale sui fattori etiopatogenetici di alcune epidermomicosi. Arch. Ital. Dermatol. Sifilogr. Venereol. 7, 415–478.

Fleer, R. 1992. Engineering yeast for high level expression. Curr. Opin. Biotechnol. 3, 486–496.

Fleet, G.H. 1990a. Food spoilage yeasts. In: J.F.T. Spencer and D.M. Spencer (Eds), Yeast Technology. Springer-Verlag, Berlin, pp. 124–166.

Fleet, G.H. 1990b. Yeasts in dairy products. J. Appl. Bacteriol. 68, 199–211.

Fleet, G.H. 1991. Cell walls. In: A.H. Rose and J.S. Harrison (Eds), The Yeasts, Vol. 4, Yeast Organelles, 2nd edn. Academic Press, London, pp. 199–277.
Fleet, G.H. 1992. Spoilage yeasts. Crit. Rev. Biotechnol. 12, 1–44.
Fleet, G.H. 1998. The microbiology of alcoholic beverages. In: B.J. Wood (Ed.), The Microbiology of Fermented Foods, 2nd edn. Vol. 1. Blackie Academic and Professional, London, pp. 217–262.
Fleet, G.H. 1999. Microorganisms in food ecosystems. Int. J. Food Microbiol. 50, 101–117.
Fleet, G.H. 2000. *Schizosaccharomyces*. In: R.K. Robinson, C. A. Batt and P. Patel (Eds), Encyclopedia of Food Microbiology. Academic Press, London, pp. 1984–1989.
Fleet, G.H. 2001. Food Microbiology. In: I. Freckelton and H. Selby (Eds), Expert Evidence. The Lawbook Company, Sydney, Section 116.
Fleet, G.H. 2003a. Yeast interactions and wine flavor. Int. J. Food Microbiol. 86, 11–32.
Fleet, G.H. 2003b. Yeasts in fruit and fruit products. In: T. Boekhout and V. Robert (Eds), Yeasts in Foods: Beneficial and Detrimental Aspects. Behrs-Verlag, Hamburg, pp. 267–287.
Fleet, G.H. 2006. *Saccharomyces* and related genera. In: C. de W. Blackburn (Ed.), Food Spoilage Microorganisms. Woodhead Publishing, Cambridge, pp. 306–335.
Fleet, G.H. 2007. Wine. In: M.P. Doyle and L.R. Beuchat (Eds), Food Microbiology Fundamentals and Frontiers, 3rd edn. ASM Press, Washington, DC, pp. 863–890.
Fleet, G.H. 2008. Wine yeasts for the future. FEMS Yeast Res. 8, 979–995.
Fleet, G.H., and R. Balia. 2006. The public health and probiotic significance of yeasts in foods and beverages. In: A. Querol and G.H. Fleet (Eds), Yeasts in Food and Beverages. Springer-Verlag, Berlin, pp. 381–398.
Fleet, G.H., and M.A. Mian. 1998. Induction and repair of sublethal injury in food spoilage yeasts. J. Food Mycol. 1, 85–93.
Flegel, T. 1976. Conjugation and growth of *Sirobasidium magnum* in laboratory culture. Can. J. Bot. 54, 411–418.
Flegel, T.W. 1977. Let's call a yeast a yeast. Can. J. Microbiol. 23, 945–946.
Flegel, T.W. 1981. The pheromonal control of mating in yeasts and its phylogenetic implication: a review. Can. J. Microbiol. 27, 373–389.
Flor, P.Q., and S. Hayashida. 1983. *Saccharomyces uvarum inulyticus* var. nov., a new high-concentration ethanol tolerant yeast from rice wine. Eur. J. Appl. Microbiol. Biotechnol. 18, 148–152.
Florenzano, G. 1950. Due nuove specie dei lieviti asporogeni, isolati da vini (*Trichosporon intermedium* nov. spec. e *Brettanomyces custersii* nov. spec.). Ric. Sci. 20, 1494–1498.
Florenzano, G. 1951. Diffusione e significato enologico dei lieviti *Brettanomyces*. Atti Accad. Ital. Vite Vino 3, 236–249.
Florenzano, G. 1953. Zimologia e zimolecnia delvino. In: P.G. Garoglio (Ed.), Nuovo Trattatodi Enologia, Vol. II. Sansoni Firenze, p. 299.
Flores, C.L., C. Rodríguez, T. Petit and C. Gancedo. 2000. Carbohydrate and energy-yielding metabolism in non-conventional yeasts. FEMS Microbiol. Rev. 24, 507–529.
Fogleman, J.C., and J.L.M. Foster. 1989. Microbial colonization of injured cactus tissue (*Stenocereus gummosus*) and its relationship to the ecology of cactophilic *Drosophila mojavensis*. Appl. Environ. Microbiol. 55, 100–105.
Fogleman, J.C., W.T. Starmer and W.B. Heed. 1981. Larval selectivity for yeast species by *Drosophila mojavensis* in natural substrates. Proc. Natl. Acad. Sci. USA 78, 4435–4439.
Fogleman, J.C., W.T. Starmer and W.B. Heed. 1982. Comparisons of yeast florae from natural substrates and larval guts of some southwestern *Drosophila*. Oecologia 52, 187–191.
Fokkema, N.J. 1976. Antagonism between fungal saprophytes and pathogens on aerial plant surfaces. In: C.H. Dickinson and T.F. Preece (Eds), Microbiology of Aerial Plant Surfaces. Academic Press, New York, pp. 487–506.
Fokkema, N.J., and F. van der Meulen. 1976. Antagonism of yeast-like phyllosphere fungi against *Septoria nodorum* on wheat leaves. Neth. J. Plant Pathol. 82, 13–16.
Fokkema, N.J., J.G. den Houter, Y.J.C. Kosterman and A.L. Nelis. 1979. Manipulation of yeasts on field-grown wheat leaves and their antagonistic effect on *Cochliobolus sativus* and *Septoria nodorum*. Trans. Br. Mycol. Soc. 72, 19–29.
Fokkema, N.J., I. Riphagen, R.J. Poot and C. de Jong. 1983. Aphid honeydew, a potential stimulant of *Cochliobolus sativus* and *Septoria nodorum* and the competitive role of saprophytic mycoflora. Trans. Br. Mycol. Soc. 81, 355–363.
Fokkema, N.J., A.J. Dik and R.A. Daamen. 1987. Use of carbendazim and carbendazim-resistant yeasts to create different yeast densities on wheat leaves for field studies on biological control. Eur. J. Plant Pathol. 93, 273–283.
Fonseca, J.J. 2007. Lobomycosis. Int. J. Surg. Pathol. 15, 62–63.
Fonseca, Á., and J. Inácio. 2006. Phylloplane yeasts. In: G. Péter and C.A. Rosa (Eds), Biodiversity and Ecophysiology of Yeasts. Springer, Berlin, pp. 263–301.
Fonseca, Á., and J.P. Sampaio. 1992. *Rhodosporidium lusitaniae* sp. nov., a novel homothallic basidiomycetous yeast species from Portugal that degrades phenolic compounds. Syst. Appl. Microbiol. 15, 47–51.
Fonseca, Á., and N. van Uden. 1991. *Cryptococcus yarrowii* sp. nov., a novel yeast species from Portugal. Antonie van Leeuwenhoek 59, 177–181.
Fonseca, Á., G. Scorzetti and J.W. Fell. 2000a. Diversity in the yeast *Cryptococcus albidus* and related species as revealed by ribosomal DNA sequence analysis. Can. J. Microbiol. 46, 7–27.
Fonseca, Á., J.P. Sampaio, J. Inácio and J.W. Fell. 2000b. Emendation of the basidiomycetous yeast genus *Kondoa* and the description of *Kondoa aeria* sp. nov. Antonie van Leeuwenhoek 77, 293–302.
Fonseca, Á., J.W. Fell, C.P. Kurtzman and I. Spencer-Martins. 2000c. *Candida tartarivorans* sp. nov., an anamorphic ascomycetous yeast with the capacity to degrade L(+)- and meso-tartaric acid. Int. J. Syst. Evol. Microbiol. 50, 389–394.
Fonseca, Á., T. Boekhout and J.W. Fell. 2008. Validation of the basidiomycetous yeast species *Cryptococcus flavus* and *C. liquefaciens*. Mycotaxon 106, 503–504.
Fontoynont, M., and H. Boucher. 1923. Contribution à l'étude des mycoses de Madagascar. Ann. Dermatol. Syph. Série VI 4, 318–344.
Forbes-Smith, M. 1999. Induced resistance for the biological control of postharvest diseases of fruits and vegetables. Food Aust. 51, 382–385.

Forche, A., G. Schönian, Y. Gräser, R. Vilgalys and T.G. Mitchell. 1999. Genetic structure of typical and atypical populations of *Candida albicans* from Africa. Fungal Genet. Biol. 28, 107–125.

Forkman, G., and S. Martens. 2001. Metabolic engineering and applications of flavonoids. Curr. Opin. Biotechnol. 12, 155–160.

Forrest, S.I., C.F. Robinow and M.-A. Lachance. 1987. Nuclear behaviour accompanying ascus formation in *Debaryomyces polymorphus*. Can. J. Microbiol. 33, 967–970.

Förster, A., A. Aurich, S. Mauersberger and G. Barth. 2007. Citric acid production from sucrose using a recombinant strain of the yeast *Yarrowia lipolytica*. Appl. Microbiol. Biotechnol. 75, 1409–1417.

Foulerton, A.G.R. 1900. On the pathogenic action of Blastomycetes. J. Pathol. Bacteriol. 6, 37–63.

Foulet, F., N. Nicolas, O. Eloy, F. Botterel, J.C. Gantier, J.M. Costa and S. Bretagne. 2005. Microsatellite marker analysis as a typing system for *Candida glabrata*. J. Clin. Microbiol. 43, 4574–4579.

Foury, F. 1997. Human genetic diseases – a cross talk between man and yeast. Gene 195, 1–10.

Fowell, R.R. 1952. Sodium acetate agar as a sporulation medium for yeasts. Nature 170, 578.

Fowell, R.R. 1969. Sporulation and hybridization of yeasts. In: A.H. Rose and J.S. Harrison (Eds), The Yeasts, Vol. 1. Biology of Yeasts. Academic Press, New York, pp. 301–383.

Fox, R.D., and G.J. Wong. 1990. Homothallism and heterothallism in *Tremella fuciformis*. Can. J. Bot. 68, 107–111.

Frágner, P. 1969. *Trichosporon jirovecii* sp. nov. Ceská Mykol. 23, 160–162.

Frágner, P. 1970. Spannweite der Art *Trichosporon cutaneum*. Ceská Mykol. 24, 153–161.

Fragoso, R.G., and R. Ciferri. 1928. Hongos parásitos y saprifitos de la Repùblica Dominicana. Boll. R. Soc. Esp. Hist. Nat. 28, 377–388.

Fraire, A.E., B. Kemp, S.D. Greenberg, H.S. Kim, R. Estrada and R.A. McBride. 1996. Calcofluor white stain for the detection of *Pneumocystis carinii* in transbronchial lung biopsy specimens: a study of 68 cases. Mod. Pathol. 9, 861–864.

Francke-Grosmann, H. 1952. Uber die Ambrosiazucht der beiden Kiefernborkenkäfer *Myelophilus minor* Htg. und Ipsäcuminatus. Gyll. Medd. Statens Skogsforskningsinst. (Swed.) 41, 1–52.

Franck-Grosmann, H. 1967. Ectosymbiosis in wood inhabiting insects. In: S.M. Henry (Ed.), Symbiosis, Vol. 2. Academic Press, New York, pp. 142–205.

François, F., T. Noël, R. Pépin, A. Brulfert, C. Chastin, A. Favel and J. Villard. 2001. Alternative identification test relying on sexual reproductive abilities of *Candida lusitaniae* strains isolated from hospitalized patients. J. Clin. Microbiol. 39, 3906.

Frank, D.N., C. Adamidi, M.A. Ehringer, C. Pitulle and N.R. Pace. 2000. Phylogenetic-comparative analysis of the eukaryal ribonuclease P RNA. RNA 6, 1895–1904.

Franzot, S.P., J. Mukherjee, R. Cherniak, L.C. Chen, J.S. Hamdan and A. Casadevall. 1998. Microevolution of a standard strain of *Cryptococcus neoformans* resulting in differences in virulence and other phenotypes. Infect. Immun. 66, 89–97.

Franzot, S.P., I.F. Salkin and A. Casadevall. 1999. *Cryptococcus neoformans* var. *grubii*: separate varietal status for *Cryptococcus neoformans* serotype A isolates. J. Clin. Microbiol. 37, 838–840.

Fraser, J.A., R.L. Subaran, C.B. Nichols and J. Heitman. 2003. Recapitulation of the sexual cycle of the primary fungal pathogen *Cryptococcus neoformans* var. *gattii*: implications for an outbreak on Vancouver Island, Canada. Eukaryot. Cell 2, 1036–1045.

Fraser, J.A., S.S. Giles, E.C. Wenink, S.G. Geunes-Boyer, J.R. Wright, S. Diezmann, A. Allen, J.E. Stajich, F.S. Dietrich, J.R. Perfect and J. Heitman. 2005. Same-sex mating and the origin of the Vancouver Island *Cryptococcus gattii* outbreak. Nature 437, 1360–1364.

Fraser, J.A., S.M.C. Lim, S. Diezmann, E.C. Wenink, C.G. Arndt, G.M. Cox, F.S. Dietrich and J. Heitman. 2006. Yeast diversity sampling on the San Juan Islands reveals no evidence for the spread of the Vancouver Island *Cryptococcus gattii* outbreak to this locale. FEMS Yeast Res. 6, 620–624.

Fraser, J.A., Y. Hsueh, K.M. Findley and J. Heitman. 2007. Evolution of the mating-type locus: the basidiomycetes. In: J. Heitman, J.W. Kronstad, J.W. Taylor and L.A. Casselton (Eds), Sex in Fungi: Molecular Determination and Evolutionary Implications. ASM Press, Washington, DC, pp. 19–34.

Frazer, H.L. 1944. Observations on the method of transmission of internal boll disease of cotton by the cotton stainer-bug. Ann. Appl. Biol. 21, 271–290.

Frederiksen, P.S. 1956. A new *Rhodotorula* species, *Rhodotorula macerans* sp. n. isolated from field retted flax straw. Friesia 5, 234–239.

Fredlund, E., U. Druvefors, M.E. Boysen, K.-J. Lingsten and J. Schnűrer. 2002. Physiological characteristics of the biocontrol yeast *Pichia anomala* J121. FEMS Yeast Res. 2, 395–402.

Freeman, W., and F.D. Weidman. 1923. Cystic blastomycosis of the cerebral gray matter caused by *Torula histolytica* Stoddard and Cutler. Arch. Neurol. Psychiatry 9, 569–603.

Freer, S.N. 1991. Fermentation and aerobic metabolism of cellodextrins by yeasts. Appl. Environ. Microb. 57, 655–659.

Frei, W. 1921. Eine Soormycose der Nägel bei einer Salvarsan-Dermatitis. Arch. Dermatol. Syph. 129, 404–433.

Frenkel, J.K. 1976. *Pneumocystis jiroveci* n. sp. from man: morphology, physiology, and immunology in relation to pathology. Natl. Cancer Inst. Monogr. 43, 13–30.

Fresenius, J.B.G.W. 1850. Beiträge zur Mykologie, Vol. 1, Frankfurt am Main.

Fric, P. 2007. Probiotics and prebiotics – renaissance of a therapeutic principle. Central Eur. J. Med. 2, 237–270.

Frieders, E.M., and D.J. McLaughlin. 1996. Mitosis in the yeast phase of *Agaricostilbum pulcherrimum* and its evolutionary significance. Can. J. Bot. 74, 1392–1406.

Friel, D., N.M. Gomez Pessoa, M. Vandenbol and H. Jijakli. 2007. Separate and combined disruption of two exo-β-1,3-glucanase genes decrease the efficiency of *Pichia anomala* (strain K) biocontrol against *Botrytis cinerea* on apple. MPMI 20, 371–379.

Frieman, M.B., J.M. McCaffery and B.P. Cormack. 2002. Modular domain structure in the *Candida glabrata* adhesin Epa-1-p, a β-1,6-glucan-cross-linked cell wall protein. Mol. Microbiol. 46, 479–492.

Fries, E. 1822. Systema Mycologicum, Vol. II, 213pp.

Fries, E.M. 1832. Systema Mycologicum, Vol. III, 2. Gryphiswaldae. Lund.

Fröhlich-Wyder, M.T. 2003. Yeasts in dairy products. In: T. Boekhout and V. Robert (Eds), Yeasts in Foods: Beneficial and Detrimental Aspects. Behrs Verlag, Hamburg, pp. 209–237.

Froilano de Mello, I., and L. Gonzaga Fernandes. 1918. Ensaio de classificação de fungos pertencentes a classe dos "Blastomyces". Arq. Hig. Patol. Exót. 6, 207–316.

Froilano de Mello, I., and A. Paes. 1918. *Endomyces cruzi*, n. sp. agente (?) duma endomicose brônquica simulando asma. Arq. Hig. Patol. Exót. 6, 51–60.

Fuchs, C.T., and G. Spiteller. 1995. 4-Pentadecylpyridine: a metabolite from *Taphrina pruni*. Z. Naturforsch. [C] 50, 766–768.

Fuchs, C.T., and G. Spiteller. 1997. Reduced indole-3-acetic acid decomposition causes enhanced growth of plums affected by the fungus *Taphrina pruni*. Z. Naturforsch. [C] 52, 504–507.

Fuchs, C.T., and G. Spiteller. 1998. Accumulation of caffeoyl-D-quinic acids and catechins in plums affected by the fungus *Taphrina pruni*. Z. Naturforsch. [C] 53, 799–805.

Fuentefria, A.M., S.-O. Suh, M.F. Landell, J. Faganello, A. Schrank, M.H. Vainstein, M. Blackwell and P. Valente. 2008. *Trichosporon insectorum* sp. nov., a new anamorphic basidiomycetous killer yeast. Mycol. Res. 112, 93–99.

Fujii, N., T. Oki, A. Sakurai, S. Suye and M. Sakakibara. 2001. Ethanol production from starch by immobilized. *Aspergillus awamori* and *Saccharomyces pastorianus* using cellulose carriers. J. Ind. Microbiol. Biotechnol. 27, 52–77.

Fujita, S., Y. Senda, T. Okusi, Y. Ota, H. Takada, K. Yamada and M. Kawano. 2007. Catheter-related fungemia due to fluconazole-resistant *Candida nivariensis*. J. Clin. Microbiol. 45, 3459–3461.

Fujiwara, A., and S. Masuda. 1981. Process for producing D-arabitol. US Patent 4,271,268.

Fukatsu, T., and H. Ishikawa. 1996. Phylogenetic position of yeast-like symbiont of *Hamiltonaphis styraci* (Homotera, Aphididae) based on 18S rDNA sequence. Insect Biochem. Mol. Biol. 26, 383–388.

Fukazawa, Y., T. Nakase, T. Shinoda, A. Nishikawa, K. Kagaya and T. Tsuchiya. 1975. Significance of cell wall structures on yeast classification: proton magnetic resonance and serological and deoxyribonucleic acid characterization of *Candida sake* and related species. Int. J. Syst. Bacteriol. 25, 304–314.

Fukuhara, H. 1995. Linear DNA plasmids of yeasts. FEMS Microbiol. Lett. 131, 1–9.

Fungsin, B., M. Hamamoto, V. Arunpairojana, J. Sukhumavasi, P. Atthasampunna and T. Nakase. 2001. *Bensingtonia thailandica* sp. nov., a novel basidiomycetous yeast species isolated from plant leaves in Thailand. Int. J. Syst. Evol. Microbiol. 51, 1209–1213.

Fungsin, B., M. Hamamoto, V. Arunpairojana, J. Sukhumavasi, P. Atthasampunna and T. Nakase. 2002a. *Kockovaella barringtoniae* sp. nov., a new basidiomycetous yeast species isolated from a plant leaf collected in a tropical rain forest in Thailand. Int. J. Syst. Evol. Microbiol. 52, 281–284.

Fungsin, B., M. Takashima, S. Artjariyasripong, V. Arunpaiojana, M. Hamamoto and T. Nakase. 2002b. *Bullera arundinariae* sp. nov., a new yeast species of ballistoconidium-forming yeast, isolated from a plant in Thailand. Microbiol. Cult. Coll. 18, 83–90.

Fungsin, B., M. Takashima, S. Artjariyasripong, W. Potacharoen and T. Nakase. 2003a. *Bullera sakaeratica* sp. nov., a new species of ballistoconidium-forming yeast found in Thailand. Microbiol. Cult. Coll. 19, 33–39.

Fungsin, B., M. Takashima, F.-Y. Bai, S. Artjariyasripong and T. Nakase. 2003b. *Bullera panici* sp. nov. and *Bullera siamensis* sp. nov., two new yeasts in the *Bullera variabilis* cluster isolated in Thailand. Microbiol. Cult. Coll. 19, 23–32.

Fungsin, B., M. Takashima, T. Sugita, S. Atjariyasripong, W. Potacharoen, M. Tanticharoen and T. Nakase. 2006. *Bullera koratensis* sp. nov. and *Bullera lagerstroemiae* sp. nov., two new ballistoconidium-forming yeast species in the Trichosporonales-clade isolated from plant leaves in Thailand. J. Gen. Appl. Microbiol. 52, 73–81.

Furman, R.M., and D.G. Ahearn. 1983. *Candida ciferrii* and *Candida chiropterorum* isolated from clinical specimens. J. Clin. Microbiol. 18, 1252–1255.

Furukawa, T., T. Matsuyoshi, Y. Minoda and K. Yamada. 1977. Fermentative production of citric acid from *n*-paraffins by yeast. J. Ferment. Technol. 55, 356–363.

Furuta, T., M. Fujita, K. Machii, K. Kobayashi, S. Kojima and K. Ueda. 1993. Fatal spontaneous pneumocystosis in nude rats. Lab. Anim. Sci. 43, 551–556.

Fuson, G.B., C.W. Price and H.J. Phaff. 1979. Deoxyribonucleic acid sequence relatedness among some members of the yeast genus *Hansenula*. Int. J. Syst. Bacteriol. 29, 64–69.

Fuson, G.B., C.W. Price and H.J. Phaff. 1980. Deoxyribonucleic acid base sequence relatedness among strains of *Pichia ohmeri* that produce dimorphic ascospores. Int. J. Syst. Bacteriol. 30, 217–219.

Fuson, G.B., H.L. Presley and H.J. Phaff. 1987. Deoxyribonucleic acid base sequence relatedness among members of the yeast genus *Kluyveromyces*. Int. J. Syst. Bacteriol. 37, 371–379.

Fuzzi, S., P. Mandrioli and A. Perfetto. 1997. Fog droplets – an atmospheric source of secondary biological aerosol particles. Atmos. Environ. 31, 287–290.

Gabriel, M., M. Kopecká, M. Yamaguchi, A. Svoboda, K. Takeo, S. Yoshida, M. Ohkusu, T. Sugita and T. Nakase. 2006. The cytoskeleton in the unique cell reproduction by conidiogenesis of the long-neck yeast *Fellomyces* (*Sterigmatomyces*) *fuzhouensis*. Protoplasma 229, 33–44.

Gácser, A., Z. Hamari, I. Pfeiffer, J. Varga, F. Keveri and J. Kuscera. 2001. Genetic diversity of the red yeast *Cryptococcus hungaricus* and its phylogenetic relationship to some related basidiomycetous yeasts. FEMS Yeast Res. 1, 213–220.

Gácser, A., W. Schäfer, J.S. Nosanchuk, S. Salomon and J.D. Nosanchuk. 2007. Virulence of *Candida parapsilosis*, *Candida orthopsilosis*, and *Candida metapsilosis* in reconstituted human tissue models. Fungal Genet. Biol. 44, 1336–1341.

Gadanho, M., and J.P. Sampaio. 2002. Polyphasic taxonomy of the basidiomycetous yeast genus *Rhodotorula*: *Rh. glutinis sensu stricto* and *Rh. dairenensis* comb. nov. FEMS Yeast Res. 2, 47–58.

Gadanho, M., and J.P. Sampaio. 2005. Occurrence and diversity of yeasts in the mid-atlantic ridge hydrothermal fields near the Azores Archipelago. Microb. Ecol. 50, 408–417.

Gadanho, M., and J.P. Sampaio. 2006. Microeukaryotic diversity in the extreme environments of the Iberian Pyrite Belt: a comparison between universal and fungi-specific primer sets, temperature gradient gel electrophoresis and cloning. FEMS Microbiol. Ecol. 57, 139–148.

Gadanho, M., and J.P. Sampaio. 2009. *Cryptococcus ibericus* sp. nov., *Cryptococcus aciditolerans* sp. nov. and *Cryptococcus metallitolerans* sp. nov., a new ecoclade of anamorphic basidiomycetous yeast species from an extreme environment associated with acid rock drainage in São Domingos pyrite mine, Portugal. Int. J. Syst. Evol. Microbiol. 59, 2375–2379.

Gadanho, M., J.P. Sampaio and I. Spencer-Martins. 2001. Polyphasic taxonomy of the basidiomycetous yeast genus *Rhodosporidium*: *R. azoricum* sp. nov. Can. J. Microbiol. 47, 213–221.

Gadanho, M., J.M.G.C.F. Almeida and J.P. Sampaio. 2003. Assessment of yeast diversity in a marine environment in the south of Portugal by microsatellite-primed PCR. Antonie van Leeuwenhoek 84, 217–227.

Gadanho, M., D. Libkind and J.P. Sampaio. 2006. Yeast diversity in the extreme acidic environments of the Iberian Pyrite Belt. Microb. Ecol. 52, 552–563.

Gadea, I., M. Cuenca-Estrella, E. Prieto, T.M. Diaz-Guerra, J.I. Garcia-Cia, E. Mellado, J.F. Tomas and J.L. Rodriguez-Tudela. 2004. Genotyping and antifungal susceptibility profile of *Dipodascus capitatus* isolates causing disseminated infection in seven hematological patients of a tertiary hospital. J. Clin. Microbiol. 42, 1832–1836.

Gadzhiev, D.M., A.M. Makuev, and R.R. Rasulov. 1976. Method for production of fruit wines. USSR Patent 501061.

Gagiano, M., F.F. Bauer and I.S. Pretorius. 2002. The sensing of nutritional status and the relationship to filamentous growth in *Saccharomyces cerevisiae*. FEMS Yeast Res. 2, 433–470.

Gaitanis, G., A. Velegraki, E. Frangoulis, A. Mitroussia, A. Tsigonia, A. Tzimogianni, Katsambas and N.J. Legakis. 2002. Identification of *Malassezia* species from skin scales by PCR-RFLP. Clin. Microbiol. Infect. 8, 162–173.

Gaitanis, G., V. Chasapi and A. Velegraki. 2005. Novel application of the Masson-Fontana stain for demonstrating *Malassezia* species melanin-like pigment production *in vitro* and in clinical specimens. J. Clin. Microbiol. 43, 4147–4151.

Galagan, J.E., M.R. Henn, L.J. Ma, C.A. Cuomo and B. Birren. 2005. Genomics of the fungal kingdom: insights into eukaryotic biology. Genome Res. 15, 1620–1631.

Galgóczy, J., and E.K. Novák. 1962. A new yeast *Paratorulopsis banhegyii* n. sp. from human skin. Acta Microbiol. Acad. Sci. Hung. 9, 77–79.

Galgóczy, J., and E.K. Novák. 1965. *Rhodotorula zsoltii* n. sp., a new species of yeasts, and some notes on the taxonomy of the genus *Rhodotorula*. Acta Microbiol. Acad. Sci. Hung. 12, 151–155.

Gallo, M.G., P. Cabeli and V. Vidotto. 1989. Presence of pathogenic yeasts in the feces of the semi-domesticated pigeon (*Columbia livia* Gmelin 1789, urban type) from the city of Turin. Parasitologia 31, 207–212.

Gams, W. 1983. Two species of mycoparasitic fungi. Sydowia 36, 46–52.

Gams, W. 2001. Proposals to conserve or reject. Report of the committee for fungi: 9. Taxon 50, 269–272.

Gams, W. 2004. Report of the Committee for Fungi: 11. Taxon 53, 1067–1069.

Gams, W., and J. Grinbergs. 1970. *Ascoidea corymbosa* n. spec., ein hefeähnlicher Pilz im Bast von *Araucaria araucana*. Acta Bot. Neerl. 19, 794–798.

Gandy, D.G. 1966. *Itersonilia perplexans* on chrysanthemum: alternative hosts and ways of overwintering. Trans. Br. Mycol. Soc. 49, 499–507.

Ganesan, A.T., and M.S. Swaminathan. 1958. Staining the nucleus in yeasts. Stain Technol. 33, 115–121.

Ganley, A.R., and T. Kobayashi. 2007. Highly efficient concerted evolution in the ribosomal DNA repeats: total rDNA repeat variation revealed by whole-genome shotgun sequence data. Genome Res. 17, 184–191.

Ganter, P.F. 1988. The vectoring of cactophilic yeasts by *Drosophila*. Oecologia 75, 400–404.

Ganter, P.F. 2006. Yeast and invertebrate associations. In: C. Rosa and G. Péter (Eds), Biodiversity and Ecophysiology of Yeasts. Springer-Verlag, Berlin, pp. 303–370.

Ganter, P.F., and W.T. Starmer. 1992. Killer factor as a mechanism of interference competition in yeasts associated with cacti. Ecology 73, 54–67.

Ganter, P.F., W.T. Starmer, M.A. Lachance and H.J. Phaff. 1986. Yeast communities from host plants and associated *Drosophila* species in southern Arizona: new isolations and analysis of the relative importance of hosts and vectors on community composition. Oecologia 70, 386–392.

Ganter, P.F., G. Cardinali, M. Giammaria and B. Quarles. 2004. Correlations among measures of phenotypic and genetic variation within an oligotrophic asexual yeast, *Candida sonorensis*, collected from *Opuntia*. FEMS Yeast Res. 4, 527–540.

Ganter, P.F., G. Cardinali and K. Boundy-Mills. 2010. *Pichia insulana* sp. nov., a novel cactophilic yeast from the Caribbean. Int. J. Syst. Evol. Microbiol. 60, 1001–1007.

Gänzle, M.G., M. Ehmann and W.P. Hammes. 1998. Modeling of growth of *Lactobacillus sanfranciscensis* and *Candida milleri* in response to process parameters of sourdough fermentation. Appl. Environ. Microbiol. 64, 2616–2623.

Gao, C., and G.H. Fleet. 1995. Degradation of malic and tartaric acids by high density cell suspensions of wine yeasts. Food Microbiol. 12, 65–71.

Gao, L., Z. Chi, J. Sheng, L. Wang, J. Li and F. Gong. 2007. Inulinase-producing marine yeasts: evaluation of their diversity and inulin hydrolysis by their crude enzymes. Microbi. Ecol. 54, 722–729.

Gao, Q., M.K. Killie, H. Chen, R. Jiang and R. Seljejid. 1997. Characterization and cytokine-stimulating activities of acidic heteroglycans from *Tremella fuciformis*. Planta Med. 63, 457–460.

Garcia, E.E., J.M. Belin and Y. Wache. 2007. Use of a Doehlert factorial design to investigate the effects of pH and aeration on the accumulation of lactones by *Yarrowia lipolytica*. J. Appl. Microbiol. 103, 1508–1515.

Garcia, R., C. Bermejo, C. Grau, R. Perez, J.M. Rodriguez-Pena, J. Francois, C. Nombela and J. Arroyo. 2004. The global transcriptional response to transient cell wall damage in *Saccharomyces cerevisiae* and its regulation by the cell integrity signaling pathway. J. Biol. Chem. 279, 15183–15195.

Garcia-Hermoso, D., O. Cabaret, G. Lecellier, M. Desnos-Ollivier, D. Hoinard, D. Raoux, J.M. Costa, F. Dromer and S. Bretagne. 2007. Comparison of microsatellite length polymorphism and multilocus sequence typing for DNA-based typing of *Candida albicans*. J. Clin. Microbiol. 45, 3958–3963.

García-Martos, P., J. Mira, F. Galán and J.M. Hernández. 1996. Sexual forms of yeasts in clinical samples. Mycopathologia 136, 67–70.

García-Martos, P., J.M. Hernández-Molina, F. Galán, J.R. Ruiz-Henestrosa, R. García-Agudo, M.J. Palomo and J. Mira. 1999. Isolation of *Hanseniaspora uvarum* (*Kloeckera apiculata*) in humans. Mycopathologia 144, 73–75.

Garcia-Martos, P., I. Dominguez, P. Marin, R. Garcia-Agudo, S. Aoufi and J. Mira. 2001. Antifungal susceptibility of emerging yeast pathogens. Enferm. Infec. Microbiol. Clin. 19, 249–256.

García-Martos, P., J.F. Noval, A. García-Tapìa, P. Marín, J.L. Puerto and A. Sepúlveda. 2002. Susceptibility to antifungal agents of *Cryptococcus* species of clinical interest. Med. Clin. 119, 211–213.

García-Martos, P., J. Ruiz-Aragón, L. García-Agudo, A. Saldarreaga, M.C. Lozanoand and P. Marín. 2004. Aislamiento de *Candida ciferrii* un paciente inmunodeficiente. Ver. Iberoam. Micol. 21, 85–86.

García-Reyero, N., E. Grau, M. Castillo, M.J.L. de Alda, D. Barcelo and B. Pina. 2001. Monitoring of endocrine disruptors in surface waters by the yeast recombinant assay. Environ. Toxicol. Chem. 20, 1152–1158.

Gardini, F., G. Suzzi, A. Lombardi, F. Galgano, M.A. Crudele, C. Andrighetto, M. Schirone and R. Tofalo. 2001. A survey of yeasts in traditional sausages of southern Italy. FEMS Yeast Res. 1, 161–167.

Gárdonyi, M., M. Österberg, C. Rodrigues, I. Spencer-Martins and B. Hahn-Hägerdal. 2003. High capacity xylose transport in *Candida intermedia* PYCC 4715. FEMS Yeast Res. 3, 45–52.

Gargas, A., P.T. DePriest, M. Grube and A. Tehler. 1995. Multiple origins of lichen symbioses in fungi suggested by SSU rDNA phylogeny. Science 268, 1492–1495.

Gargeya, I.B., W.R. Pruitt, R.B. Simmons, S.A. Meyer and D.G. Ahearn. 1990. Occurrence of *Clavispora lusitaniae*, the teleomorph of *Candida lusitaniae*, among clinical isolates. J. Clin. Microbiol. 28, 2224–2227.

Gargeya, I.B., W.R. Pruitt, S.A. Meyer and D.G. Ahearn. 1991. *Candida haemulonii* from clinical specimens in the USA. J. Med. Vet. Mycol. 29, 335–338.

Garrait, G., J.F. Jarrige, S. Blanquet, E. Beyssac and M. Alric. 2007. Recombinant *Saccharomyces cerevisiae* strain expressing a model cytochrome P450 in the rat digestive environment: viability and bioconversion activity. Appl. Environ. Microbiol. 73, 3566–3574.

Garrison, R.G. 1981. Vegetative ultrastructure. In: W.N. Arnold (Ed.), Yeast Cell Envelopes: Biochemistry, Biophysics, and Ultrastructure, Vol. 2. CRC Press, Boca Raton, FL, pp. 139–160.

Gartshore, J., D.G. Cooper and J.A. Nicell. 2003. Biodegradation of plasticizers by *Rhodotorula rubra*. Environ. Toxic. Chem. 22, 1244–1251.

Gascuel, O. 1997. BIONJ: an improved version of the NJ algorithm based on a simple model of sequence data. Mol. Biol. Evol. 14, 685–695.

Gascuel, O., and M. Steel. 2006. Neighbor-joining revealed. Mol. Biol. Evol. 23, 1997–2000.

Gassem, M.A.A. 2002. A microbiological study of sobia: a fermented beverage in the Western province of Saudi Arabia. World J. Microbiol. Biotechnol. 18, 173–177.

Gasser, B., and D. Mattanovich. 2007. Antibody production with yeasts and filamentous fungi: on the road to large scale? Biotechnol. Lett. 29, 201–212.

Gastmann, S., A. Dunkler, A. Walther, K. Klein and J. Wendland. 2007. A molecular toolbox for manipulating *Eremothecium coryli*. Microbiol. Res. 162, 299–307.

Gatesy, J. 2002. Relative quality of different systematic datasets for cerartiodactyl mammals: assessments within a combined analysis framework. In: R. DeSalle, G. Giribet and W. Wheeler (Eds), Molecular Systematics and Evolution: Theory and Practice. Birkhäuser, Basel, pp. 45–67.

Gatesy, J., R. DeSalle and W. Wheeler. 1993. Alignment-ambiguous nucleotide sites and exclusion of systematic data. Mol. Phylogenet. Evol. 2, 152–157.

Gattiker, A., R. Rischatsch, P. Demougin, S. Voegeli, F.S. Dietrich, P. Philippsen and M. Primig. 2007. *Ashbya* Genome Database 3.0: a cross-species genome and transcriptome browser for yeast biologists. BMC Genomics 8, 9.

Gatzidou, E.T., A.N. Zira and S.E. Theocharis. 2007. Toxicogenomics: a pivotal piece in the puzzle of toxicological research. J. Appl. Toxicol. 27, 302–309.

Gedoelst, L. 1902. Les Champignons Parasites de l'Homme et des Animaux Domestiques. Lamertin, Brussels.

Gedoelst, L. 1911. Synopsis de Parasitologie de l'Homme et des Animaux Domestiques. Lierre, Bruxelles.

Gee, S.F., S. Joly, D.R. Soll, J.F. Meis, P.E. Verweij, I. Polacheck, D.J. Sullivan and D.C. Coleman. 2002. Identification of four distinct genotypes of *Candida dubliniensis* and detection of microevolution *in vitro* and *in vivo*. J. Clin. Microbiol. 40, 556–574.

Geerlings, A., F.J. Redondo, A. Contin, J. Memelink, R. van der Heijden and R. Verpoorte. 2001. Biotransformation of tryptamine and secologanin into plant terpenoid indole alkaloids by transgenic yeast. Appl. Microbiol. Biotechnol. 56, 420–424.

Geiger, A. 1910. Beiträge zur Kenntnis der Sprosspilze ohne Sporenbildung. Zentralbl. Bakteriol. Parasitenkd. Abt. II, 27, 97–149.

Gellissen, G. (Ed.) 2002. *Hansenula polymorpha*. Biology and Applications. Wiley-VCH, Weinheim.

Gellissen, G. (Ed.) 2005. Production of Recombinant Proteins. Wiley-VCH, Weinheim.

Gellissen, G., G. Kunze, C. Gaillardin, J.M. Cregg, E. Berardi, M. Veenhuis and I. van der Klei. 2005. New yeast expression platforms based on methylotrophic *Hansenula polymorpha* and *Pichia pastoris* and on dimorphic *Arxula adeninivorans* and *Yarrowia lipolytica* – a comparison. FEMS Yeast Res. 5, 1079–1096.

Gemmer, C.M., Y.M. DeAngelis, B. Theelen, T. Boekhout and T.L. Dawson. 2002. Fast, noninvasive method for molecular detection and differentiation of *Malassezia* yeast species on human skin and application of the method to dandruff microbiology. J. Clin. Microbiol. 40, 3350–3357.

Gemmill, T.R., and R.B. Trimble. 1999. Overview of N- and O-linked oligosaccharide structures found in various yeast species. Biochim. Biophys. Acta 1426, 227–237.

Genestar Serra, R. 1956. Nueva especie de levadura aislada de concentrado de tanino *Candida majoricensis* nov. sp. Microbiol. Esp. 9, 275–279.

Gente, S., D. Sohier, E. Coton, C. Duhamel and M. Guéguen. 2006. Identification of *Geotrichum candidum* at the species and strain level: proposal for a standardized protocol. J. Ind. Microbiol. Biotechnol. 33, 1019–1031.

Gente, S., N. Desmasures, C. Jacopin, G. Plessis, M. Beliard, J.-M. Panoff and M. Guéguen. 2002a. Intraspecies chromosome length polymorphism in *Geotrichum candidum* revealed by pulsed field gel electrophoresis. Int. J. Food Microbiol. 76, 127–134.

Gente, S., N. Desmasures, J.-M. Panoff and M. Guéguen. 2002b. Genetic diversity among *Geotrichum candidum* strains from various substrates studied using RAM and RAPD PRC. J. Appl. Microbiol. 92, 491–501.

Gerardo, N.M., U.G. Mueller, S.L. Price and C.R. Currie. 2004. Exploiting a mutualism: parasite specialization on cultivars within the fungus-growing ant symbiosis. Proc. R. Soc. Lond. B 271, 1791–1798.

Gerngross, T.U. 2004. Advances in the production of human therapeutic proteins in yeasts and filamentous fungi. Nat. Biotechnol. 22, 1409–1414.

Gerson, U., Z. Paz, L. Kushnir and A. Sztejnberg. 2005. New fungi to control phytophagous mites and phytopathogenic fungi. Int. Org. Biol. Control IOBC/WPRS Bull. 28, 103–106.

Geueke, D.J., and C. Brunkhorst. 2003. Inactivation of *Saccharomyces cerevisiae* with radio frequency electric fields. J. Food Prot. 66, 1712–1715.

Ghadeer, F., M.I. Mihyar, I. Yamani and A.K. Al-Sa'ed. 1997. Resistance of yeast flora of labeneh to potassium sorbate and sodium benzoate. J. Dairy Sci. 80, 2304–2309.

Ghang, D.M., L. Yu, M.H. Lim, H.M. Ko, S.Y. Im, H.B. Lee and S. Bai. 2007. Efficient one-step starch utilization by industrial strains of *Saccharomyces cerevisiae* expressing the glucoamylase and alpha-amylase genes from *Debaryomyces occidentalis*. Biotechnol. Lett. 29, 1203–1208.

Ghoneum, M., L. Wang, S. Agrawal and S. Gollapudi. 2007. Yeast therapy for the treatment of breast cancer: a nude mice model. In Vivo 21, 251–258.

Ghoshroy, S., R. Lartey, J. Sheng and V. Citovsky. 1997. Transport of proteins and nuclic acids through plasmodesmata. Annu. Rev. Plant Physiol. Plant Mol. Biol. 48, 27–50.

Gibson, B.R., S.J. Lawrence, J.P.R. Leclaire, C.D. Powell and K.A. Smart. 2007. Yeast responses to stresses associated with industrial brewery handling. FEMS Microbiol. Rev. 31, 535–569.

Giese, R.L. 1966. The bioecology of *Corthylus columbianus* Hopkins. Holz und Org. Int. Symp. Berlin-Dahlem-1965 1, 361–370.

Giesenhagen, K. 1895. Die entwickelungsreiben der parasitischen Exoasceen. Flora 81, 267–361.

Giesenhagen, K. 1901. *Taphrina*, *Exoascus* and *Magnusiella*. Bot. Zeit. 50, 115–142.

Giga-Hama, Y., and H. Kumagai. 1998. Foreign gene expression in fission yeast *Schizosaccharomyces pombe*. Springer-Verlag, Berlin.

Gigioli, I. 1897. Insects and yeasts. Nature 56, 575–577.

Gilbert, D.G. 1980. Dispersal of yeasts and bacteria by *Drosophila* in a temperate forest. Oecologia 46, 135–137.

Gildemacher, P.R., B. Heijne, J. Houbraken, T. Vromans, E.S. Hoekstra and T. Boekhout. 2004. Can phyllosphere yeasts explain the effect of scab fungicides on russeting of Elstar apples? Eur. J. Plant Pathol. 110, 929–937.

Gildemacher, P., B. Heijne, M. Silvestri, J. Houbraken, E. Hoekstra and T. Boekhout. 2006. Interactions between yeasts, fungicides and apple fruit russeting. FEMS Yeast Res. 6, 1149–1156.

Gilfillan, G.D., D.J. Sullivan, K. Haynes, T. Parkinson, D.C. Coleman and N.A. Gow. 1998. *Candida dubliniensis*, phylogeny and putative virulence factors. Microbiology 144, 829–838.

Gill, C.O., M.J. Hall and C. Ratledge. 1977. Lipid accumulation in an oleaginous yeast (*Candida* 107) growing on glucose in single-stage continuous culture. Appl. Environ. Microbiol. 33, 231–239.

Gilliland, R.B. 1962. The *Brettanomyces* II. Taxonomic significance of slow fermentations and description of a new species. J. Inst. Brew. 68, 51–59.

Gillings, M.R., M.P. Holley and M. Selleck. 2006. Molecular identification of species comprising an unusual biofilm from a groundwater treatment plant. Biofilms 3, 19–24.

Gilloteaux, J., and J. Naud. 1979. The zinc iodide–osmium tetroxide staining-fixative of Maillet. Nature of the precipitate studied by x-ray microanalysis and detection of Ca^{2+}-affinity subcellular sites in a tonic smooth muscle. Histochemistry 63, 227–243.

Giménez-Jurado, G. 1992. *Metschnikowia gruessii*, sp. nov., the teleomorph of *Nectaromyces reukaufii* but not of *Candida reukaufii*. Syst. Appl. Microbiol. 15, 432–438.

Giménez-Jurado, G., and N. van Uden. 1989. *Leucosporidium fellii* sp. nov., a basidiomycetous yeast that degrades L(+)-tartaric acid. Antonie van Leeuwenhoek 55, 133–141.

Giménez-Jurado, G., T. Plácido, A.J. Cidadão, C. Cabeça-Silva, E. Fonseca and H.J. Roeijmans. 1990. *Kurtzmanomyces tardus* sp. nov., a new anamorphic yeast species of basidiomycetous affinity. Antonie van Leeuwenhoek 58, 129–135.

Giménez-Jurado, G., A.J. Cidadão and A. Beijn-van der Waaij. 1994. A novel heterothallic ascomycetous yeast species: *Stephanoascus smithiae*, teleomorph of *Candida edax*. Syst. Appl. Microbiol. 17, 237–246.

Giménez-Jurado, G., M.J. Valderrama, I. Sá-Nogueira and I. Spencer-Martins. 1995. Assessment of phenotypic and genetic diversity in the yeast genus *Metschnikowia*. Antonie van Leeuwenhoek 68, 101–110.

Giménez-Jurado, G., C.P. Kurtzman, W.T. Starmer and I. Spencer-Martins. 2003. *Metschnikowia vanudenii* sp. nov. and *Metschnikowia lachancei* sp. nov., from flowers and associated insects in North America. Int. J. Syst. Evol. Microbiol. 53, 1665–1670.

Gimeno, C.J., P.O. Ljungdahl, C.A. Styles and G.R. Fink. 1992. Unipolar cell divisions in the yeast *S. cerevisiae* lead to filamentous growth: regulation by starvation and RAS. Cell 68, 1077–1090.

Ginns, J. 1986. The genus *Syzygospora* (Heterobasidiomycetes, Syzygosporaceae). Mycologia 78, 619–636.

Ginns, J., and A. Bernicchia. 2000. *Filobasidiella lutea*: parasitism of *Hypochnicium vellereum*. Karstenia 40, 49–51.

Ginns, J., and P.W. Malloch. 2003. *Filobasidiella depauperata* (Tremellales): haustorial branches and parasitism of *Verticillium lecanii*. Mycol. Prog. 2, 137–140.

Ginns, J., and S. Sunhede. 1978. Three species of *Christiansenia* (Corticiaceae) and the teratological galls on *Collybia dryophila*. Bot. Not. 131, 167–173.

Giobbe, S., S. Marceddu, B. Scherm, G. Zara, V.L. Mazzarello, M. Budroni and Q. Migheli. 2007. The stange case of a biofilm-forming strain of *Pichia fermentans*, which controls *Monilinia* brown rot on apple but is pathogenic on peach fruit. FEMS Yeast Res. 7, 1389–1398.

Giordano, A. 1935. Rôle du *Torulopsis neoformans* (Sanfelice) Red. en pathologie humaine. Boll. Sez. Ital. Soc. Intern. Microbiol. 7, 119–123.

Giosué, S., G. Spada, V. Rossi, G. Carli and I. Ponti. 2000. Forecasting infections of the leaf curl disease on peaches caused by *Taphrina deformans*. Eur. J. Plant Pathol. 106, 563–571.

Giovannozzi, M. 1939. Studi sulla fermentazione del tabacco. IV nota. Sui blastomiceti del tabacco Kentucky in fermentazione – i lieviti sporigeni. Boll. Tec. Regio Ist. Sper. Colt. Tab. "Leonardo Angeloni", Scafati, no. 1.

Giovannozzi, M. 1941. Studi sulla fermentazione dei tabacchi. Vl nota. I blastomiceti del tabacco in fermentazione – i lieviti asporigeni. Boll. Tec. Regio Ist. Sper. Colt. Tab. "Leonardo Angeloni", Scafati, no. 3–4.

Giovannozzi, M. 1948. Microflora blastomicetica dei tabacchi. Mycopathologia 4, 260–267.

Girbardt, M. 1958. Über die Substruktur von *Polystictus* versicolor L. Arch. Mikrobiol. 28, 255–269.

Girbardt, M. 1961. Licht-und Elektronenmikroskopische Untersuchungen an *Polystictus* versicolor. Arch. Mikrobiol. 39, 351–359.

Giribet, G., W. Wheeler and J. Muona. 2002. DNA multiple sequence alignments. In: R. De-Salle, G. Giribet and W. Wheeler (Eds), Molecular Systematics and Evolution: Theory and Practice. Birkhäuser, Basel, pp. 45–67.

Girmenia, C., L. Pagano, B. Martino, D. d'Antonio, R. Franci, G. Specchia, L. Melillo, M. Buelli, G. Pizzarelli, M. Venditti and P. Martino. 2005. Invasive infections caused by *Trichosporon* species and *Geotrichum capitatum* in patients with hematological malignancies: a retrospective multicenter study from Italy and review of the literature. J. Clin. Microbiol. 43, 1818–1828.

Girmenia, C., G. Pizzarelli, F. Cristini, F. Barchiesi, E. Spreghini, G. Scalise and P. Martino. 2006. *Candida guilliermondii* fungemia in patients with hematologic malignancies. J. Clin. Microbiol. 44, 2458–2464.

Giudici, P. 1990. Inhibitory action of acetic acid on osmophilic yeasts isolated from traditional balsamic vinegar. Industrie della Bevande 19, 475–477.

Giusiano, G., M. Mangiaterra, V.G. Saito, F. Rojas, V. Gomez and M.C. Diaz. 2006. Etiology of fungaemia and catheter colonisation in Argentinean paediatric patients. Mycoses 49, 49–54.

Gjaerum, H.B. 1964. The genus *Taphrina* Fr. in Norway. Nytt Mag. Bot. 11, 5–26.

Gjaerum, H.B. 1966. Oretunge forarsaket av *Taphrina alni* (B. and Br.) n. comb. i Norge. Blyttia 24, 188–195.

Glaever, G., A.M. Chu, L. Ni, C. Connelly, L. Riles, S. Veronneau, S. Dow, A. Lucau-Danila, K. Anderson, B. Andre, A.P. Arkin, A. Astromoff, M. El-Bakkoury, R. Bangham, R. Benito, S. Brachat, S. Campanaro, M. Curtiss, K. Davis, A. Deutschbauer, K.D. Entian, P. Flaherty, F. Foury, D.J. Garfinkel, M. Gerstein, D. Gotte, U. Guldener, J.H. Hegemann, S. Hempel, Z. Herman, D.F. Jaramillo, D.E. Kelly, S.L. Kelly, P. Kotter, D. LaBonte, D.C. Lamb, N. Lan, H. Liang, H. Liao, L. Liu, C. Luo, M. Lussier, R. Mao, P. Menard, S.L. Ooi, J.L. Revuelta, C.J. Roberts, M. Rose, P. Ross-Macdonald, B. Scherens, G. Schimmack, B. Shafer, D.D. Shoemaker, S. Sookhai-Mahadeo, R.K. Storms, J.N. Strathern, G. Valle, M. Voet, G. Volckaert, C.Y. Wang, T.R. Ward, J. Wilhelmy, E.A. Winzeler, Y. Yang, G. Yen, E. Youngman, K. Yu, H. Bussey, J.D. Boeke, M. Snyder, P. Philippsen, R.W. Davis and M. Johnston. 2002. Functional profiling of the *Saccharomyces cerevisiae* genome. Nature 418, 387–391.

Glanser, M., and S.N. Ban. 1983. Degradation of lignin of corn stover by means of yeasts: *Trichosporon*. Process Biochem. 19, 105–110.

Glushakova, A.M., and I.Y. Chernov. 2004. Seasonal dynamics in a yeast population on leaves of the common wood sorrel *Oxalis acetosella* L. Mikrobiologiia 73, 226–232. In Russian.

Glushakova, A.M., Iu.V. Ivannikova, E.S. Naumova, I.Iu. Chernov and G.I. Naumov. 2007. Massive isolation and identification of *Saccharomyces paradoxus* yeasts from plant phyllosphere. Mikrobiologiia 76, 236–242. In Russian.

Gochenaur, S.E. 1981. *Cyrenella elegans* gen. et sp. nov., a dikaryotic anamorph. Mycotaxon 13, 267–277.

Godjevargova, T., D. Ivanova, Z. Alexieva and N. Dimova. 2003. Biodegradation of toxic organic components from industrial phenol production waste waters by free and immobilized *Trichosporon cutaneum*. Process Biochem. 38, 915–920.

Goffeau, A. 1996. A vintage year for yeast and Yeast. Yeast 12, 1603–1605.

Goffeau, A., B.G. Barrell, H. Bussey, R.W. Davis, B. Dujon, H. Feldmann, F. Galibert, J.D. Hoheisel, C. Jacq, M. Johnston, E.J. Louis, H.W. Mewes, Y. Murakami, P. Philippsen, H. Tettelin and S.G. Oliver. 1996. Life with 6000 genes. Science 274, 546, 563–567.

Goffeau, A., R. Aert, M.L. Agostini-Carbone, A. Ahmed, M. Aigle, L. Alberghina, E. Allen, J. Alt-Mörbe, B. André, S. Andrews, W. Ansorge, G. Antoine, R. Anwar, A. Aparicio, R. Araujo, J. Arino, F. Arnold, J. Arroyo, E. Aviles, et al. 1997. The yeast genome directory. Nature 387 (Suppl.), 5–105.

Goh, E.L.C., A.D. Hocking, C.M. Stewart, K.A. Buckle and G.H. Fleet. 2007. Bioprotective effect of increased solute concentration on yeasts and moulds during high pressure processing. Innov. Food Sci. Emerg. Technol. 8, 535–542.

Gojkovic, Z., M.P. Sandrini and J. Piśkur. 2001. Eukaryotic beta-alanine synthases are functionally related but have a high degree of structural diversity. Genetics 158, 999–1011.

Gojkovic, Z., W. Knecht, E. Zameitat, J. Warneboldt, J.B. Coutelis, Y. Pynyaha, C. Neuvéglise, K. Moller, M. Loffler and J. Piśkur. 2004. Horizontal gene transfer promoted evolution of the ability to propagate under anaerobic conditions in yeasts. Mol. Genet. Genomics 271, 387–393.

Gokhale, A.A. 1972. Studies on the genus *Tilletiopsis*. Nova Hedwigia 23, 795–809.

Goldani, L.Z., D.E. Craven and A.M. Sugar. 1995. Central venous catheter infection with *Rhodotorula minuta* in a patient with AIDS taking suppressive doses of fluconazole. J. Med. Vet. Mycol. 33, 267–270.

Goldemberg, J. 2007. Ethanol for a sustainable energy future. Science 315, 808–810.

Goldman, N. 1993. Statistical tests of models of DNA substitution. J. Mol. Evol. 36, 182–198.

Goldman, N., and S. Whelan. 2000. Statistical tests of gamma-distributed rate heterogeneity in models of sequence evolution in phylogenetics. Mol. Biol. Evol. 17, 975–978.

Goloboff, P.A. 1999. Analyzing large data sets in reasonable times: solutions for composite optima. Cladistics 15, 415–428.

Golonka, A.M. 2002. Nectar-inhabiting microorganisms and the dioecious plant species *Silene latifolia*. PhD Thesis, Duke University, Durham, NC.

Golubev, W.I. 1973. *Nadsonia commutata* nov. sp. Mikrobiologiia 42, 1058–1061.

Golubev, W.I. 1977. *Metschnikowia lunata* sp. nov. Antonie van Leeuwenhoek 43, 317–322.
Golubev, W.I. 1981. Novye kombinatsii drozhzhevykh gribov roda *Cryptococcus*. Mikol. Fitopatol. 15, 467–468.
Golubev, W.I. 1984. *Cryptococcus fuscescens* sp. nov., and a diagnostic key to the nitrate-positive species of the genus *Cryptococcus*. J. Gen. Appl. Microbiol. 30, 427–433.
Golubev, W.I. 1989a. The action spectrum of killer toxin produced by *Rhodotorula glutinis* and its taxonomic significance. Mikrobiologiia 58, 99–103. In Russian.
Golubev, W.I. 1989b. Catabolism of *m*-inositol and taxonomic value of D-glucuronate assimilation in yeasts. Mikrobiologiia 58, 276–283. In Russian.
Golubev, W.I. 1990. Killer-sensitive relationships among yeast-like fungi: physiogenic implications. Proc. 14th Int. Spec. Symp. Yeasts, Smolenice, pp. 36–38.
Golubev, W.I. 1991a. Capsules. In: A.H. Rose and J.S. Harrison (Eds), The Yeasts, 2nd edn. Vol. 4. Academic Press, London, pp. 175–197.
Golubev, W.I. 1991b. Taxonomic evaluation of mycocins produced by basidiomycetous yeast *Cryptococcus podzolicus*. Mikrobiologiia 60, 115–121. In Russian.
Golubev, W.I. 1993. *Rhodosporidium babjevae*, a new heterothallic yeast species (Ustilaginales). Syst. Appl. Microbiol. 16, 445–449.
Golubev, W.I. 1995. Perfect state of *Rhodomyces dendrorhous* (*Phaffia rhodozyma*). Yeast 11, 101–110.
Golubev, W.I. 1998a. Mycocins (killer toxins). In: C.P. Kurtzman and J.W. Fell (Eds), The Yeasts, A Taxonomic Study, 4th edn. Elsevier, Amsterdam, pp. 55–62.
Golubev, W.I. 1998b. *Xanthophyllomyces* Golubev. In: C.P. Kurtzman and J.W. Fell (Eds), The Yeasts, A Taxonomic Study, 4th edn. Elsevier, Amsterdam, pp. 718–719.
Golubev, W.I. 1998c. *Rhodotorula creatinivora* and *Rh. yakutica* – new species of basidiomycetous yeasts extracted from permafrost soils on eastern Siberian Arctic. Mikrobiologiia 32, 8–13.
Golubev, W. 1998d. Killer activity of *Tilletiopsis albescens* Gokhale: taxonomic and phylogenetic implication. Syst. Appl. Microbiol. 21, 429–432.
Golubev, W.I. 1999. *Mastigobasidium*, a new teleomorphic genus for the perfect state of ballistosporous yeast *Bensingtonia intermedia*. Int. J. Syst. Bacteriol. 49, 1301–1305.
Golubev, W.I. 2000. Isolation of tremelloid yeasts on glucuronate medium. Mikrobiologiia 69, 490–493.
Golubev, W.I., and I.P. Bab′eva. 1972. *Debaryomyces formicarius* sp. n. and *Debaryomyces cantarellii* associated with the ants of the group *Formica rufa* L. J. Gen. Appl. Microbiol. 18, 249–254.
Golubev, W.I., and I.P. Bab′eva. 1977. *Torulopsis apis* var. *galacta* var. nov. Int. J. Syst. Bacteriol. 27, 165–167.
Golubev, W.I., and V.M. Blagodatskaya. 1978. The significance of the ability to assimilate d-glucuronic acid, D-glucono-D-lactone and 5-keto-D-gluconate in identification of species of *Candida* Berkhout. Mikrobiologiia 47, 841–848. In Russian.
Golubev, W.I., and T. Boekhout. 1992. Dimorphism in *Itersonilia perplexans*: differences between yeast and hyphal forms in sensitivity to mycocins produced by Tremellaceous yeasts. FEMS Microbiol. Lett. 98, 187–190.
Golubev, W.I., and T. Boekhout. 1995. Sensitivity to killer toxins as a taxonomic tool among heterobasidiomycetous yeasts. Stud. Mycol. 38, 47–58.
Golubev, W.I., and I.G. Churkina. 1993. Intrageneric killing patterns of *Rhodotorula mucilaginosa* mycocins. Proc. Russian Acad. Sci. (Ser. Biol.) 4, 550–557. In Russian.
Golubev, W.I., and L.G. Churkina. 2001. Specificity of sensitivity to mycocin from *Tilletiopsis flava* BKM Y-2838. Mikrobiologiia 70, 51–54.
Golubev, W.I., and N.V. Golubev. 2002. Selenium tolerance of yeasts. Microbiology (Moscow) 71, 386–390 (translated from Mikrobiologiia 71, 455–459).
Golubev, W.I., and N.W. Golubev. 2003. A new basidiomycetous yeast species, *Cryptococcus mycelialis*, related to *Holtermannia* Saccardo et Traverso. Microbiology (Moscow) 72, 728–732 (translated from Mikrobiologiia 72, 822–827).
Golubev, W.I., and L.B. Kuznetsova. 1989. Formation and spectrum of action of mycocins of the basidiomycetous yeast *Cryptococcus laurentii* (Kufferath) Skinner. Mikrobiologiia 58, 980–984. In Russian.
Golubev, W.I., and T. Nakase. 1997. Mycocinogeny in the genus *Bullera*: taxonomic specificity of sensitivity to the mycocin produced by *Bullera sinensis*. FEMS Microbiol. Lett. 146, 59–64.
Golubev, W.I., and T. Nakase. 1998. Mycocinogeny in the genus *Bullera*: killer activity of *Bullera unica* and intrageneric killer-sensitive relationships. Microbiology (Moscow) 67, 184–188.
Golubev, W.I., and J.P. Sampaio. 2009. New filobasidiaceous yeasts found in the phylloplane of a fern. J. Gen. Appl. Microbiol. 55, 441–446.
Golubev, W., and Y. Shabalin. 1994. Microcin production by the yeast *Cryptococcus humicola*. FEMS Microbiol. Lett. 119, 105–110.
Golubev, W.I., and F. Staib. 2000. Green and brown colour effects in Tremellaceous yeast fungi on Staib agar. Mycoses 43, 1–5.
Golubev, W.I., and A.B. Tsiomenko. 1985. Killer strains of ballistosporogenous yeast fungus of the genus *Sporidiobolus* Nyland. Dokl. Akad. Nauk SSSR 282, 425–428. In Russian.
Golubev, W.I., and L.M. Vagabova. 1977. Deoxyribonucleic acid base composition in some yeast species. Izv. Akad. Nauk SSSR, Ser. Biol. 6, 933–936. In Russian.
Golubev, W.I., and N.V. Vdovina. 1973. Soil Yeasts of Rice Fields Treated by Pesticides. The Behavior, Conversion and Analysis of Pesticides and their Metabolites in Soil. USSR Academy of Sciences, Pushchino, pp. 66–73. In Russian.
Golubev, W.I., N. Okunevo and W. Vdavinan. 1974. Assimilation of inositol as a criterion in yeast identification. Mikrobiologiia 6, 1047–1050. In Russian.
Golubev, W.I., I.P. Bab′eva, V.M. Blagodatskaya and I.S. Reshetova. 1977. Taxonomic study of yeasts isolated from spring sap flows of birch (*Betula verrucosa* Ehrh.). Mikrobiologiia 46, 564–568. In Russian.
Golubev, W.I., V.M. Blagodatskaya, S.O. Suetin and R.S. Trotsenko. 1981. *Pichia inositovora* and *Candida paludigena*, two new species of yeasts isolated from peat. Int. J. Syst. Bacteriol. 31, 91–96.
Golubev, W.I., I.P. Bab'eva, M.E. Vimovarova and V.S. Tyurin. 1987. Additional strains of rare *Nadsonia* species. Mikrobiologiia 56, 454–459. In Russian.
Golubev, W.I., A.B. Tsiomenko and L.P. Tikhomirova. 1988. Plasmid-free killer strains of the yeast *Sporidiobolus pararoseus*. Mikrobiologiia 57, 805–809. In Russian.

Golubev, W.I., M.Th. Smith, G.A. Poot and J.L.F. Kock. 1989. Species delineation in the genus *Nadsonia* Sydow. Antonie van Leeuwenhoek 55, 369–382.

Golubev, W.I., L.G. Churkina and S.A. Seregina. 1996a. Intergeneric action spectra of the *Rhodotorula mucilaginosa* mycocins. Izv. Ross. Akad. Nauk, Ser. Biol. N 5, 523–529. In Russian.

Golubev, W.I., R. Ikeda, T. Shinoda and T. Nakase. 1996b. Mycocinogeny in the genus *Bullera*: anti-Tremellaceous yeast activity of killer toxin produced by *Bullera hannae*. J. Gen. Appl. Microbiol. 42, 471–479.

Golubev, W.I., T.V. Kulakovskaia and E.V. Golubeva. 2001. *Pseudozyma fusiformata* BKM Y-2821 – a producer of antifungal glycolipid. Mikrobiologiia 70, 642–646. In Russian.

Golubev, W.I., M. Gadanho, J.P. Sampaio and N.W. Golubev. 2003. *Cryptococcus nemorosus* sp. nov. and *Cryptococcus perniciosus* sp. nov., related to *Papiliotrema* Sampaio et al. (Tremellales). Int. J. Syst. Evol. Microbiol. 53, 905–911.

Golubev, W.I., J.P. Sampaio, M. Gadanho and E.W. Golubeva. 2004a. *Cryptococcus paraflavus* sp. nov. (Tremellales), isolated from steppe plants in Russia. J. Gen. Appl. Microbiol. 50, 65–69.

Golubev, W.I., J.P. Sampaio, L. Alves and N.W. Golubev. 2004b. *Cryptococcus festucosus* sp. nov.: a new hymenomycetous yeast in the *Holtermannia* clade. Can. J. Microbiol. 50, 1001–1006.

Golubev, W.I., T.V. Kulakovskaya, E.V. Kulakovskaya and N.W. Golubev. 2004c. The fungicidal activity of an extracellular glycolipid from *Sympodiomycopsis paphiopedili* Sugiyama et al. Microbiology (Moscow) 73, 724–728.

Golubev, W.I., J.P. Sampaio, L. Alves and E.W. Golubeva. 2006a. *Cryptococcus silvicola* nov. sp. from nature reserves of Russia and Portugal. Antonie van Leeuwenhoek 89, 45–51.

Golubev, W.I., J.P. Sampaio and E.W. Golubeva. 2006b. *Cryptococcus stepposus*, a new filobasidiaceous yeast species found in the Prioksko-terrasny biosphere reserve in Russia. Mycol. Res. 110, 957–961.

Golubev, W., T. Sugita and N. Golubev. 2007. An ustilaginomycetous yeast, *Pseudozyma graminicola* sp. nov., isolated from the leaves of pasture plants. Mycoscience 48, 29–33.

Golubev, W.I., I. Pfeiffer and M.A. Tomashevskaya. 2008. *Cryptococcus pinus* sp. nov., an anamorphic basidiomycetous yeast isolated from pine litter. Int. J. Syst. Evol. Microbiol. 58, 1968–1971.

Golubev, W.I., and J.P. Sampaio. 2009. New filobasidiaceous yeasts found in the phylloplane of a fern. J. Gen. Appl. Microbiol. 55, 441–446.

Gomes, J., I. Gomes and W. Steiner. 2000. Thermolabile xylanase of the Antarctic yeast *Cryptococcus adeliae*: production and properties. Extremophiles 4, 227–235.

Gomes, J.M. 1924. Mycose broncho-pulmonar *Monilia butantanensis* (n. sp.). Ann. Paulistas Med. Cirurg. 15, 246–251.

Gomez-Lopez, A., A. Alastruey-Izquierdo, D. Rodriguez, B. Almirante, A. Pahissa, J.L. Rodriguez-Tudela and M. Cuenca-Estrella. 2008. Prevalence and susceptibility profile of *Candida metapsilosis* and *Candida orthopsilosis*: results from population–based surveillance of candidemia in Spain. Antimicrob. Agents Chemother. 52, 1506–1509.

Gomez-Ruiz, L., M. Garcia-Garibay and E. Barzana. 1988. Utilization of endo-polygalacturonase from *Kluyveromyces fragilis* in the clarification of apple juice. J. Food Sci. 53, 12–36.

Gondé, P., B. Blondin, M. Leclerc, R. Ratomahenina, A. Arnaud and P. Glazy. 1984. Fermentation of cellodextrins by different yeast strains. Appl. Environ. Microb. 48, 265–269.

Gondé, P., R. Ratomahenina, A. Arnaud and P. Glazy. 1985. Purification and properties of an extracellular β-glucosidase of *Candida molischiana* (Zikes) Meyer & Yarrow capable of hydrolyzing soluble cellodextrins. Can. J. Biochem. Cell Biol. 63, 1160–1166.

Gong, X., and B. Kendrick. 1995. *Agaricostilbum nova-zelandica*, a new auricularioid fungus on *Rhopalostylis sapida* from New Zealand. Mycotaxon 54, 19–25.

Gonzáles, S., J. Gafnerand and A. Querol. 2006. Natural hybrids from *Saccharomyces cerevisiae*, *Saccharomyces bayanus* and *Saccharomyces kudriavzevii* in wine fermentations. FEMS Yeast Res. 6, 1221–1234.

González, R.N., D.J. Wilson, S.A. Sickles, M.J. Zurakowski, P.M. Weybrecht and A.K. Walsh. 2001. Outbreaks of clinical mastitis caused by *Trichosporon beigelii* in dairy herds. J. Am. Vet. Med. Assoc. 218, 238–242.

Goodman, M. 1976. Protein sequences in phylogeny. In: F.J. Ayala (Ed.), Molecular Evolution. Sinauer Associates, Sunderland, MA, pp. 141–159.

Gordon, M.A. 1951. The lipophilic mycoflora of the skin. I. *In vitro* culture of *Pityrosporum orbiculare* n. sp. Mycologiia 43, 524–535.

Goremykin, V.V., K.I. Hirsch-Ernst, S. Wolfl and F.H. Hellwig. 2003. Analysis of the *Amborella trichopoda* chloroplast genome sequence suggests that *Amborella* is not a basal angiosperm. Mol. Biol. Evol. 20, 1499–1505.

Gori, K., M. Hebraud, C. Chambon, H.D. Mortensen, N. Arneborg and L. Jespersen. 2007. Proteomic changes in *Debaryomyces hansenii* upon exposure to NaCl stress. FEMS Yeast Res. 7, 293–303.

Gorin, P.A.J. 1973. The position of phosphate groups in the phosphomannans of *Hansenula capsulata*, as determined by carbon-13 magnetic resonance spectroscopy. Can. J. Chem. 51, 2105–2109.

Gorin, P.A.J., and J.F.T. Spencer. 1968. Galactomannans of *Trichosporon fermentans* and other yeasts; proton magnetic resonance and chemical studies. Can. J. Chem. 46, 2299–2304.

Gorin, P.A.J., and J.F.T. Spencer. 1970. Proton magnetic resonance spectroscopy – an aid in identification and chemotaxonomy of yeasts. Adv. Appl. Microbiol. 13, 25–89.

Goto, K., T. Iwase, K. Kichise, K. Kitano, A. Totuka, T. Obata and S. Hara. 1990. Isolation and properties of a chromosome-dependent KHR killer toxin in *Saccharomyces cerevisiae*. Agric. Biol. Chem. 54, 505–509.

Goto, K., H. Fukuda, K. Kichise, K. Kitano and S. Hara. 1991. Cloning and nucleotide sequence of the KHS killer gene of *Saccharomyces cerevisiae*. Agric. Biol. Chem. 55, 1953–1958.

Goto, S. 1980. *Saccharomyces placentae* Goto sp. nov. J. Gen. Appl. Microbiol. 26, 311–313.

Goto, S. 1979a. A new yeast species, *Candida acutus*, isolated from sulfited grape must. J. Gen. Appl. Microbiol. 25, 145–148.

Goto, S. 1979b. Two new yeast species belonging to the genus *Candida*. J. Gen. Appl. Microbiol. 25, 293–297.

Goto, S., and H. Oguri. 1983. Two new species of the genus *Candida* from wild grapes. J. Gen. Appl. Microbiol. 29, 85–90.

Goto, S., and J. Sugiyama. 1968. Studies on the Himalayan yeasts and molds (I). A new species of *Debaryomyces* and some asporogenous yeasts. J. Jpn. Bot. 43, 102–108.

Goto, S., and J. Sugiyama. 1970. Studies on Himalayan yeasts and molds (IV). Several asporogenous yeasts, including two new taxa of *Cryptococcus*. Can. J. Bot. 48, 2097–2101.

Goto, S., and H. Takami. 1986. Classification of Ascoideaceous yeasts based on the electrophoretic comparison of enzymes and coenzyme Q systems. J. Gen. Appl. Microbiol. 32, 271–282.

Goto, S., and I. Yokotsuka. 1962b. Classification of the film yeasts maintained in Japan. Part 2. Genus *Hansenula*. Bull. R. Inst. Ferment., Yamanashi Univ. 9, 79–87.

Goto, S., J. Sugiyama and H. Iizuka. 1969. A taxonomic study of Antarctic yeasts. Mycologia 61, 748–774.

Goto, S., K. Yamasato and H. Iizuka. 1974. Identification of yeasts isolated from the Pacific Ocean. J. Gen. Appl. Microbiol. 20, 309–316.

Goto, S., Y. Yamakawa and I. Yokotsuka. 1975. Classification of fragrant odor producing *Geotrichum* (Studies on fragrant odor producing microorganisms, Part II). J. Agric. Chem. Soc. Jpn 49, 519–525.

Goto, S., J. Sugiyama, M. Hamamoto and K. Komagata. 1987a. *Saitoella*, a new anamorphic genus in the Cryptococcaceae to accommodate two Himalayan yeast isolates formerly identified as *Rhodotorula glutinis*. J. Gen. Appl. Microbiol. 33, 75–85.

Goto, S., H. Iwasaki, Y. Okuma, Y. Ito and A. Endo. 1987b. New species belonging to the genera *Pichia* and *Candida*. J. Gen. Appl. Microbiol. 33, 275–286.

Goto, S., S. Horiguchi, H. Kaneko and T. Itoh. 1988. Distribution of pyrophosphatidic acid in yeast species. J. Gen. Appl. Microbiol. 34, 165–182.

Gotor-Fernández, V., E. Busto and V. Gotor. 2006. *Candida antarctica* lipase B: an ideal catalyst for the preparation of nitrogenated organic compounds. Adv. Synth. Catal. 348, 797–812.

Gottschalk, M. 1985. Untersuchungen zur Phylogenie der Basidiomyceten anhand des Vergleichs der Nucleotidsequenzen ihrer 5S ribosomalen Ribonukleinsäuren. Thesis, Universität Tübingen.

Gottschalk, M., and P.A. Blanz. 1985. Untersuchungen an 5S ribosomalen Ribonukleinsäuren als Beitrag zur Klärung von Systematik und Phylogenie der Basidiomyceten. Z. Mykol. 51, 205–244.

Gouger, R.J. 1972. Interrelations of *Ips avulsus* (Eichh.) and associated fungi. Diss. Abstr. 6453–B, 32.

Gouliamova, D.E., G.L. Hennebert, M.T. Smith and J.P. van der Walt. 1998. Diversity and affinities among species and strains of *Lipomyces*. Antonie van Leeuwenhoek 74, 283–291.

Gounot, A.M. 2001. Ecology of psychrophilic and psychrotrophic microorganisms in cold and frozen soils. In: R. Paepe and V. Melnikov (Eds), Permafrost Response on Economic Development, Environmental Security and Natural Resources. Kluwer, Dordrecht, pp. 543–551.

Gow, N.A.R., and G.W. Gooday. 1983. Ultrastructure of chitin in hyphae of *Candida albicans* and other dimorphic and mycelial fungi. Protoplasma 155, 52–85.

Gow, N.A.R., G.W. Gooday, R.J. Newsam and K. Gull. 1980. Ultrastructure of the septum in *Candida albicans*. Curr. Microbiol. 4, 357–359.

Graham, L.A., A.R. Flannery and T.H. Stevens. 2003. Structure and assembly of the yeast V-ATPase. J. Bioenerg. Biomembr. 35, 301–312.

Granchi, L., N. Bosco, A. Messini and M. Vincenzini. 1999. Rapid detection and quantification of yeast species during spontaneous wine fermentation by PCR-RFLP analysis of the rDNA ITS region. J. Appl. Microbiol. 87, 949–956.

Granchi, L., D. Ganucci, A. Messini and M. Vincenzini. 2002. Oenological properties of *Hanseniaspora osmophila* and *Kloeckera corticis* from wines produced by spontaneous *fermentati*ons of normal and dried grapes. FEMS Yeast Res. 2, 403–407.

Granick, S. 1948. Protoporphyrin 9 as a precursor of chlorophyll. J. Biol. Chem. 172, 717–727.

Gravesse, C., M.H. Jijakli and P. Lipoivre. 1998. Study of the exo-β-1,3-glucanase activity production by yeast *Pichia anomala* in relation to its antagonistic properties against *Botrytis cinerea* on postharvest apples. Meded. Fac. Landbouwwet.-Rijksuniv. Gent. 63, 1682–1685.

Grawitz, P. 1877. Zur Botanik des Soors und der Dermatomycosen. Dtsch. Z. Prakt. Med., No. 20, 19 May, 209–211.

Gray, K.A., L. Zhao and M. Emptage. 2006. Bioethanol. Curr. Opin. Chem. Biol. 10, 141–146.

Graybeal, A. 1998. Is it better to add taxa or characters to a difficult phylogenetic problem? Syst. Biol. 47, 9–17.

Graziano, F. 1930. La presenza di eumiceti nelle feci dei lattanti sani ed ammalati. G. Batteriol. Immunol. 5, 1061–1077.

Greene, C.E., D.M. Miller and J.L. Blue. 1985. *Trichosporon* infection in a cat. J. Am. Vet. Med. Assoc. 187, 946–948.

Greenwalt, C.J., J.B. Hunter, S. Lin, S. McKenzie and A. Denvir. 2001. Ozonation and alkaline-peroxide pretreatment of wheat straw for *Cryptococcus curvatus* fermentation. Life Support Biosph. Sci. 7, 243–249.

Greuter, W., H.M. Burdet, V. Demoulin, R. Grolle, D.L. Hawksworth, D.H. Nicholson, P.C. Silva, F.A. Stafleu, E.G. Voss and J. McNeill (Eds). 1988. International Code of Botanical Nomenclature. Koeltz Scientific Books, Königstein, Germany.

Greuter, W., F.R. Barrie, H.M. Burdet, W.G. Chaloner, V. Demoulin, D.L. Hawksworth, P.M. Jørgensen, D.H. Nicolson, P.C. Silva, P. Trehane and J. McNeill (Eds). 1994. International Code of Botanical Nomenclature. Koeltz Scientific Books, Königstein, Germany

Grevesse, C., P. Lepoivre and H. Jijakli. 2003. Characterization of the exo-glucanase-encoding gene PaEXG2 and study of its role in the biocontrol activity of *Pichia anomala* strain K. Phytopathology 93, 1145–1152.

Grewal, S.I., and S.C. Elgin. 2002. Heterochromatin: new possibilities for the inheritance of structure. Curr. Opin. Genet. Dev. 12, 178–187.

Griffin, D.H. 1994. Molecular architecture. In: D.H. Griffin (Ed.), Fungal Physiology, 2nd edn. Wiley, New York, pp. 63–101.

Grigoraki, L., and G. Péju. 1921. Sur une nouvelle espèce de levure du genre *Debaryomyces* (*D. matruchoti*). C.R. Soc. Biol. 85, 459–462.

Grinbaum, A., I. Ashkenazi, G. Treister, A. Goldschmied-Reouven and C.S. Block. 1994. Exploding bottles: eye injury due to yeast fermentation of an uncarbonated soft drink. Br. J. Opthalmol. 78, 883.

Grinbergs, J. 1967. Zur Kenntnis einer neuen Hefeart: *Candida tepae* sp. nov. Arch. Mikrobiol. 56, 202–204.

Grinbergs, J., and D. Yarrow. 1970a. Two new *Candida* species: *Candida chilensis* sp. n. and *Candida valdiviana* sp. n. Antonie van Leeuwenhoek 36, 143–148.

Grinbergs, J., and D. Yarrow. 1970b. *Rhodotorula araucariae* sp. n. Antonie van Leeuwenhoek 36, 455–457.

Groenewald, M., H.-M. Daniel, V. Robert, G.A. Poot and M.Th. Smith. 2008. Polyphasic reexamination of *Debaryomyces hansenii* strains and reinstatement of *D. hansenii, D. fabryi* and *D. subglobosus*. Persoonia 21, 17–27.

Groenewege, J. 1921a. Ueber das Vorkommen von Emulsin bei Saccharomyceten und das Vorhandensein eines spezifischen Enzyms Zellobiase. Meded. Algem. Proefstn. Landbouw Ned. Indië No. 9, 1–12.

Groenewege, J. 1921b. Over de oorzaak van rustiness op rubber van *Hevea brasiliensis*. Meded. Algem. Proefstn. Landbouw Ned. Indië No. 11, 5–19.

Groll, A.H., and T.J. Walsh. 2001. Uncommon opportunistic fungi: new nosocomial threats. Clin. Microbiol. Infect. 7 (Suppl. 2), 8–24.

Grönlund, C. 1892. Eine neue *Torula*-Art und zwei neue *Saccharomyces*-Arten im Neu-Carlsberg Laboratorium untersucht. Z. Gesamte Brauwes 15, 281.

Grosbüsch, J. 1915. Über eine farblose, stark roten Farbstoff erzeugende *Torula*. Zentralbl. Bakteriol. Parasitenkd Abt. II, 42, 625–638.

Grose, E.S., and C.J. Marinkelle. 1968. A new species of *Candida* from Colombian bats. Mycopathol. Mycol. Appl. 36, 225–227.

Gross, M., I.J. Kosmowsky, R. Lorenz, H.P. Molitoris and R. Jaenicke. 1994. Response of bacteria and fungi to high-pressure stress as investigated by two-dimensional polyacrylamide gel electrophoresis. Electrophoresis 15, 1559–1569.

Groth, C., J. Hansenand and J. Piśkur. 1999. A natural chimeric yeast containing genetic material from three species. Int. J. Syst. Bacteriol. 49, 1933–1938.

Grün, C.H., F. Hochstenbach, B.M. Humbel, A.J. Verkleij, J.H. Sietsma, F.M. Klis, J.P. Kamerling and J.F. Vliegenthart. 2005. The structure of cell wall a-glucan from fission yeast. Glycobiology 15, 245–257.

Gründer, S., P. Mayser, T. Redmann and E.F. Kaleta. 2005. Mycological examinations on the fungal flora of the chicken comb. Mycoses 48, 114–119.

Grüss, J. 1918. Die Anpassung eines Pilzes (*Anthomyces reukaufii*) an den Blütenbau und den Bienenrüssel. Ber. Dtsch. Bot. Ges. 35, 746–761.

Grüss, J. 1926. Genetische und gärungsphysiologische Untersuchungen an Nektarhefen. Jahrb. Wiss. Bot. 66, 109–182.

Grüss, J. 1927. Über hochalpine Nektarhefen. II. *Mikroanthomyces alpinus* nov. gen. et spec. Wochenschr. Brau. 243–246, 253–257.

Gu, W.L., G.-H. An and E.A. Johnson. 1997. Ethanol increases carotenoid production in *Phaffia rhodozyma*. J. Ind. Microbiol. Biotechnol. 19, 114–117.

Gu, Z., L. David, D. Petrov, T. Jones, R.W. Davis and L.M. Steinmetz. 2005. Elevated evolutionary rates in the laboratory strain of *Saccharomyces cerevisiae*. Proc. Natl. Acad. Sci. USA 102, 1092–1097.

Guéguen, F. 1904. Les champignons parasites de l'homme et des animaux. Thèse, Paris.

Gueguen, Y., P. Chemardin, S. Pien, A. Arnaud and P. Glazy. 1997. Enhancement of aromatic quality of Muscat wine by the use of immobilized β-glucosidase. J. Biotechnol. 55, 151–156.

Guého, E. 1979. Deoxyribonucleic acid base composition and taxonomy in the genus *Geotrichum* Link. Antonie van Leeuwenhoek 45, 199–210.

Guého, E., and J. Guillot. 1999. Comments on *Malassezia* species from dogs and cats. Mycoses 42, 673–674.

Guého, E., and S.A. Meyer. 1989. A re-evaluation of the genus *Malassezia* by means of genome comparison. Antonie van Leewenhoek 55, 245–253.

Guého, E., and H.J. Phaff. 1983. *Pichia norvegensis*, telemorphe de *Candida norvegensis*: validation per homologie chromosomique. Bull. Soc. Fr. Mycol. Med. 12, 203–208.

Guého, E., J. Tredick and H.J. Phaff. 1984. DNA base composition and DNA relatedness among species of *Trichosporon* Behrend. Antonie van Leeuwenhoek 50, 17–32.

Guého, E., J. Tredick and H.J. Phaff. 1985. DNA relatedness among species of *Geotrichum* and *Dipodascus*. Can. J. Bot. 63, 961–966.

Guého, E., G.S. de Hoog, M.Th. Smith and S.A. Meyer. 1987a. DNA relatedness, taxonomy, and medical significance of *Geotrichum capitatum*. J. Clin. Microbiol. 25, 1191–1194.

Guého, E., R.B. Simmons, W.R. Pruitt, S.A. Meyer and D.G. Ahearn. 1987b. Association of *Malassezia pachydermatis* with systemic infections of humans. J. Clin. Microbiol. 25, 1789–1790.

Guého, E., C.P. Kurtzman and S.W. Peterson. 1989. Evolutionary affinities of heterobasidiomycetous yeasts estimated from 18S and 25S ribosomal RNA sequence divergence. Syst. Appl. Microbiol. 12, 230–236.

Guého, E., C.P. Kurtzman and S.W. Peterson. 1990. Phylogenetic relationships among species of *Sterigmatomyces* and *Fellomyces* as determined from partial rRNA sequences. Int. J. Syst. Bacteriol. 40, 60–65.

Guého, E., G.S. de Hoog and M.Th. Smith. 1992a. Neotypification of the genus *Trichosporon*. Antonie van Leeuwenhoek 61, 285–288.

Guého, E., M.Th. Smith, G.S. de Hoog, G. Billon-Grand, R. Christen and W.H. Batenburg-van der Vegte. 1992b. Contributions to a revision of the genus *Trichosporon*. Antonie van Leeuwenhoek 61, 289–316.

Guého, E., L. Improvisi, R. Christen and G.S. de Hoog. 1993. Phylogenetic relationships of *Cryptococcus neoformans* and some related basidiomycetous yeasts determined from partial large subunit rRNA sequences. Antonie van Leeuwenhoek 63, 175–189.

Guého, E., L. Improvisi, G.S. de Hoog and B. Dupont. 1994. *Trichosporon* on humans: a practical account. Mycoses 37, 3–10.

Guého, E., G. Midgley and J. Guillot. 1996. The genus *Malassezia* with description of four new species. Antonie van Leeuwenhoek 69, 337–355.

Guého, E., T. Boekhout, H.R. Ashbee, J. Guillot and A. van Belkum. 1998a. The role of *Malassezia* species in the ecology of human skin and as pathogen. Med. Mycol. 36 (Suppl. 1), 220–229.

Guého, E., M.Th. Smith and G.S. de Hoog. 1998b. *Trichosporon* Behrend. In: C.P. Kurtzman and J.W. Fell (Eds), The Yeasts, A Taxonomic Study, 4th edn. Elsevier, Amsterdam, pp. 854–872.

Guerra, P. 1935. Rôle des levures en dermatologie. Étude clinique et mycologique. Thèse, Faculté de Médecine de Paris.

Guerra, R., G.M. Cavallini, L. Longanesi, C. Casolari, G. Bertoli, F. Rivasi and U. Fabio. 1992. *Rhodotorula glutinis* keratitis. Int. Ophthalmol. 16, 187–190.

Guerzoni, M.E., R. Lancotti and R. Marchetti. 1993. Survey of the physiological properties of the most frequent yeasts associated with commercial chilled foods. Int. J. Food Microbiol. 17, 329–341.

Guetsky, R., D. Shtienberg, Y. Elad and A. Dinoor. 2001. Combining biocontrol agents to reduce the variability of biological control. Phytopathology 91, 621–627.

Guetsky, R., D. Shtienberg, Y. Elad, E. Fischer and A. Dinoor. 2002a. Improving biological control by combining biocontrol agents each with several mechanisms of disease suppression. Phytopathology 92, 976–985.

Guetsky, R., D. Shtienberg, A. Dinoor and Y. Elad. 2002b. Establishment, survival and activity of the biocontrol agents *Pichia guilliermondii* and *Bacillus mycoides* applied as a mixture on strawberry plants. Biocontrol Sci. Technol. 12, 705–714.

Guffogg, S.O., S. Thomas-Hall, P. Holloway and K. Watson. 2004. A novel psychrotolerant member of the hymenomycetous yeasts from Antarctica: *Cryptococcus watticus* sp. nov. Int. J. Syst. Evol. Microbiol. 54, 275–277.

Gugnani, H.C., T.G. Mitchell, A.P. Litvintseva, K.B. Lengeler, J. Heitman, A. Kumar, S. Basu and A. Paliwal-Joshi. 2005. Isolation of *Cryptococcus gattii* and *Cryptococcus neoformans* var. *grubii* from the flowers and bark of *Eucalyptus* trees in India. Med. Mycol. 43, 565–569.

Guiart, J. 1910. Saccharomycoses. Précis de Parasitologie. Bibliothèque Gilbert et Fournier, pp. 106–109.

Guidi, G. 1896. Mughetto. Micologia e Metastasi del Mughetto. Stabilimento Tipografico Fiorentino, Firenze, 82pp.

Guilliermond, A. 1909. Recherches cytologiques et taxonomiquies sur les Endomycétacées. Rev. Gen. Bot. 21, 353–391, 401–419, 865.

Guilliermond, A. 1912. Les Levures. Encyclopédie Scientifique. O. Doin et Fils, Paris.

Guilliermond, A. 1913. Nouvelles observations sur la sexualité des levures. 1. Existence d'une copulation hétérogamique observée dans une espèce nouvelle. 2. Sur la copulation de *Debaryomyces globosus*. 3. Sur les phénomènes de retrogradation de la sexualité constatés dans plusieurs levures. Arch. Protistenkd. 28, 52–77.

Guilliermond, A. 1914. Monographie des levures d'Afrique occidentale par la mission chevalière. Ann. Sci. Nat. Bot. Biol. Végétale. Sér. 19, 1–32.

Guilliermond, A. 1918. *Zygosaccharomyces nadsonii*: nouvelle espéce de levures à conjugaison hétérogamique. Bull. Soc. Mycol. Fr. 34, 1–16.

Guilliermond, A. 1919. Sur une nouvelle levure à copulation hétérogamique. C.R. Soc. Biol. 82, 466–470.

Guilliermond, A. 1928. Recherches sur quelques Ascomycètes inférieurs isolés de la stigmatomycose des graines de cotonnier: essai sur la phylogénie des Ascomycètes. Rev. Gen. Bot. 40, 328–342, 397–414, 474–485, 555–574, 606–624, 690–704.

Guilliermond, A. 1930. Homo- et hétérothallisme chez les levures. C.R. Soc. Biol. 190, 1316–1318.

Guilliermond, A. 1935. Sur un champignon nouveau isolé de la stigmatomycose des graines de cotonnier, l'*Eremothecium ashbyi* et ses relations possibles avec le *Spermophthora gossypii*. C.R. Hebd. Acad. Sci. 200, 1556–1558.

Guilliermond, A. 1936. L'*Eremothecium ashbyi*, nouveau champignon parasite des capsules du cotonnier. Rev. Mycol. 1, 115–156.

Guilliermond, A., and P. Negroni. 1929. Sur la présence d'une copulation hétérogamique dans le *Saccharomyces marxianus*. C.R. Soc. Biol. 101, 564–566.

Guilliermond, A., and G. Péju. 1919. Sur un nouveau champignon présentant des caractères intermédiaires entre les levures et les *Endomyces*. C.R. Soc. Biol. 82, 13–43.

Guillot, J., and R. Bond. 1999. *Malassezia pachydermatis*: a review. Med. Mycol. 37, 295–306.

Guillot, J., and E. Guého. 1995. The diversity of *Malassezia* yeasts confirmed by rRNA sequence and nuclear DNA comparisons. Antonie van Leeuwenhoek 67, 297–314.

Guillot, J., E. Guého and M.C. Prévost. 1995a. Ultrastructural features of the dimorphic yeast *Malassezia furfur*. J. Mycol. Méd. 5, 86–91.

Guillot, J., E. Guého and R. Chermette. 1995b. Confirmation of the nomenclatural status of *Malassezia pachydermatis*. Antonie van Leeuwenhoek 67, 173–176.

Guillot, J., E. Guého, M. Lesourd, G. Midgley, G. Chévrier and B. Dupont. 1996. Identification of *Malassezia* species, a practical approach. J. Mycol. Méd. 6, 103–110.

Guillot, J., E. Guého, G. Chévrier and R. Chermette. 1997. Epidemiological analysis of *Malassezia pachydermatis* isolates by partial sequencing of the large subunit ribosomal RNA. Res. Vet. Sci. 62, 22–25.

Guillot, J., E. Guého, M. Mialot and R. Chermette. 1998a. Importance des levures du genre *Malassezia* en dermatologie vétérinaire. Point Véet. 29, 21–31.

Guillot, J., T. Petit, F. Degorce-Rubiales, E. Guého and R. Chermette. 1998b. Dermatitis caused by *Malassezia pachydermatis* in a California sea lion (*Zalophus californianus*). Vet. Rec. 142, 311–312.

Guillot, J., M. Deville, M. Berthelemy, F. Provost and E. Guého. 2000. A single PCR-restriction endonuclease analysis for rapid identification of *Malassezia* species. Lett. Appl. Microbiol. 31, 400–403.

Guillou, S., and N. El Murr. 2002. Inactivation of *Saccharomyces cerevisiae* in solutions by low amperage electric treatment. J. Appl. Microbiol. 92, 860–865.

Guindon, S., and O. Gascuel. 2002. Efficient biased estimation of evolutionary distances when substitution rates vary across sites. Mol. Biol. Evol. 19, 534–543.

Guindon, S., and O. Gascuel. 2003. A simple, fast, and accurate algorithm to estimate large phylogenies by maximum likelihood. Syst. Biol. 52, 696–704.

Guldener, U., M. Munsterkotter, G. Kastenmuller, N. Strack, J. van Helden, C. Lemer, J. Richelles, S.J. Wodak, J. Garcia-Martinez, J.E. Perez-Ortin, H. Michael, A. Kaps, E. Talla, B. Dujon, B. Andre, J.L. Souciet, J. de Montigny, E. Bon, C. Gaillardin and H.W. Mewes. 2005. CYGD: the Comprehensive Yeast Genome Database. Nucleic Acids Res. 33, D364–D368.

Gull, K. 1976. Differentiation of septal ultrastructure according to cell type in the basidiomycete *Agrocybe praecox*. J. Ultrastruct. Res. 54, 89–94.

Gull, K. 1978. Form and function of septa in filamentous fungi. In: J.E. Smith (Ed.), The filamentous fungi: developmental mycology, Vol. 3. Edward Arnold, London, pp. 78–93.

Gullo, M., A.D. Romano, A. Pulvirenti and P. Giudici. 2003. *Candida humilis* – dominant species in sourdoughs for the production of durum wheat bran flour bread. Int. J. Food Microbiol. 80, 55–59.

Gunge, N. 1995. Plasmid DNA and the killer phenomenon in *Kluyveromyces*. In: U. Kück (Ed.), Genetics and Biotechnology, The Mycota, Vol. 2. Springer-Verlag, Berlin, pp. 189–209.

Gunge, N., A. Tamaru, F. Ozawa and K. Sakaguchi. 1981. Isolation and characterization of linear deoxyribonucleic acid plasmids from *Kluyveromyces lactis* and the plasmid-associated killer character. J. Bacteriol. 145, 382–390.

Gunn, S.R., X.T. Reveles, J.D. Hamlington, L.C. Sadkowski, T.L. Johnson-Pais and J.H. Jorgensen. 2006. Use of DNA sequencing analysis to confirm fungemia due to *Trichosporon dermatis* in a pediatric patient. J. Clin. Microbiol. 44, 1175–1177.

Gunsilius, E., C. Lass-Flörl, C.M. Kähler, G. Gastl and A.L. Petzer. 2001. *Candida ciferrii*, a new fluconazole-resistant yeast causing systemic mycosis in immunocompromised patients. Ann. Hematol. 80, 178–179.

Guo, C., C. Zhao, P. He, D. Lu, A. Shen and N. Jiang. 2006. Screening and characterization of yeasts for xylitol production. J. Appl. Microbiol. 101, 1096–1104.

Guo, Z., and X. Xu. 2005. New opportunity for enzymatic modification of fats and oils with industrial potentials. Org. Biomol. Chem. 3, 2615–2619.

Gupta, A.K., Y. Kohli, J. Faergemann and R.C. Summerbell. 2001a. Epidemiology of *Malassezia* yeasts associated with pityriasis versicolor in Ontario, Canada. Med. Mycol. 39, 199–206.

Gupta, A.K., Y. Kohli, R.C. Summerbell and J. Faergemann. 2001b. Quantitative culture of *Malassezia* species from different body sites of individuals with or without dermatoses. Med. Mycol. 39, 243–251.

Gupta, A.K., R. Batra, R. Bluhm, T. Boekhout and T.L. Dawson Jr. 2004a. Skin diseases associated with *Malassezia* species. J. Am. Acad. Dermatol. 51, 785–798.

Gupta, A.K., T. Boekhout, B. Theelen, R.C. Summerbell and R. Batra. 2004b. Identification and typing of *Malassezia* species by amplified fragment length polymorphism (AFLP) and sequence analyses of the internal transcribed spacer (ITS) and large subunit (LSU) regions of ribosomal DNA. J. Clin. Microbiol. 42, 4253–4260.

Gupta, R. 1996. Growth of marine yeast on different strength of stress solutes. Proc. 2nd Workshop on Scientific Results of FORV Sagar Sampa. Department of Ocean Development, New Delhi, pp. 91–95.

Gupthar, A.S. 1994. Theoretical and practical aspects of ploidy estimation in *Pichia stipitis*. Mycol. Res. 98, 716–718.

Gustafson, B.A. 1955. Otitis externa in the dog. A bacteriological and experimental study. Thesis, Stockholm.

Guyard, C., E. Dehecq, J.-P. Tissier, L. Pononelli, E. Dei-Cas, J.C. Cailliez and F.D. Menozzi. 2002a. Involvement of beta-glucans in the wide-spectrum antimicrobial *Williopsis saturnus* var. *mrakii* MUCL 41968 killer toxin. Mol. Med. 8, 686–694.

Guyard, C., N. Séguy, J.C. Cailliez, H. Drobecq, L. Pononelli, E. Dei-Cas, A. Mercenier and F.D. Menozzi. 2002b. Characterization of a *Williopsis saturnus* var. *mrakii* high molecular weight secreted killer toxin with broadspectrum antimicrobial activity. J. Antimicrob. Chemother. 49, 961–971.

Gyaurgieva, O.H., T.S. Bogomolova and G.I. Gorshkova. 1996. Meningitis caused by *Rhodotorula rubra* in an HIV-infected patient. J. Med. Vet. Mycol. 34, 357–359.

Hadfield, C., K.K. Raina, K. Shahimenon and R.C. Mount. 1993. The expression and performance of cloned genes in yeasts. Mycol. Res. 97, 897–944.

Hagedorn, S., and B. Kaphammer. 1994. Microbial biocatalysis in the generation of flavor and fragrance chemicals. Annu. Rev. Microbiol. 48, 773–800.

Hagen, K.S., and R.L. Tassan. 1972. Exploring nutritional roles of extracellular symbiotes on the reproduction of honeydew feeding adult chrysopids and tephritids. In: J.G. Rodriguez (Ed.), Insect and Mite Nutrition. North-Holland, Amsterdam, pp. 323–351.

Hagen, K.S., R.L. Tassan and E.F. Sawill Jr. 1970. Some ecophysiological relationships between certain *Chrysopa* honeydews and yeasts. Bollettino del Laboratorio di Entomolgia Agraria "Filippo Silvestri" di Portici 28, 113.

Hagler, A.N., and D.G. Ahearn. 1981. Rapid diazonium blue B test to detect basidiomycetous yeasts. Int. J. Syst. Bacteriol. 31, 204–208.

Hagler, A.N., and D.G. Ahearn. 1987. Ecology of aquatic yeasts. In: A.H. Rose and J.S. Harrison (Eds), The Yeasts, 2nd edn. Vol. 1. Academic Press, London, pp. 181–205.

Hagler, A.N., and L.C. Mendonça-Hagler. 1979. *Candida lipolytica* isolated from Guanabara Bay and its ability to grow in marine and estuarine conditions. Rev. Bras. Pesqui. Med. Biol. 12, 273–277.

Hagler, A.N., and L.C. Mendonça-Hagler. 1981. Yeasts from marine and estuarine waters with different levels of pollution in the state of Rio de Janeiro, Brazil. Appl. Environ. Microbiol. 41, 173–178.

Hagler, A.N., L.C. Mendonça-Hagler and H.J. Phaff. 1989. *Candida populi*, a new species of yeast occurring in the exudates of *Populus* and *Betula* species. Int. J. Syst. Bacteriol. 39, 97–99.

Hahn, T., K. Tag, K. Riedel, S. Uhlig, K. Baronian, G. Gellisen and G. Kunze. 2006. A novel estrogen sensor based on recombinant *Arxula* cells. Biosensors Bioelectron. 21, 2078–2085.

Hahn-Hägerdahl, B., K. Karhummaa, C. Fonseca, I. Spencer-Martins and M.F. Gorwa-Grausland. 2007. Towards industrial pentose-fermenting yeast strains. Appl. Microbiol. Biotechnol. 74, 937–953.

Hajlaoui, M., and R.R. Bélanger. 1991. Comparative effects of temperature and humidity on the activity of three potential antagonists of rose powdery mildew. Neth. J. Plant Pathol. 97, 203–208.

Hajlaoui, M., and R.R. Bélanger. 1993. Antagonism of the yeast-like phylloplane fungus *Sporothrix flocculosa* against *Erysiphe graminis* var. *tritici*. Biocon. Sci. Technol. 3, 427–434.

Hajlaoui, M.R., N. Benhamou and R.R. Bélanger. 1992. Cytochemical study of the antagonistic activity of *Sporothrix flocculosa* on rose powdery mildew, *Sphaerotheca pannosa* var. *rosae*. Phytopathology 82, 583–589.

Hajsig, M. 1958. *Torulopsis apicola* nov. spec., new isolates from bees. Antonie van Leeuwenhoek 24, 18–22.

Halász, A., and R. Lásztity. 1991. Use of Yeast Biomass in Food Production. CRC Press, Boca Raton, FL, 312pp.

Hall, C., D. Brachatand and F.S. Dietrich. 2005. Contribution of horizontal gene transfer to the evolution of *Saccharomyces cerevisiae*. Eukaryot. Cell 4, 1102–1115.

Hall, L., S. Wohlfiel and G.D. Roberts. 2003. Experience with the MicroSeq D2 large-subunit ribosomal DNA sequencing kit for identification of commonly encountered, clinically important yeast species. J. Clin. Microbiol. 41, 5099–5102.

Hall, N. 2007. Advanced sequencing technologies and their wider impact in microbiology. J. Exp. Biol. 210, 1518–1525.

Halls, C., and O. Yu. 2008. Potential for metabolic engineering of resveratrol biosynthesis. Trends Biotechnol. 26, 77–81.

Hamajima, K., A. Nishikawa, T. Shinoda and Y. Fukazawa. 1987. Deoxyribonucleic acid base composition and its homology between two forms of *Candida parapsilosis* and *Lodderomyces elongisporus*. J. Gen. Appl. Microbiol. 33, 299–302.

Hamamoto, M., and T. Nakase. 1995. Ballistosporous yeasts found on the surface of plant materials collected in New Zealand. 1. Six new species in the genus *Sporobolomyces*. Antonie van Leeuwenhoek 67, 151–171.

Hamamoto, M., and T. Nakase. 1996. Ballistosporous yeasts found on the surface of plant materials collected in New Zealand. The genera *Bensingtonia* and *Bullera* with descriptions of five new species. Antonie van Leeuwenhoek 69, 279–291.

Hamamoto, M., and T. Nakase. 2000. Phylogenetic analysis of the ballistoconidium-forming yeast genus *Sporobolomyces* based on 18S rDNA sequences. Int. J. Syst. Evol. Microbiol. 50, 1373–1380.

Hamamoto, M., J. Sugiyama and K. Komagata. 1984. Identification of *Rhodotorula glutinis* YK 108 (AJ 5015, IFO 0667) as *Rhodosporidium diobovatum* mating type a. J. Gen. Appl. Microbiol. 30, 527–530.

Hamamoto, M., J. Sugiyama, S. Goto and K. Komagata. 1986a. Numerical taxonomy based on the electrophoretic mobility of enzymes in the genera *Rhodosporidium*, *Cystofilobasidium* and *Rhodotorula*. J. Gen. Appl. Microbiol. 32, 89–99.

Hamamoto, M., J. Sugiyama and K. Komagata. 1986b. DNA base composition of strains in the genera *Rhodosporidium*, *Cystofilobasidium*, and *Rhodotorula* determined by reversed-phase high-performance liquid chromatography. J. Gen. Appl. Microbiol. 32, 215–223.

Hamamoto, M., J. Sugiyama and K. Komagata. 1987. DNA–DNA reassociation studies of strains in the genera *Rhodosporidium* and *Rhodotorula*. J. Gen. Appl. Microbiol. 33, 57–73.

Hamamoto, M., J. Sugiyama and K. Komagata. 1988a. *Rhodosporidium kratochvilovae* sp. nov., a new basidiomycetous yeast species. J. Gen. Appl. Microbiol. 34, 119–125.

Hamamoto, M., J. Sugiyama and K. Komagata. 1988b. Transfer of *Rhodosporidium infirmominiatum* to the genus *Cystofilobasidium* as *Cystofilobasidium infirmominiatum* comb. nov. J. Gen. Appl. Microbiol. 34, 271–278.

Hamamoto, M., J. Sugiyama and K. Komagata. 1988c. Transfer of *Rhodotorula hasegawae* to a new basidiomycetous genus *Erythrobasidium* as *Erythrobasidium hasegawae* comb. nov. J. Gen. Appl. Microbiol. 34, 279–287.

Hamamoto, M., J. Sugiyama and K. Komagata. 1991. Nomenclature of the basidiomycetous yeast species *Erythrobasidium hasegawae*. J. Gen. Appl. Microbiol. 37, 131–132.

Hamamoto, M., K. Uchida and H. Yamaguchi. 1992. Ubiquinone system and DNA base composition of strains in the genus *Malassezia* determined by high-performance liquid chromatography. J. Gen. Appl. Microbiol. 38, 79–82.

Hamamoto, M., K. Kuroyanagi and T. Nakase. 1998. *Fellomyces ogasawarensis* sp. nov. and *Fellomyces distylii* sp. nov., yeasts isolated from a plant in Japan. Int. J. Syst. Bacteriol. 48, 287–293.

Hamamoto, M., M. Tamura and T. Nakase. 2000. Emended descriptions of *Tilletiopsis washingtonensis*, *Tilletiopsis cremea* and *Tilletiopsis lilacina*. Int. J. Syst. Evol. Microbiol. 50, 925–930.

Hamamoto, M., V.N. Thanh and T. Nakase. 2002a. *Bannoa hahajimensis* gen. nov., sp. nov., and three related anamorphs, *Sporobolomyces bischofiae* sp. nov., *Sporobolomyces ogasawarensis* sp. nov. and *Sporobolomyces syzygii* sp. nov., yeasts isolated from plants in Japan. Int. J. Syst. Evol. Microbiol. 52, 1023–1032.

Hamamoto, M., T. Nagahama and M. Tamura. 2002b. Systematic study of basidiomycetous yeasts: evaluation of the ITS regions of rDNA to delimit species of the genus *Rhodosporidium*. FEMS Yeast Res. 2, 409–413.

Hamann, T., and B.L. Møller. 2007. Cloning and expression of cytochrome P450s and cytochrome P450 reductases in yeast. Prot. Exp. Purif. 56, 121–127.

Hamilton, S.R., and T.U. Gerngross. 2007. Glycosylation engineering in yeast: the advent of fully humanized yeast. Curr. Opin. Biotechnol. 18, 387–392.

Hammer, B.W. 1919. Studies on formation of gas in sweetened condensed milk. Iowa State Coll. Agric. Exp. Stat. Res. Bull. 54, 211–220.

Hammer, B.W., and W.A. Cordes. 1920. A study of lactose-fermenting yeasts in "yeasty" cream. Agric. Exp. Stat. Iowa State Coll. Agric. Mech. Arts Res. Bull. 61, 1–24.

Hammer, E., D. Krowas, A. Schäfer, M. Specht, W. Francke and F. Schauer. 1998. Isolation and characterization of a dibenzofuran-degrading yeast: identification of oxidation and ring cleavage products. Appl. Environ. Microbiol. 64, 2215–2219.

Han, J.R., D.Y. Huang and G.H. Liu. 2002. Effect of microbial elicitors on sclerotia biomass and carotenoid yield in surface cultures of *Penicillium* sp. PT95. Sheng Wu Gong Cheng Xue Bao 18, 369–372. In Chinese.

Hanawa, S. 1920. Studien über die auf gesunder und kranker Haut angesiedelten Pilzkeime. Jpn. J. Dermatol. Urol. 20, 103–131.

Hancioğlu, O., and M. Karapinar. 1997. Microflora of Boza, a traditional fermented Turkish beverage. Int. J. Food Microbiol. 35, 271–274.

Hannafusa, Y., A. Bradley, E.E. Tomaszewski, M.C. Libal and D.N. Phalen. 2007. Growth and metabolic characterization of *Macrorhabdus ornithogaster*. J. Vet. Diagn. Invest. 19, 256–265.

Hansen, E.B. 2004. Microorganisms. In: Y.H. Hui, L. Meunier-Goddik, A.S. Hansen, J. Josephsen, W.-K. Nip, P.S. Stanfield and F. Toldrá (Eds), Handbook of Food and Beverage Fermentation Technology. Marcel-Dekker, New York, pp. 9–22.

Hansen, E.C. 1883. Undersogelser over alkoholgjaersvampenes fysiologi og morfologi. II. Om askosporedannelsen

hos slaegten *Saccharomyces*. Medd. Carlsberg Lab. 2, 29–86.
Hansen, E.C. 1888a. Recherches sur la physiologie et la morphologie des ferments alcooliques. VII. Action des ferments alcooliques sur les diverses especes de sucre. C.R. Trav. Lab. Carlsberg 2, 143–167.
Hansen, E.C. 1888b. Undersøgelser over alkoholgjaensvampenes fysiologi og morfologi. VII. Om alkoholgjaersvampenes forhold til sukkerarterne. Medd. Carlsberg Lab. 2, 220–256.
Hansen, E.C. 1889. Über die im Schleimflusse lebender Bäume beobachteten Mikroorganismen. Zentralbl. Bakteriol. Parasitenkd., Abt. II, 5, 632–640.
Hansen, E.C. 1891. Sur la germination des spores chez les *Saccharomyces*. Ann. Micrographic. 3, 449–474.
Hansen, E.C. 1904. Grundlinien zur Systematik der Saccharomyceten. Zentralbl. Bakteriol. Parasitenkd., Abt. II, Hansen Hjort 1954. [979] 12, 529–538.
Hansen, E.C. 1908. Recherches sur la physiologie et la morphologie des ferments alcooliques. XIII. Nouvelles études sur les levures de brasserie à fermentation basse. C.R. Trav. Lab. Carlsberg 7, 179–217.
Hansson, L., and M. Dostálek. 1986a. Influence of cultivation conditions on lipid production by *Cryptococcus albidus*. Appl. Microbiol. Biotechnol. 24, 12–18.
Hansson, L., and M. Dostálek. 1986b. Lipid formation by *Cryptococcus albidus* in nitrogen-limited and in carbon-limited chemostat cultures. Appl. Microbiol. Biotechnol. 24, 187–192.
Hansen, T.K., and M. Jakobsen. 2001. Taxonomical and technological characteristics of *Saccharomyces* spp. associated with blue veined cheese. Int. J. Food Microbiol. 69, 59–68.
Hanya, Y., and T. Nakadai. 2003. Yeasts and soy products. In: T. Boekhout and V. Robert (Eds), Yeasts in Food: Beneficial and Detrimental Aspects. Behrs Verlag, Hamburg, pp. 413–428.
Hara, N., Y. Tubota, K. Saito and T. Suto. 1989. Biochemical characteristics and ubiquinone of 44 strains of *Trichosporon beigelii* and related organisms. J. Gen. Appl. Microbiol. 35, 1–10.
Hara, S., Y. Iimura and K.I. Otsuka. 1983. Development of the new winemaking method for pure culture using useful killer wine yeasts and prevention of film-forming spoilage of wines. J. Agric. Chem. Soc. Jpn 57, 897–907.
Harris, H., and D.A. Hopkinson. 1976. Handbook of Enzyme Electrophoresis in Human Genetics. North-Holland Publishing Co., American Elsevier Publishing Co., New York.
Harrison, F.C. 1927. Cheese torulae. Trans. R. Soc. Can. 3rd Ser. 21, Sect. 5, 341–380.
Harrison, F.C. 1928. A systematic study of some torulae. Trans. R. Soc. Can., Sect. V, 22, 187–225.
Hartland, R.P., C.A. Vermeulen, F.M. Klis, J.H. Sietsma and J.G. Wessels. 1994. The linkage of (1-3)-beta-glucan to chitin during cell wall assembly in *Saccharomyces cerevisiae*. Yeast 10, 1591–1599.
Hartmann, L.M., P.J. Craig and R.O. Jenkins. 2003. Influence of arsenic on antimony methylation by the aerobic yeast *Cryptococcus humicolus*. Arch. Microbiol. 180, 347–352.
Hartmann, M. 1903. Eine rassenspaltige *Torula*-Art, welche nur zeitweise Maltose zu vergären vermag (*Torula colliculosa* n. sp.). Wochenschr. Brau. 20, 113–114.
Hartner, F.S., and A. Glieder. 2006. Regulation of methanol utilization pathway genes in yeasts. Microb. Cell Factories 5, 39.
Hartwell, L.H. 2002. Nobel lecture. Yeast and cancer. Biosci. Rep. 22, 373–394.
Hasan, F., A.A. Shah and A. Hameed. 2006. Industrial applications of lipases. Enzyme Microb. Technol. 39, 235–251.
Hasegawa, M., H. Kishino and T. Yano. 1985. Dating of the human–ape splitting by a molecular clock of mitochondrial DNA. J. Mol. Evol. 22, 160–174.
Hasegawa, M., H. Kishino and T. Yano. 1987. Man's place in Hominoidea as inferred from molecular clocks of DNA. J. Mol. Evol. 26, 132–147.
Hasegawa, T. 1959. The lactose assimilating species in the genus *Rhodotorula*. J. Gen. Appl. Microbiol. 5, 30–34.
Hasegawa, T. 1965. A report on the taxonomy of red to orange *Rhodotorula*. Ann. Rep. Inst. Ferment. Osaka 2, 1–25.
Hasegawa, T., and I. Banno. 1958. Studies on the genus *Rhodotorula* (III). On the nitrate utilization of *Rhodotorula*. J. Ferment. Technol. (Jpn) 36, 403–406.
Hasegawa, T., and I. Banno. 1964. *Rhodotorula infirmominiata* (Okunuki) comb. n. Antonie van Leeuwenhoek 30, 65–67.
Hasegawa, T., I. Banno and S. Yamauchi. 1960. A taxonomic study on the genus *Rhodotorula*. J. Gen. Appl. Microbiol. 6, 196–215.
Hasegawa, Y., S. Adachi and R. Matsuno. 1997. Production of homochiral 1-phenylethanol through enantioselective oxidation of its racemate with whole cells of the yeast *Hansenula capsulata* IFO 0974. J. Ferment. Bioeng. 83, 346–351.
Hasegawa, Y., S. Adachi and R. Matsuno. 1998. Asymmetric reduction of acetophenon by immobilized *Hansenula capsulata* cells. J. Ferment. Bioeng. 85, 322–327.
Haseltine, E.L., and F.H. Arnold. 2007. Synthetic gene circuits: design with directed evolution. Annu. Rev. Biophys. Biomol. Struct. 36, 1–19.
Haser, K., H.H. Wenk and W. Schwab. 2006. Biocatalytic production of dihydrocoumarin from coumarin by *Saccharomyces cerevisiae*. J. Agric. Food Chem. 54, 6236–6340.
Hashimoto, S., K. Aritomi, T. Minohara, Y. Nishizawa, H. Hoshida, S. Kashiwagi and R. Akada. 2006. Direct mating between diploid sake strains of *Saccharomyces cerevisiae*. Appl. Microbiol. Biotechnol. 69, 689–696.
Haskins, R.H., and J.F.T. Spencer. 1967. *Trichosporonoides oedocephalis* n. gen., n. sp. I. Morphology, development, and taxonomy. Can. J. Bot. 45, 515–520.
Hasnip, S., C. Crews, N. Potter, J. Christy, D. Chan, T. Bondu, W. Matthews, B. Walters and K. Patel. 2007. Survey of ethyl carbamate in fermented foods sold in the United Kingdom in 2004. J. Agric. Food Chem. 55, 2755–2759.
Hassan, M., P.J. Blanc, A. Pareilleux and G. Goma. 1995. Production of cocoa butter equivalents from prickly-pear juice fermentation by an unsaturated fatty acid auxotroph of *Cryptococcus curvatus* grown in batch culture. Process Biochem. 30, 629–634.
Hassan, M., P.J. Blanc, L.M. Franger, A. Pareilleux and G. Goma. 1996. Influence of nitrogen and iron limitations on lipid production by *Cryptococcus curvatus* grown in batch and fed-batch culture. Process Biochem. 31, 355–361.
Hassan, S.S., A.F. el-Baz and H.S. Abd-Rabboh. 2007. A novel potentiometric biosensor for selective L-cysteine

determination using L-cysteine-desulfhydrase producing *Trichosporon jirovecii* yeast cells coupled with sulfide electrode. Anal. Chim. Acta 602, 108–113.

Hastings, W.K. 1970. Monte Carlo sampling methods using Markov chains and their applications. Biometrika 57, 97–109.

Hattori, H., C. Inoue, Y. Tomita and T. Kanbe. 2007. A case of oral geotrichosis caused by *Geotrichum capitatum* in an old patient. Jpn. J. Infect. Dis. 60, 300–301.

Haubold, E.M., J.F. Aronson, D.F. Cowan, M.R. McGinnis and C.R. Cooper. 1998. Isolation of fungal rDNA from bottlenose dolphin skin infected with *Loboa loboi*. Med. Mycol. 36, 263–267.

Haubold, E.M., C.R. Cooper Jr., J.W. Wen, McGinnis and D.F. Cowan. 2000. Comparative morphology of *Lacazia loboi* (syn. *Loboa loboi*) in dolphins and humans. Med. Mycol. 38, 9–14.

Hauck, T., F. Brühlmann and W. Schwab. 2003. Formation of 4-hydroxy-2,5-dimethyl-3[2H]-furanone by *Zygosaccharomyces rouxii*: identification of an intermediate. Appl. Environ. Microbiol. 69, 3911–3918.

Hauerslev, K. 1987. Three new or rare resupinate fungi from Denmark. Friesia 11, 281–286.

Hausner, G., J. Reid and G.R. Klassen. 1992. Do galeate-ascospore members of the Cephaloascaceae, Endomycetaceae and Ophiostomataceae share a common phylogeny? Mycologia 84, 870–881.

Hawker, L.E., M.A. Gooday and C.E. Bracker. 1966. Plasmodesmata in fungal cell walls. Nature 212, 635.

Hawkins, J.L., and L.M. Baddour. 2003. *Candida lusitaniae* infections in the era of fluconazole availability. Clin. Infect. Dis. 36, e14–18.

Hawksworth, D.L. 2004. Fungal diversity and its implications for genetic resource collections. Stud. Mycol. 50, 9–18.

Hawksworth, D.L., P.M. Kirk, B.C. Sutton and D.N. Pegler. 1995. Ainsworth & Bisby's Dictionary of the Fungi, 8th edn. CAB International, Egham.

Hawthorne, D. 1963. Directed mutation of the mating type alleles as an explanation of homothallism in yeast. Proc. 11th Int. Congr. Genet. 1, 34–35.

Hawthorne, D., and P. Philippsen. 1994. Genetic and molecular analysis of hybrids in the genus *Saccharomyces* involving *S. cerevisiae*, *S. uvarum* and a new species *S. douglasii*. Yeast 10, 1285–1296.

Hayashi, N., R. Arai, S. Tada, H. Taguchi and Y. Ogawa. 2007. Detection and identification of *Brettanomyces*/*Dekkera* sp. yeasts with a loopmediated isothermal amplification method. Food Microbiol. 24, 778–785.

Hayashida, Y., K. Nishimura and J.C. Slaughter. 1997. The influence of mash pre-aging on the development of the flavour-active compound, 4-hydroxy-2(or 5)-ethyl-5(or 2)-methyl- 3(2H)-furanone (HEMF) during soy sauce fermentation. Int. J. Food Sci. Technol. 32, 11–14.

Hayles, J., and P. Nurse. 2001. A journey into space. Nat. Rev. Mol. Cell Biol. 2, 647–656.

Hayman, G.T., and P.L. Bolen. 1991. Linear DNA plasmids of *Pichia inositovora* are associated with a novel killer toxin activity. Curr. Genet. 19, 389–393.

Hazen, K.C. 1995. New and emerging yeast pathogens. Clin. Microbiol. Rev. 8, 462–478.

Hazen, K.C., J. Stei, C. Darracott, A. Breathnach, J. May and S.A. Howell. 2005. Isolation of cholesterol-dependent *Candida glabrata* from clinical specimens. Diagn. Microbiol. Infect. Dis. 52, 35–37.

He, F., and Y.T. Chen. 2005. Cloning and heterologous expression of NADPH cytochrome P450 oxidoreductase genes from an industrial dicarboxylic acid-producing *Candida tropicalis*. Yeast 22, 481–491.

Heard, G.M. 1999. Novel yeasts in winemaking – looking to the future. Food Austral. 51, 347–352.

Heard, G.M., and G.H. Fleet. 2000. *Yarrowia* (*Candida*) *lipolytica*. In: R.K. Robinson, C.A. Batt and P. Patel (Eds), Encyclopedia of Food Microbiology. Academic Press, London, pp. 360–365.

Heath, I.B. (Ed.) 1978. Nuclear Division in the Fungi. Academic Press, New York.

Heath, I.B. 1981. Nucleus-associated organelles in fungi. Int. Rev. Cytol. 69, 191–221.

Heath, I.B., M.-L. Ashton, K. Rethoret and M.C. Heath. 1982. Mitosis and the phylogeny of *Taphrina*. Can. J. Bot. 60, 1696–1725.

Heath, I.B., M.L. Ashton and S.G.W. Kamlinskyj. 1987. Mitosis as a phylogenetic marker among the yeasts – review and observations on novel mitotic systems in freeze substituted cells of the Taphrinales. In: G.S. de Hoog, M.Th. Smith and A.C.M. Weijman (Eds), The Expanding Realm of Yeast-like Fungi. Elsevier, Amsterdam, pp. 279–297. (Stud. Mycol. 30, 279–297).

Heath, I.B., M. Bonham, A. Akram and G.D. Gupta. 2003. The interrelationships of actin and hyphal tip growth in the ascomycete *Geotrichum candidum*. Fungal Genet. Biol. 38, 85–97.

Hébrard, G., S. Blanqòuet, E.R. Beyssac, G. Remondetto, M. Subirade and M. Alric. 2006. Use of whey protein beads as a new carrier system for recombinant yeasts in human digestive tract. J. Biotechnol. 127, 151–160.

Hechler, H.C. 1971. Taxonomic notes on four species of *Panagrellus* Thorne (Nematoda: Cephalobidae). J. Nematol. 3, 227–236.

Hedrick, L.R. 1976. *Candida fluviatilis* sp. nov. and other yeasts from aquatic environments. Antonie van Leeuwenhoek 42, 329–332.

Hedrick, L.R., and G.C. Burke. 1951. Two new yeasts from Hawaiian fruit flies. Mycopathol. Mycol. Appl. 6, 92–95.

Hedrick, L.R., and P.D. Dupont. 1968. Two new yeasts: *Trichosporon aquatile* and *Trichosporon eriense* spp. n. Antonie van Leeuwenhoek 34, 474–482.

Hedtke, S.M., T.M. Townsend and D.M. Hillis. 2006. Resolution of phylogenetic conflict in large data sets by increased taxon sampling. Syst. Biol. 55, 522–529.

Heed, W.B., W.T. Starmer, M. Miranda, M. Miller and H.J. Phaff. 1976. An analysis of the yeast flora associated with cactophilic *Drosophila* and their host plants in the Sonoran Desert and its relation to temperate and tropical associations. Ecology 57, 151–160.

Hegarty, M.J., and S.J. Hiscock. 2005. Hybrid speciation in plants: new insights from molecular studies. New Phytol. 165, 411–423.

Heise, N., A.L.S. Gutierrez, K.A. Mattos, C. Jones, R. Wait, J.O. Previato and L.M. Medonca-Previato. 2002. Molecular analysis of a novel family of complex glycoinositolphosphoryl ceramides from *Cryptococccus neoformans*: structural differences between encapsulated and acapsular yeast forms. Glycobiology 12, 409–420.

Heitman, J., S.G. Filler, J.E. Edwards Jr. and A.P. Mitchell (Eds). 2006. Molecular Principles of Fungal Pathogenesis. ASM Press, Washington, DC.

Hektoen, L., and C.F. Perkins. 1900. Refractory subcutaneous abscesses caused by *Sporothrix schenckii*. A new pathogenic fungus. J. Exp. Med. 5, 77–89.

Helbig, J. 2002. Ability of the antagonistic yeast *Cryptococcus albidus* to control *Botrytis cinerea* in strawberry. BioControl 47, 85–99.

Helston, R.M., J.A. Box, W. Tang and P. Baumann. 2010. http://www.ncbi.nlm.nih.gov/pubmed/20618870. *Schizosaccharomyces cryophilus* sp. nov., a new species of fission yeast. FEMS Yeast Res. 10, 779–786.

Helfer, W. 1991. Pilze auf Fruchtkörpern. Untersuchungen zur Okologie. Systematik und Chemie. Libri Bot. 1, 1–157.

Hemmingway, J.S. 1980. International infection of juncea mustard seed by *Nematospora* yeast. Rev. Progress Rept. Reckitt and Colman, Norwich.

Hendriks, L., A. Goris, Y. van de Peer, J.-M. Neefs, M. Vancanneyt, K. Kersters, J.-F. Berny, G.L. Hennebert and R. de Wachter. 1992. Phylogenetic relationships among ascomycetes and ascomycete-like yeasts as deduced from small ribosomal subunit RNA sequences. Syst. Appl. Microbiol. 15, 98–104.

Henick–Kling, Th., C. Egli, J. Licker, C. Mitrakul and T.E. Acree. 2000. *Brettanomyces* in wine. Proc. 5th Int. Symp. Cool Climate Viticulture and Oenology, Melbourne, Australia.

Henk, D.A., and R. Vilgalys. 2007. Molecular phylogeny suggests a single origin of insect symbiosis in the Pucciniomycetes with support for some relationships within the genus *Septobasidium*. Am. J. Bot. 94, 1515–1526.

Henneberg, W. 1926. Handbuch der Gärungsbakteriologie. II. 2te Aufl. Berlin.

Hennequin, C., A. Thierry, G.F. Richard, G. Lecointre, H.V. Nguyen, C. Gaillardin and B. Dujon. 2001. Microsatellite typing as a new tool for identification of *Saccharomyces cerevisiae* strains. J. Clin. Microbiol. 39, 551–559.

Henninger, W., and S. Windisch. 1975a. *Pichia lindnerii* sp. n., eine neue Methanol assimilierende Hefe aus Erde. Arch. Microbiol. 105, 47–48.

Henninger, W., and S. Windisch. 1975b. A new yeast of *Sterigmatomyces*, *S. aphidis* sp. n. Arch. Microbiol. 105, 49–50.

Henninger, W., and S. Windisch. 1976a. *Kluyveromyces blattae* sp. n., eine neue vielsporige Hefe aus Blatta *orientalis*. Arch. Microbiol. 109, 153–156.

Henninger, W., and S. Windisch. 1976b. *Torulopsis spandovensis* sp. n., a new yeast from beer. Arch. Microbiol. 107, 205–206.

Hennings, P.C. 1902. Engler's Bot. Jahrb. 32, 34.

Henriques, M., I. Sá-Nogueira, G. Giménez-Jurado and N. van Uden. 1991. Ribosomal DNA spacer probes for yeast identification: studies in the genus *Metschnikowia*. Yeast 7, 167–172.

Henz, S.R., D.H. Huson, A.F. Auch, K. Nieselt-Struwe and S.C. Schuster. 2005. Whole-genome prokaryotic phylogeny. Bioinformatics 21, 2329–2335.

Herbrecht, R., and Y. Nivoix. 2005. *Saccharomyces cerevisiae* fungemia, an adverse effect of *Saccharomyces boulardii* probiotic administration. Clin. Infect. Dis. 40, 1635–1637.

Herbrecht, R., H. Koening, J. Waller, L. Liu and E. Guého. 1993. *Trichosporon* infection: clinical manifestations and treatment. J. Mycol. Med. 3, 129–136.

Herman, A.I., L.J. Wickerham and P. Griffin. 1966. Allelic determinants of agglutination in the yeast *Hansenula wingei*. Genetics 54, 339.

Herman, A.I. 1971a. Mating responses in the yeast *Hansenula holstii*. Antonie van Leeuwenhoek 37, 275–280.

Herman, A.I. 1971b. Mating responses in *Candida lipolytica*. J. Bacteriol. 107, 371.

Hernández, A., A. Martín, M.G. Córdoba, M.J. Benito, E. Aranda and F. Pérez-Nevado. 2008. Determination of killer activity in yeasts isolated from the elaboration of seasoned green table olives. Int. J. Food Microbiol. 121, 178–188.

Hernández-López, M.J., J.A. Prieto and F. Randez-Gil. 2003. Osmotolerance and leavening ability in sweet and frozen sweet dough. Comparative analysis between *Torulaspora delbrueckii* and *Saccharomyces cerevisiae* baker's yeast strains. Antonie van Leeuwenhoek 84, 125–134.

Hernández-López, M.J., C. Pallotti, P. Andreu, J. Aguilera, J.A. Prieto and F. Randez-Gil. 2007. Characterization of a *Torulaspora delbrueckii* diploid strain with optimized performance in sweet and frozen sweet dough. Int. J. Food Microbiol. 116, 103–110.

Hernandez-Saavedra, N.Y., J.L. Ochoa and R. Vazquez-Duhalt. 1994. Effect of salinity in the growth of the marine yeast *Rhodotorula rubra*. Microbios 80, 99–106.

Hernandez-Saavedra, N.Y., J.L. Ochoa and R. Vazquez-Duhalt. 1995. Osmotic adjustment in marine yeast. J. Plankton Res. 17, 59–69.

Hernandez-Saavedra, N.Y., S.D. Hernandez, J.R. Vazquesm and J.L. Ochoa. 1990. Distribution of *Sporobolomyces* (Kluyver et van Niel) genera in the western coast of Baja California Sur, Mexico. In: Yeast Taxonomy: Theoretical and Practical Aspects, Proc. 14th Int. Symp. Yeasts, Smolenice, Slovak Republic, p. 74.

Hernandez-Saavedra, N.Y., D. Hernandez-Saavedra and J.L. Ochoa. 1992. Distribution of *Sporobolomyces* (Kluyver et van Niel) genus in the western coast of Baja California Sur, Mexico. Syst. Appl. Microbiol. 15, 319–322.

Hernawan, T., and G.H. Fleet. 1995. Chemical and cytological changes during the autolysis of yeasts. J. Ind. Microbiol. 14, 440–450.

Herr, R.A., E.J. Tarcha, P.R. Taborda, J.W. Taylor, L. Ajello and L. Mendoza. 2001. Phylogenetic analysis of *Lacazia loboi* places this previously uncharacterized pathogen within the dimorphic Onygenales. J. Clin. Microbiol. 39, 309–314.

Herrera, T., and M. Ulloa. 1978. Descripcion de una especie nueva de levadura *Candida queretana*, aislada del tepache de queretaro, Mexico. Bol. Soc. Mex. Microbiol. 12, 13–18.

Herrera, T., M. Ulloa and I. Fuentes. 1973. Descripcion de una especie nueva de *Hansenula* y una variedada nueva de *Candida parapsilosis* aisladas del pozol. Bol. Soc. Mex. Microbiol. 7, 17–26.

Herrero, M., L.A. Garcia and M. Diaz. 2003. The effect of SO_2 on the production of ethanol, acetaldehyde, organic acids, and flavor volatiles during industrial cider fermentation. J. Agric. Food Chem. 51, 3455–3459.

Herrero, M., E. Noriega, L. Garcia and M. Diaz. 2005. Influence of malolactic starter on the quality of the cider produced on an industrial scale. Eur. Food Res. Technol. 221, 168–174.

Herrero, M., C. Quirós, L.A. García and M. Díaz. 2006. Use of flow cytometry to follow the physiological states of

microorganisms in cider fermentation processes. Appl. Environ. Microbiol. 72, 6725–6733.
Herzberg, M., R. Fischer and A. Titze. 2002. Conflicting results obtained by RAPD-PCR and large-subunit rDNA sequences in determining and comparing yeast strains isolated from flowers: a comparison of two methods. Int. J. Syst. Evol. Microbiol. 52, 1423–1433.
Hesseltine, C.W. 1965. A millennium of fungi, food and fermentation. Mycologia 57, 149–197.
Hesseltine, C.W., and C.P. Kurtzman. 1990. Yeasts in amylolytic food starters. Anal. Inst. Biol. Univ. Nac. Autón. México, Ser. Bot. 60, 1–7.
Hesseltine, C.W., and H.L. Wang (Eds). 1986. Indigenous Fermented Food of Non-Western Origin. Mycologia Memoir No. 11. J. Cramer, Berlin.
Hewald, S., K. Josephs and M. Bolker. 2005. Genetic analysis of biosurfactant production in *Ustilago maydis*. Appl. Environ. Microbiol. 71, 3033–3040.
Hibbett, D.S. 2006. A phylogenetic overview of the Agaricomycotina. Mycologia 98, 917–925.
Hibbett, D.S., and R.G. Thorn. 2001. Basidiomycota: Homobasidiomycetes. In: D.J. McLaughlin, E.G. McLaughlin and P.A. Lemke (Eds), The Mycota VII, Systematics and Evolution, Part B. Springer-Verlag, Berlin, pp. 121–168.
Hibbett, D.S., M. Binder, J.F. Bischoff, M. Blackwell, P.F. Cannon, O.E. Eriksson, S. Huhndorf, T. James, P.M. Kirk, R. Lücking, T. Lumbsch, F. Lutzoni, P.B. Matheny, D.J. McLaughlin, M.J. Powell, S. Redhead, C.L. Schoch, J.W. Spatafora, J.A. Stalpers, R. Vilgalys, M.C. Aime, A. Aptroot, R. Bauer, D. Begerow, G.L. Benny, L.A. Castlebury, P.W. Crous, Y.-C. Dai, W. Gams, D.M. Geiser, G.W. Griffith, C. Gueidan, D. Hawksworth, G. Hestmark, K. Hosaka, R.A. Humber, K. Hyde, J.E. Ironside, U. Kõljalg, C.P. Kurtzman, K.-H. Larson, R. Lichtwardt, J. Longcore, J. Miadlikowska, A. Miller, J.-M. Moncalvo, S. Mozley-Standridge, F. Oberwinkler, E. Parmasto, V. Reeb, J.D. Rogers, C. Roux, L. Ryvarden, J.P. Sampaio, A. Schüssler, J. Sugiyama, R.G. Thorn, L. Tibell, W. Untereiner, C. Walker, Z. Wang, A. Weir, M. Weiss, M.M. White, K. Winka, Y.-J. Yao and N. Zhang. 2007. A higher-level phylogenetic classification of the Fungi. Mycol. Res. 111, 509–547.
Hicks, J.B., and I. Herskowitz. 1976. Interconversion of yeast mating types. I. Direct observations on the action of the homothallism (HO) gene. Genetics 83, 245–258.
Hierro, N., A. González, A. Mas and J.M. Guillamón. 2006a. Diversity and evolution of non-*Saccharomyces* yeast populations during wine fermentation: effect of grape ripeness and cold maceration. FEMS Yeast Res. 6, 102–111.
Hierro, N., B. Esteve-Zarzoso, A. Gonzalez, A. Mas and J.M. Guillamon. 2006b. Real-time quantitative PCR (QPCR) and reverse transcription-QPCR for detection and enumeration of total yeasts in wine. Appl. Environ. Microbiol. 72, 7148–7155.
Higgins, V.J., P.J. Bell, I.W. Dawes and P.V. Attfield. 2001. Generation of a novel *Saccharomyces cerevisiae* strain that exhibits strong maltose utilization and hyperosmotic resistance using nonrecombinant techniques. Appl. Environ. Microbiol. 67, 4346–4348.
Higham, J. 1970. Studies in the genus *Sporidiobolus*. MSc Thesis, University of British Columbia, BC, Canada.
Higuera-Ciapara, I., L. Félix-Valenzuela and F.M. Goycoolea. 2006. Astaxanthin: a review of its chemistry and applications. Crit. Rev. Food Sci. Nutr. 46, 185–196.
Hijwegen, T. 1986. Biological control of cucumber powdery mildew by *Tilletiopsis minor*. Neth. J. Plant Pathol. 92, 93–95.
Hijwegen, T. 1988. Effect of seventeen fungicolous fungi on sporulation of cucumber powdery mildew. Neth. J. Plant Pathol. 94, 185–190.
Hill, J., E. Nelson, D. Tilman, S. Polasky and D. Tiffany. 2006. Environmental, economic, and energetic costs and benefits of biodiesel and ethanol biofuels. Proc. Natl. Acad. Sci. USA 103, 11206–11210.
Hillis, D.M., and J.J. Bull. 1993. An empirical test of bootstrapping as a method for assessing confidence in phylogenetic analysis. Syst. Biol. 42, 182–192.
Himmel, M.E., S.Y. Ding, D.K. Johnson, W.S. Adney, M.R. Nimios, J.W. Brady and T.D. Foust. 2007. Biomass recalcitrance: engineering plants and enzymes for biofuels production. Science 315, 804–807.
Hinton, A., J.A. Cason and K.D. Ingram. 2002. Enumeration and identification of yeasts associated with commercial poultry processing and spoilage of refrigerated broiler carcasses. J. Food Prot. 65, 993–998.
Hinzelin, F., C.P. Kurtzman and M.Th. Smith. 1991. *Williopsis salicorniae* sp. nov. Antonie van Leeuwenhoek 59, 125–127.
Hipkin, C.R., D.A. Kau and A.C. Cannons. 1993. Evidence that the glutamine-stimulated loss of nitrate reductase protein from the yeast *Candida nitratophila* is not the result of inducer exclusion. Biochem. J. 295, 611–615.
Hirai, A., R. Kano, K. Makimura, E.R. Duarte, J.S. Hamdan, M.A. Lachance, A. Yamaguchi and A. Hasegawa. 2004. *Malassezia nana* sp. nov., a novel lipid-dependent yeast species isolated from animals. Int. J. Syst. Evol. Microbiol. 54, 623–627.
Hiraoka, C., M. Matsuda, Y. Suzuki, S. Fujieda, M. Tomita, K. Fuhshuku, R. Obata, S. Nishiyama and T. Sugai. 2006. Screening, substrate specificity and stereoselectivity of yeast strains, which reduce sterically hindered isopropyl ketones. Tetrahedron Asymmetry 17, 3358–3367.
Hirosawa, N., and H. Takada. 1969. Salt susceptibility of *Rhodotorula glutinis* var. *salinaria* isolated from salt farm in Japan. Trans. Mycol. Soc. Jpn. 10, 35–39.
Hirst, J.M. 1953. Changes in atmospheric spore content: diurnal periodicity and the effects of water. Trans. Br. Mycol. Soc. 36, 375–393.
Hisatomi, T., N. Yanagishima and I. Banno. 1986. Induction of heterothallic strains and their genetic and physiological characterization in a homothallic strain of the yeast *Saccharomyces exiguus*. Curr. Genet. 10, 887–892.
Hisatomi, T., N. Yanagishima, A. Sakurai and H. Kobayashi. 1988. Interspecific actions of a mating pheromones on the a matingtype cells of three *Saccharomyces* yeasts. Curr. Genet. 13, 25–27.
Hislop, E.C., and T.W. Cox. 1969. Effects of captan on the non-parasitic microflora of apple leaves. Trans. Br. Mycol. Soc. 52, 223–235.
Hittinger, C.T., A. Rokas and S.B. Carrol. 2004. Parallel inactivation of multiple GAL pathway genes and ecological diversification in yeasts. Proc. Natl. Acad. Sci. USA 101, 14144–14149.
Hitzeman, R.A., F.E. Hagie, H.L. Levine, D.V. Goeddel, G. Ammerere and B.D. Hall. 1981. Expression of a human gene for interferon in yeast. Nature 293, 717–722.

Hjort, A. 1954. Some studies on the genus *Saccharomycodes* Hansen. C.R. Trav. Lab. Carlsberg, Ser. Physiol. 25, 259–284.

Hoang, L.M., J.A. Maguire, P. Doyle, M. Fyfe and D.L. Roscoe. 2004. *Cryptococcus neoformans* infections at Vancouver Hospital and Health Sciences Centre (1997–2002): epidemiology, microbiology and histopathology. J. Med. Microbiol. 53, 935–940.

Hoch, H.C., and R.J. Howard. 1981. Conventional chemical fixations induce artifactual swelling of dolipore septa. Exp. Mycol. 5, 167–172.

Hoch, H.C., and R. Provvidenti. 1979. Mycoparasitic relationships: cytology of the *Sphaerotheca fuliginea–Tilletiopsis* sp. interaction. Phytopathology 69, 359–362.

Hochstenbach, F., F.M. Klis, H. van den Ende, E. van Donselaar, P.J. Peters and R.D. Klausner. 1998. Identification of a putative a-glucan synthase essential for cell wall construction and morphogenesis in fission yeast. Proc. Natl. Acad. Sci. USA 95, 9161–9166.

Hocking, A.D., and J.I. Pitt. 1981. *Trichosporonoides nigrescens* sp. nov., a new xerophilic yeast-like fungus. Antonie van Leeuwenhoek 47, 411–421.

Hodgson, V.J., D. Button and G.M. Walker. 1995. Anti-*Candida* activity of a novel killer toxin from the yeast *Williopsis mrakii*. Microbiology 141, 2003–2012.

Hoeben, P., and G.D. Clark-Walker. 1986. An approach to yeast classification by mapping mitochondrial DNA from *Dekkera*/*Brettanomyces* and *Eeniella* genera. Curr. Genet. 10, 371–379.

Hoeben, P., G. Weiller and G.D. Clark-Walker. 1993. Larger rearranged mitochondrial genomes in *Dekkera*/*Brettanomyces* yeasts are more closely related than smaller genomes with a conserved gene order. J. Mol. Evol. 36, 263–269.

Hoeg, L., G. Schönian, M. Ollert and H.C. Korting. 1998. *Candida sake*: a relevant species in the context of HIV-associated oropharyngeal candidosis? J. Mol. Med. 76, 70–73.

Hogan, D.A. 2006. Quorum sensing: alcohols in a social situation. Curr. Biol. 16, R457–R458.

Hogan, L.H., and B.S. Klein. 1994. Altered expression of surface α-1,3-glucan in genetically related strains of *Blastomyces dermatitidis* that differ in virulence. Infect. Immun. 62, 3543–3546.

Höhl, M., and M.A. Ragan. 2007. Is multiple-sequence alignment required for accurate inference of phylogeny? Syst. Biol. 56, 206–221.

Hohmann, S. 2005. The yeast systems biology network: mating communities. Curr. Opin. Biotechnol. 16, 356–360.

Holck, P., M. Sletmoen, B.T. Stokke, H. Permin and S. Norn. 2007. Potentiation of histamine release by microfungal (1-3) and (1-6)-beta-D-glucans. Basic Clin. Pharmacol. Toxicol. 101, 455–458.

Holgersson, J., and A. Gustafsson. 2007. Production of proteins carrying oligomannose or humanlike glycans in yeast and methods of use thereof. US Patent 20070184063.

Holland, B.R., K.T. Huber, V. Moulton and P.J. Lockhart. 2004. Using consensus networks to visualize contradictory evidence for species phylogeny. Mol. Biol. Evol. 21, 1459–1461.

Holland, S.M., Y.R. Shea and J. Kwon-Chung. 2004. Regarding "*Trichosporon pullulans* infection in 2 patients with chronic granulomatous disease". J. Allergy Clin. Immunol. 114, 205–206.

Holley, R.A., and G.E. Timbers. 1983. *Nematospora* destruction in mustard seed by microwave and moisture treatments. Can. Inst. Food Sci. Technol. J. 16, 68–75.

Holley, R.A., P. Allan-Wojtas and B.E. Phipps-Todd. 1984. *Nematospora sinecauda* sp. nov., a yeast pathogen of mustard seeds. Antonie van Leeuwenhoek 50, 305–320.

Holloway, P., R. Subden and M.-A. Lachance. 1990. The yeasts in a Riesling must from the Niagara grape-growing region of Ontario. Can. J. Food Sci. Technol. 23, 212–216.

Holloway, R., A. van Twest, R.E. Subden and M.-A. Lachance. 1992. A strain of *Candida stellata* of special interest to oenologists. Food Res. Int. 25, 147–149.

Holm Hansen, E., P. Nissen, P. Sommer, J.C. Nielsen and N. Arneborg. 2001. The effect of oxygen on the survival of non-*Saccharomyces* yeasts during mixed culture fermentations of grape juice with *Saccharomyces cerevisiae*. J. Appl. Microbiol. 91, 541–547.

Holmberg, S. 1982. Genetic differences between *Saccharomyces carlsbergensis* and *S. cerevisiae*. II. Restriction endonuclease analysis of genes of chromosome III. Carlsberg Res. Commun. 47, 233–244.

Holst, E.C. 1936. *Zygosaccharomyces pini*, a new species of yeast associated with bark beetles in pines. J. Agric. Res. 53, 513–518.

Holtermann, C. 1898. Mykologische Untersuchungen aus den Tropen. Berlin, 122pp.

Holtz, W. 1901. Beitrag zur Kenntnis der Baumflusse und einiger ihrer Bewohner. Zentralbl. Bakteriol. Parasitenkd. Abt. 2, 7, 179–189.

Holzapfel, W.H. 2002. Appropriate starter culture technologies for small-scale fermentation in developing countries. Int. J. Food Microbiol. 75, 197–212.

Holzschu, D.L., and H.J. Phaff. 1982. Taxonomy and evolution of some ascomycetous cactophilic yeasts. In: J.S.F. Barker and W.T. Starmer (Eds), Ecological Genetics and Evolution, The Cactus–Yeast–*Drosophila* Model System. Academic Press, Sydney, pp. 127–141.

Holzschu, D.L., H.L. Presley, M. Miranda and H.J. Phaff. 1979. Identification of *Candida lusitaniae* as an opportunistic yeast in humans. J. Clin. Microbiol. 10, 202–205.

Holzschu, D.L., J. Tredick and H.J. Phaff. 1981. Validation of the yeast *Sporidiobolus ruinenii* based on its DNA relatedness to other species of the genus *Sporidiobolus*. Curr. Microbiol. 5, 73–76.

Holzschu, D.L., H.J. Phaff, J. Tredick and D. Hedgecock. 1983. *Pichia pseudocactophila*, a new species of yeast occurring in necrotic tissue of columnar cacti in the North American Sonoran Desert. Can. J. Microbiol. 29, 1314–1322.

Holzschu, D.L., H.J. Phaff, J. Tredick and D. Hedgecock. 1985. Resolution of the varietal relationship within the species *Pichia opuntiae* and establishment of a new species, *Pichia thermotolerans* comb. nov. Int. J. Syst. Bacteriol. Holzschu 35, 457–461.

Hong, S.G., J. Chun, H.W. Oh and K.S. Bae. 2001. *Metschnikowia koreensis* sp. nov., a novel yeast species isolated from flowers in Korea. Int. J. Syst. Evol. Microbiol. 51, 1927–1931.

Hong, S.G., K.H. Lee and K.S. Bae. 2002. Diversity of yeasts associated with natural environments in Korea. J. Microbiol. 40, 55–62.

Hong, S.G., K.S. Bae, M. Herzberg, A. Titze and M.-A. Lachance. 2003. *Candida kunwiensis* sp. nov., a yeast associated with flowers and bumblebees. Int. J. Syst. Evol. Microbiol. 53, 367–372.

Hong, S.G., K.H. Lee, J. Kwak and K.S. Bae. 2006. Diversity of yeasts associated with *Panax ginseng*. J. Microbiol. 44, 674–679.

Höötmann, U., B. Bisping and H.J. Rehm. 1991. Physiology of polyol formation by free and immobilized cells of the osmotolerant yeast *Pichia farinosa*. Appl. Microbiol. Biotechnol. 35, 258–263.

Hopfer, R.L., and F. Blank. 1975. Caffeic acid-containing medium for identification of *Cryptococcus neoformans*. J. Clin. Microbiol. 2, 115–120.

Hopfer, R.L., and D. Gröschel. 1975. Six hour pigmentation test for the identification of *Cryptococcus neoformans*. J. Clin. Microbiol. 2, 96–98.

Hopsu-Havu, V.K., E. Tunnela and D. Yarrow. 1978. *Candida sonckii* sp. nov. Antonie van Leeuwenhoek 44, 425–438.

Hordijk, W., and O. Gascuel. 2005. Improving the efficiency of SPR moves in phylogenetic tree search methods based on maximum likelihood. Bioinformatics 21, 4338–4347.

Horisberger, M., and M. Rouvet-Vauthey. 1985. Cell wall architecture in the fission yeast *Schizosaccharomyces pombe*. Experientia 41, 748–750.

Horita, H., and S. Yasuoka. 2002. Black streak of edible burdock caused by *Itersonilia perplexans* in Japan. J. Gen. Plant Pathol. 68, 277–283.

Horn, S.J., I.M. Aasen and K. Østgaard. 2000. Ethanol production from seaweed extract. J. Ind. Microbiol. Biotechnol. 25, 249–254.

Hoshino, T., K. Ojima, and Y. Setoguchi. 2000. Astaxanthin synthase. Hoffmann-LaRoche, European Patent 1035206–A3.

Hospenthal, D.R., M.L. Beckius, K.L. Floyd, L.L. Horvath and C. K. Murray. 2006. Presumptive identification of *Candida* species other than *C. albicans*, *C. krusei*, and *C. tropicalis* with the chromogenic medium CHROMagar Candida. Ann. Clin. Microbiol. Antimicrob. 5, 1.

Hossack, J.A., and I. Spencer-Martins. 1978. Lipid composition of the yeast *Lipomyces kononenkoae*. Eur. J. Appl. Microbiol. 5, 273–278.

Hou, C.T. 1994. pH Dependence and thermostability of lipases from cultures from the ARS culture collection. J. Ind. Microbiol. Biotechnol. 13, 242–248.

Houard, S., M. Heinderyckx and A. Bollen. 2002. Engineering of non-conventional yeasts for efficient synthesis of macromolecules: the methylotrophic genera. Biochimie 84, 1089–1093.

Houde, A., A. Kademi and D. Leblanc. 2004. Lipases and their industrial applications – an overview. Appl. Biochem. Biotechnol. 118, 155–170.

Houwers, D., and B. Blankenstein. 2001. *Cyniclomyces guttuatus* and diarrhea in dogs. Tijdschr. Diergeneeskd. 126, 502.

Howell, K., D. Cozzolino, E. Bartowsky, G.H. Fleet and P.A. Henschke. 2006. Metabolic profiling as a tool for revealing *Saccharomyces* interactions during wine making. FEMS Yeast Res. 6, 91–101.

Hoyos, P., G. Sansottera, M. Fernández, F. Molinari, J.V. Sinisterra and A.R. Alcántara. 2008. Enantioselective monoreduction of different 1,2-diaryl-1,2-diketones catalysed by lyophilised whole cells from *Pichia glucozyma*. Tetrahedron 64, 7929–7936.

Hsueh, P.-R., L.J. Teng, S.W. Ho and K.T. Luh. 2003. Catheter-related sepsis due to *Rhodotorula glutinis*. J. Clin. Microbiol. 41, 857–859.

Hu, C.-K., F.-W. Bai and L.-J. An. 2003. Enhancing ethanol tolerance of a self-flocculating fusant of *Schizosaccharomyces pombe* and *Saccharomyces cerevisiae* by Mg^{2+} via reduction in plasma membrane permeability. Biotechnol. Lett. 25, 1191–1194.

Huang, W.P., and D.J. Klionsky. 2002. Autophagy in yeast: a review of the molecular machinery. Cell Struct. Funct. 27, 409–420.

Huchzermyer, F., and N.M. Henton. 2000. Megabacteria in mammals. Vet. Rec. 146, 768.

Huchzermeyer, F.W., M.M. Henton and R.H. Keffen. 1993. High mortality associated with megabacteriosis of proventriculus and gizzard in ostrich chicks. Vet. Rec. 133, 143–144.

Huelsenbeck, J.P., and B. Rannala. 2004. Frequentist properties of Bayesian posterior probabilities of phylogenetic trees under simple and complex substitution models. Syst. Biol. 53, 904–913.

Huelsenbeck, J.P., and F.R. Ronquist. 2001. Mr Bayes: Bayesian inference of phylogenetic trees. Bioinformatics 17, 754–755.

Huelsenbeck, J.P., J.J. Bull and C.W. Cunningham. 1996. Parametric bootstrapping in molecular phylogenetics: applications and performance. In: J.D. Ferraris and S.R. Palumbi (Eds), Molecular Zoology: Advances, Strategies, and Protocols. Wiley-Liss, New York, pp. 19–45.

Huelsenbeck, J.P., B. Larget and M.E. Alfaro. 2004. Bayesian phylogenetic model selection using reversible jump Markov chain Monte Carlo. Mol. Biol. Evol. 21, 1123–1133.

Huerfano, S., A. Castañeda and E. Castañeda. 2001. Experimental infection of almond trees seedlings (*Terminia catappa*) with environmental isolate of *Cryptococcus neoformans* var. *gattii*, serotype C. Rev. Iberoam Micol. 18, 131–132.

Hughes, W.T., and F. Gigliotti. 1988. Nomenclature for *Pneumocystis carinii*. J. Infect. Dis. 157, 432–433.

Hughes-Schrader, S. 1948. Cytology of coccids (Coccoidae-Homoptera). Adv. Genet. 2, 127–203.

Hui, M., and W.T. Kwok. 2006. *Pneumocystis carinii* pneumonia in Hong Kong: a 10 year retrospective study. J. Med. Microbiol. 55, 85–88.

Hui, Y.H., and G.G. Khachatourians (Eds). 1995. Food Biotechnology. VCH Publishers, New York.

Hui, Y.H., L. Meunier-Goddik, A. Solvejg Hansen, J. Josephson, W.-K. Nip, P.S. Stanfield and F. Toldrá (Eds). 2004. Handbook of Food Fermentation and Beverage Fermentation Technology. Marcel-Dekker, New York.

Hull, C.M., and A.D. Johnson. 1999. Identification of a mating type-like locus in the asexual pathogenic yeast *Candida albicans*. Science 285, 1271–1275.

Hull, C.M., R.M. Raisner and A.D. Johnson. 2000. Evidence for mating of the "asexual" yeast *Candida albicans* in a mammalian host. Science 289, 307–310.

Hull, C.M., M.J. Boily and J. Heitman. 2005. Sex-specific homeodomain proteins Sxi1alpha and Sxi2a coordinately regulate sexual development in *Cryptococcus neoformans*. Eukaryot. Cell 4, 526–535.

Humbel, B.M., M. Konomi, T. Takagi, N. Kamasawa, S.A. Ishijima and M. Osumi. 2001. *In situ* localization of β-glucans in the cell wall of *Schizosaccharomyces pombe*. Yeast 18, 433–444.

Hunt, D.W.A., and J.H. Borden. 1990. Conversion of verbenols to verbenone by yeasts isolated from *Dendroctonus ponderosae* (Coleoptera: Scolytidae). J. Chem. Ecol. 16, 1385–1398.

Hunt, D.E., and P.L. Carpenter. 1963. Sterols as components in the mating reaction of *Hansenula wingei*. J. Bacteriol. 86, 845–847.

Hurley, R., J. de Louvois and A. Mulhall. 1987. Yeasts as human and animal pathogens. In: A.H. Rose and J.S. Harrison (Eds), The Yeasts, Vol. I, Biology of Yeasts. Academic Press, London, pp. 207–281.

Hurt, R.A. 1997. A molecular analysis of the relatedness of anamorphic yeasts currently classified as *Candida pintolopesii*. PhD Thesis, University of Tennessee, Knoxville, TN.

Husnik, J.I., H. Volschenk, J. Bauer, D. Colavizza, Z.L. Luo and H.J.J. Vuuren. 2006. Metabolic engineering of malolactic wine yeast. Metab. Eng. 8, 315–323.

Huson, D.H., and D. Bryant. 2006. Application of phylogenetic networks in evolutionary studies. Mol. Biol. Evol. 23, 254–267.

Huson, D.H., T. Dezulian, T. Klopper and M.A. Steel. 2004. Phylogenetic super-networks from partial trees. IEEE/ACM Trans. Comput. Biol. Bioinform. 1, 151–158.

Huss, V.A.R., and M.L. Sogin. 1990. Phylogenetic position of some *Chlorella* species within the Chlorococcales based upon complete small-subunit ribosomal RNA sequences. J. Mol. Evol. 31, 432–442.

Huss, V.A.R., K.H. Wein and E. Kessler. 1988. Deoxyribonucleic acid reassociation in the taxonomy of the genus *Chlorella*. Arch. Microbiol. 150, 509–511.

Hussein, G., U. Sankawa, H. Goto, K. Matsumoto and H. Watanabe. 2006. Astaxanthin, a carotenoid with potential in human health. J. Nat. Prod. 69, 443–449.

Hussein, L., S. El Sayed and S. Foda. 1989. Reduction of lactose in milk by purified lactase produced by *Kluyveromyces lactis*. J. Food Prot. 52, 30–34.

Hutchinson, G.E. 1957. Concluding remarks. Cold Spring Harb. Symp. Quant. Biol. 22, 415–427.

Hutchinson, G.E. 1959. Homage to Santa Rosalia, or why are there so many kinds of animals? Am. Nat. 93, 145–159.

Hutchison, L.J., and G.L. Barron. 1995. Parasitism of yeasts by lignicolous Basidiomycota and other fungi. Can. J. Bot. 74, 735–742.

Hutchison, L.J., and Y. Hiratsuka. 1994. Some wood-inhabiting yeasts of trembling aspen (*Populus tremuloides*) from Alberta and northeastern British Columbia. Mycologia 86, 386–391.

Hutkins, R.W. 2006. Microbiology and Technology of Fermented Foods. Blackwell Publishing, Oxford.

Ibeas, J., J. Lozano, F. Perdigones and J. Jimenez. 1996. Detection of *Brettanomyces/Dekkera* strains in sherry by nested PCR method. Appl. Environ. Microbiol. 62, 998–1003.

Icenhour, C.R., S.L. Rebholz, M.S. Collins and M.T. Cushion. 2001a. Early acquisition of *Pneumocystis carinii* in neonatal rats using targeted PCR and oral swabs. J. Eukaryot. Microbiol. (Suppl.) 135S–136S.

Icenhour, C.R., S.L. Rebholz, M.S. Collins and M.T. Cushion. 2001b. Widespread occurrence of *Pneumocystis carinii* in commercial rat colonies detected using targeted PCR and oral swabs. J. Clin. Microbiol. 39, 3437–3441.

Icenhour, C.R., J. Arnold, M. Medvedovic and M.T. Cushion. 2006. Competitive coexistence of two *Pneumocystis* species. Infect. Genet. Evol. 6, 177–186.

Ichikawa, T., A. Nishikawa, R. Ikeda and T. Shinoda. 2001a. Structural studies of a cell wall polysaccharide of *Trichosporon asahii* containing antigen II. Eur. J. Biochem. 268, 5098–5106.

Ichikawa, T., A. Nishikawa, H. Wada, R. Ikeda and T. Shinoda. 2001b. Studies of the antigen III cell wall polysaccharide of *Trichosporon domesticum*. Carbohydr. Res. 330, 495–503.

Ichikawa, T., T. Sugita, L. Wang, K. Yokoyama, K. Nishimura and A. Nishikawa. 2004. Phenotypic switching and beta-*N*-acetylhexosaminidase activity of the pathogenic yeast *Trichosporon asahii*. Microbiol. Immunol. 48, 237–242.

Iguchi, K., M. Kishida and T. Sakai. 1996. Purification and characterization of three extracellular protopectinases with polygalacturonase activities from *Trichosporon penicillatum*. Biosci. Biotechnol. Biochem. 60, 603–607.

Iizuka, H., and S. Goto. 1965. Microbiological studies on petroleum and natural gas. VIII. Determination of red yeasts isolated from oil brines and related materials. J. Gen. Appl. Microbiol. 11, 331–337.

Iizuka, H., Shimizu, J., Ishii, K. and Nakajima, Y. 1967. Verfahren zur biotechnischen Herstellung von Zitronsäure und ihren Salzen durch Mikroorganismen. German Patent 1,812,710.

Ikeda, R., and T. Maeda. 2004. Structural studies of the capsular polysaccharide of a non-*neoformans Cryptococcus* species identified as *C. laurentii* which was reclassified as *Cryptococcus flavescens* from a patient with AIDS. Carbohydr. Res. 339, 503–509.

Ikeda, R., H. Matsuyama, A. Nishikawa, T. Shinoda and Y. Fukazawa. 1991. Comparison of serological and chemical characteristics of capsular polysaccharides of *Cryptococcus neoformans* var. *neoformans* serotype A and *Cryptococcus albidus* var. *albidus*. Microbiol. Immunol. 35, 125–138.

Ikeda, R., M. Yokota and T. Shinoda. 1996. Serological characterization of *Trichosporon cutaneum* and related species. Microbiol. Immunol. 40, 813–819.

Ikeda, R., T. Sugita and T. Shinoda. 2000. Serological relationships of *Cryptococcus* spp.: distribution of antigenic factors in *Cryptococcus* and intraspecies diversity. J. Clin. Microbiol. 38, 4021–4025.

Ikeda, R., T. Sugita, E.S. Jacobson and T. Shinoda. 2002. Laccase and melanization in clinically important *Cryptococcus* species other than *Cryptococcus neoformans*. J. Clin. Microbiol. 40, 1214–1218.

Ikeda, S., S.-I. Fuji, T. Sato, N. Ytow, H. Ezura, K. Minamisawa and T. Fujimura. 2006. Community analysis of seed-associated microbes in forage crops using culture-independent methods. Microbes Environ. 21, 112–121.

Iliades, P., S.R. Meshnick and I.G. Macreadie. 2005. Mutations in the *Pneumocystis jirovecii* DHPS gene confer cross-resistance to sulfa drugs. Antimicrob. Agents Chemother. 49, 741–748.

Ilmén, M., K. Koivuranta, P. Suominen and M. Pentilä. 2007. Efficient production of L-lactic acid from xylose by *Pichia stipitis*. Appl. Environ. Microbiol. 73, 117–123.

Imanishi, Y., K. Ueda-Nishimura and K. Mikata. 2007. Two new species of *Kazachstania* that form ascospores

connected by a beltlike intersporal body: *Kazachstania zonata* and *Kazachstania gamospora*. FEMS Yeast Res. 7, 330–338.

Imanishi, Y., S. Jindamorakot, K. Mikata, A. Nakagiri, S. Limtong, W. Potacharoen, M. Tanticharoen and T. Nakase. 2008. Two new ascomycetous anamorphic yeast species related to *Candida friedrichii* – *Candida jaroonii* sp. nov., and *Candida songkhlaensis* sp. nov. – isolated in Thailand. Antonie van Leeuwenhoek 94, 267–276.

Imazeki, R., Y. Imazeki, Y. Otani and T. Hongo. 1988. Nihon no Kinoko ("Fungi of Japan"). Yama-Kei Publishers Co., Tokyo, pp. 1–623. In Japanese; names in Latin/English.

Imshenetskii, A.A., and A.E. Kriss. 1933. Matériaux pour l'étude des fungi imperfecti 1. Un nouveau champignon, le *Mastigomyces phillippovi* (nov. gen. nov. sp.) trouvé sur les fruits de *Terminalia chebula*. Dokl. Akad. Nauk SSSR. 7, 111–116. In Russian.

Inácio, J. 2003. Ocorrência e diversidade de leveduras no filoplano de plantas seleccionadas do Parque Natural da Serra da Arrábida. PhD Thesis, Universidade Nova de Lisboa, Portugal. In Portuguese.

Inácio, J., and Á. Fonseca. 2004. Reinstatement of *Rhodotorula colostri* (Castelli) Lodder and *Rhodotorula crocea* Shifrine & Phaff, former synonyms of *Rhodotorula aurantiaca* (Saito) Lodder. FEMS Yeast Res. 4, 557–561.

Inácio, J., P. Pereira, M. de Carvalho, Á. Fonseca, M.T. Amaral-Collaço and I. Spencer-Martins. 2002. Estimation and diversity of phylloplane mycobiota on selected plants in a Mediterranean-type ecosystem in Portugal. Microb. Ecol. 44, 344–353.

Inácio, J., M.G. Rodrigues, P. Sobral and Á. Fonseca. 2004. Characterisation and classification of phylloplane yeasts from Portugal related to the genus *Taphrina* and description of five novel *Lalaria* species. FEMS Yeast Res. 4, 541–555.

Inácio, J., L. Portugal, I. Spencer-Martins and Á. Fonseca. 2005. Phylloplane yeasts from Portugal: seven novel anamorphic species in the *Tremellales* lineage of the Hymenomycetes (Basidiomycota) producing orange-coloured colonies. FEMS Yeast Res. 5, 1167–1183.

Inácio, J., M.F. Landell, P. Valente, P.-H. Wang, Y.-T. Wang, S.-H. Yang, J.S. Manson, M.-A. Lachance, C.A. Rosa and Á. Fonseca. 2008. *Farysizyma* gen. nov., an anamorphic genus in the Ustilaginales to accommodate three novel epiphytic basidiomycetous yeast species from America, Europe and Asia. FEMS Yeast Res. 8, 499–508.

Ingledew, W.M. 1987. *Schwanniomyces* – a potential super-yeast. CRC Crit. Rev. Biotechnol. 5, 159–176.

Inglis, G.D., L. Sigler and M.S. Goettel. 1992. *Trichosporon*oides *megachiliensis*, a new hyphomycete associated with alfalfa leafcutter bees, with notes on *Trichosporon*oides and *Moniliella*. Mycologia 84, 555–570.

Inglis, G.D., L. Sigler and M.S. Goettel. 1993. Aerobic microorganisms associated with alfalfa leafcutter bees (*Megachile rotundata*). Microb. Ecol. 26, 125–143.

Ingold, C. 1979. Advances in the study of the so-called aquatic hyphomycetes. Am. J. Bot. 66, 218–226.

Ingold, C.T. 1982. Basidiospore germination and conidium formation of *Exidia glandulosa* and *Tremella mesenterica*. Trans. Br. Mycol. Soc. 79, 370–373.

Ingold, C.T. 1985. Observations on spores and their germination in certain Heterobasidiomycetes. Trans. Br. Mycol. Soc. 85, 417–423.

Ingold, C.T. 1986. *Bensingtonia ciliata* gen. et sp. nov., a ballistosporic fungus. Trans. Br. Mycol. Soc. 86, 325–328.

Ingold, C.T. 1988. Further observations on *Bensingtonia ciliata*. Trans. Br. Mycol. Soc. 91, 162–166.

Ingold, C.T. 1995. Types of reproductive cell in *Exidia recisa* and *Sirobasidium intermediae*. Mycol. Res. 99, 1187–1190.

Ingram, M. 1958. Yeasts in food spoilage. In: A.H. Cook (Ed.), Chemistry and Biology of Yeasts. Academic Press, New York, pp. 603–633.

Ippolito, A., and F. Nigro. 2000. Impact of preharvest application of biological control agents on postharvest diseases of fresh fruits and vegetables. Crop Prot. 19, 715–723.

Ippolito, A., L. Schena, I. Pentimone and F. Nigro. 2005. Control of postharvest rots of sweet cherries by pre- and postharvest applications of *Aureobasidium pullulans* in combination with calcium chloride or sodium bicarbonate. Postharvest Biol. Technol. 36, 245–252.

Ishibashi, Y., Y. Sakagami, A. Isogai, A. Suzuki and R.J. Bandoni. 1983a. Sex hormones of *Tremella brasiliensis*. Peptide Chem. 1982, 201–206.

Ishibashi, Y., Y. Sakagami, A. Isogai, A. Suzuki and R.J. Bandoni. 1983b. Isolation of tremerogens A-9291-1 and A-9291-11, novel hormones of *Tremella brasiliensis*. Can. J. Biochem. 61, 796–801.

Ishida, N., S. Saitoh, T. Ohnishi, K. Tokuhiro, E. Nagamori, K. Kitamoto and H. Takahashi. 2006. Metabolic engineering of *Saccharomyces* for efficient production of pure L-(+)-lactic acid. Appl. Biochem. Biotechnol. 129–132, 795–807.

Ishikawa, E., T. Sakai, H. Ikemura, K. Matsumoto and H. Abe. 2005. Identification, cloning, and characterization of a *Sporobolomyces singularis* beta-galactosidase-like enzyme involved in galacto-oligosaccharide production. J. Biosci. Bioeng. 99, 331–339.

Ismail, S.A., T. Deák, H.A. El-Rahman, M.A. Yassien and L.R. Beuchat. 2000. Presence and changes in populations of yeasts on raw and processed poultry products stored at refrigeration temperature. Int. J. Food. Microbiol. 62, 113–121.

Itah, A.Y., and J.P. Essien. 2005. Growth profile and hydrocarbonoclastic potential of microorganisms isolated from tarballs in the Bight of Bonny, Nigeria. World J. Microbiol. Biotechnol. 21, 1317–1322.

Itatani, C.A. 1996. Ultrastructural morphology of intermediate forms and forms suggestive of conjugation in the life cycle of *Pneumocystis carinii*. J. Parasitol. 82, 163–171.

Ito, H., H. Iizuka and T. Sato. 1974. A new radio-resistant yeast of *Trichosporon oryzae* nov. sp. isolated from rice. Agric. Biol. Chem. 38, 1597–1620.

IUBMB. 1992. Enzyme Nomenclature. Academic Press, New York.

Izumchenko, E., M. Wolfson, E.A. Golemis and I.G. Serebriiski. 2007. Yeast hybrid approaches. Methods Microbiol. 36, 103–137.

Jaafar, L., and J. Zueco. 2004. Characterization of a glycosylphosphatidylinositol-bound cell-wall protein (GPI-CWP) in *Yarrowia lipolytica*. Microbiology 150, 53–60.

Jaafar, L., I. Moukadiri and J. Zueco. 2003. Characterization of a disulphide-bound Pir-cell wall protein (Pir-CWP) of *Yarrowia lipolytica*. Yeast 20, 417–426.

Jablonowski, D., and R. Shcaffrath. 2007. Zymocin, a composite chitinase and tRNase killer toxin from yeast. Biochem. Soc. Trans. 35, 1533–1537.

Jabra-Rizk, M.A., T.M. Brenner, M. Romagnoli, A.A. Baqui, W.G. Merz, W.A. Falkler Jr. and T.F. Meiller. 2001. Evaluation of a reformulated CHROMagar *Candida*. J. Clin. Microbiol. 39, 2015–2016.

Jackson, A.P., J.A. Gamble, T. Yeomans, G.P. Moran, D. Saunders, D. Harris, M. Aslett, J.F. Barrell, G. Butler, F. Citiulo, D.C. Coleman, P.W. de Groot, T.J. Goodwin, M.A. Quail, J. McQuillan, C.A. Munro, A. Pain, R.T. Poulter, M.A. Rajandream, H. Renauld, M.J. Spiering, A. Tivey, N.A. Gow, B. Barrell, D.J. Sullivan and M. Berriman. 2009. Comparative genomics of the fungal pathogens *Candida dubliniensis* and *Candida albicans*. Genome Res. 19, 2231–2244.

Jackson, H.S. 1947. *Trichomonascus*, a new genus among simple Ascomycetes. Mycologia 39, 709–715.

Jacob, F.H. 1969a. *Pichia tannicola*, nouvelle espèce de levure isolée de liqueurs tannantes végétales. Bull. Soc. Mycol. Fr. 85, 111–115.

Jacob, F.H. 1969b. *Pichia adzetii* et *Pichia abadiae*, nouvelles espèces de levures isolées de liqueurs tannantes végétales. Bull. Soc. Mycol. Fr. 85, 117–127.

Jacob, F.H. 1970. Deux espèces nouvelles de levures asporogènes isolées de liqueurs tannantes végétales. Ann. Inst. Pasteur 118, 207–213.

Jacob, F.H., M. Faure-Raynaud and M.C. Berton. 1979. *Torulopsis pilati* nov. sp., une nouvelle espèce de levure isolée de la litière du sapin d'*Abies alba* Mill. Mycopathol. 69, 83–85.

Jacobsen, M.D., N.A. Gow, M.C. Maiden, D.J. Shaw and F.C. Odds. 2007. Strain typing and determination of population structure of *Candida krusei* by multilocus sequence typing. J. Clin. Microbiol. 45, 317–323.

Jacobsen, M.D., T. Boekhout and F.C. Odds. 2008. Multilocus sequence typing reveals synonymy and indicates differences between *Candida albicans* and *Candida stellatoidea*. FEMS Yeast Res. 8, 764–770.

Jacques, N., and S. Casaregola. 2008. Safety assessment of dairy microorganisms: the hemiascomycetous yeasts. Int. J. Food Microbiol. 126, 321–326.

Jacques, N., S. Mallet and S. Casaregola. 2009. Delimitation of the species of the *Debaryomyces hansenii* complex by intron sequence analysis. Int. J. Syst. Evol. Microbiol. 59, 1242–1251.

Jaeger, K.E., and T. Eggert. 2002. Lipases for biotechnology. Curr. Opin. Biotechnol. 13, 390–397.

Jahic, M., A. Veide, T. Charoenrat, T. Teeri and S.O. Enfors. 2006. Process technology for production and recovery of heterologous proteins with *Pichia pastoris*. Biotechnol. Prog. 22, 1465–1473.

Jain, M.R., S.S. Zinjarde, D.D. Deobagkar and D.N. Deobagkar. 2004. 2,4,6-Trinitrotoluene transformation by a tropical marine yeast, *Yarrowia lipolytica* NCIM 3589 Mar. Pollut. Bull. 49, 783–789.

Jakobsen, M., and J. Narvhus. 1996. Yeasts and their possible beneficial and negative effects on the quality of dairy products. Int. Dairy J. 6, 8–9.

James, P.G., R. Cherniak, R.G. Jones, C.A. Stortz and E. Reiss. 1990. Cell-wall glucans of *Cryptococcus neoformans* Cap 67. Carbohydr. Res. 198, 23–38.

James, S.A., and M. Stratford. 2003. Spoilage yeasts with emphasis on the genus *Zygosaccharomyces*. In: T. Boekhout and V. Robert (Eds), Yeasts in Food, Beneficial and Detrimental Aspects. Behr's Verlag, Hamburg, pp. 171–187.

James, S.A., M.D. Collins and I.N. Roberts. 1994a. The genetic relationship of *Lodderomyces elongisporus* to other ascomycete yeast species as revealed by small-subunit rRNA gene sequences. Lett. Appl. Microbiol. 19, 308–311.

James, S.A., M.D. Collins and I.N. Roberts. 1994b. Genetic interrelationship among species of the genus *Zygosaccharomyces* as revealed by small-subunit rRNA gene sequences. Yeast 10, 871–881.

James, S.A., M.D. Collins and I.N. Roberts. 1996. Use of an rRNA internal transcribed spacer region to distinguish phylogenetically closely related species of the genera *Zygosaccharomyces* and *Torulaspora*. Int. J. Syst. Bacteriol. 46, 189–194.

James, S.A., J. Cai, I.N. Roberts and M.D. Collins. 1997. A phylogenetic analysis of the genus *Saccharomyces* based on 18S rRNA gene sequences: description of *Saccharomyces kunashirensis* sp. nov. and *Saccharomyces martiniae* sp. nov. Int. J. Syst. Bacteriol. 47, 453–460.

James, S.A., I.N. Roberts and M.D. Collins. 1998. Phylogenetic heterogeneity of the genus *Williopsis* as revealed by 18S rRNA gene sequences. Int. J. Syst. Bacteriol. 48, 591–596.

James, S.A., M.D. Collins and I.N. Roberts. 2001a. Phylogenetic analysis of the psychrophobic yeast *Arxiozyma telluris* and the reinstatement of *Candida pintolopesii* (van Uden) Meyer et Yarrow and *Candida slooffii* van Uden et do Carmo Sousa. Int. J. Syst. Evol. Microbiol. 51, 191–725.

James, S.A., C.J. Bond and I.N. Roberts. 2001b. *Candida sorbosivorans* sp. nov., a new member of the genus *Candida* Berkhout. Int. J. Syst. Evol. Microbiol. 51, 1215–1219.

James, S.A., C.J. Bond, M. Stratford and I.N. Roberts. 2005. Molecular evidence for the existence of natural hybrids in the genus *Zygosaccharomyces*. FEMS Yeast Res. 5, 747–755.

James, T.Y., F. Kauff, C. Schoch, B. Matheny, V. Hofstetter, C.J. Cox, G. Celio, C. Guiedan, E. Fraker, J. Miadlikowska, T. Lumbsh, A. Rauhut, V. Reeb, A. Arnold, A. Amtoft, J.E. Stajich, K. Hosaka, G. Sung, D. Johnson, B. O'Rourke, M. Crockett, M. Binder, J.M. Curtis, J.C. Slot, Z. Wang, A.W. Wilson, A. Schueller, J.E. Longcore, K.O. Donnell, S. Mozley-Standridge, D. Porter, P.M. Letcher, M.J. Powell, J. W. Taylor, M.M. White, G.W. Griffith, D.R. Davies, R.A. Humber, J.B. Morton, J. Sugiyama, A.Y. Rossman, J.D. Rogers, D.H. Pfister, D. Hewitt, K. Hansen, S. Hambleton, R. A. Shoemaker, J. Kohlmeyer, B. Volkmann-Kohlmeyer, R.A. Spotts, M. Serdani, P.W. Crous, K.W. Hughes, K. Matsuura, E. Langer, G. Langer, W.A. Untereiner, R. Lucking, B. Budel, D.M. Geiser, D.M. Aptroot, P. Diederich, I. Schmitt, M. Schultz, R. Yahr, D.S. Hibbett, F. Lutzoni, D.J. Mclaughlin, J. W. Spatafora and R. Vilgalys. 2006. Reconstructing the early evolution of fungi using a six-gene phylogeny. Nature 443, 818–822.

Janbon, G. 2004. *Cryptococcus neoformans* capsule biosynthesis and regulation. FEMS Yeast Res. 4, 765–771.

Janbon, G., J. Derancourt, P. Chemardin, A. Arnaud and P. Glazy. 1995a. A very stable β-glucosidase from *Candida* mutant strain: enzymatic properties, sequencing, and homology with other yeast β-glucosidases. Biosci. Biotechnol. Biochem. 59, 1320–1322.

Janbon, G., R. Magnet, F. Bigey, A. Arnaud and P. Glazy. 1995b. Karyotype studies on different strains on *Candida*

molischiana by pulsed-field gel electrophoresis. Curr. Genet. 28, 150–154.

Janisiewicz, W.J. 1987. Postharvest biological control of blue mold on apples. Phytopathology 77, 481–485.

Janisiewicz, W.J., and B. Bors. 1995. Development of a microbial community of bacterial and yeast antagonists to control wound-invading postharvest pathogens of fruits. Appl. Environ. Microbiol. 61, 3261–3267.

Janisiewicz, W.J., and L. Korsten. 2002. Biological control of postharvest diseases of fruits. Annu. Rev. Phytopathol. 40, 411–441.

Janisiewicz, W.J., D.L. Peterson and R. Bors. 1994. Control of storage decay of apples with *Sporobolomyces roseus*. Plant Dis. 78, 466–470.

Janisiewicz, W.J., T.J. Tworkoski and C.P. Kurtzman. 2001. Biocontrol potential of *Metschnikowia pulcherrima* strains against blue mold of apple. Phytopathology 91, 1098–1108.

Janisiewicz, W.J., I. Bastos-Pereira, M.S. Almeida, D.P. Roberts, M. Wisniewski and E. Kurtenbach. 2008. Improved biocontrol of fruit decay fungi with *Pichia pastoris* recombinant strains expressing Psd1 antifungal peptide. Postharvest Biol. Technol. 47, 218–225.

Janke, A. 1924. Allgemeine Technische Mikrobiologie. I. Teil: Die Mikroorganismen. Technische Fortschrittberichte Band IV. Verlag Steinkopff, Dresden.

Janke, A. 1928. Über die Formgattung *Kloeckera* Janke. Zentralbl. Bakteriol. Parasitenkd., Abt. II, 76, 161.

Janke, A. 1930. *Mycoderma lafarii* n. sp. Arch. Mikrobiol. 1, 176–180.

Janke, A. 1954. *Sporobolomyces roseus* var. *madurae* var. nov. und die Beziehungen zwischen den Genera *Sporobolomyces* und *Bullera*. Zentralbl. Bakteriol. Parasitenkd., Orig. 161, 514–520.

Jansen van Rensburg, E.L., J.L.F. Kock, A. Botha, D.J. Coetzee and P.J. Botes. 1992. The characterization of lipomycetaceous yeasts from South African soils. SuidAfrik. Tydskr. Wetensk. 88, 387–389.

Jansen van Rensburg, E.L., J.L.F. Kock, D.J. Coetzee, A. Botha and P.J. Botes. 1995. Lipid composition and DNA band patterns in the yeast family Lipomycetaceae. Syst. Appl. Microbiol. 18, 410–424.

Janszen, F.H., and J.G. Wessels. 1970. Enzymic dissolution of hyphal septa in a basidiomycete. Antonie van Leeuwenhoek 36, 255–257.

Jarl, K. 1969. Symba yeast process. Food Technol. 23, 1009–1012.

Jarvis, W.R. 1995. Epidemiology of nosocomial fungal infections, with emphasis on *Candida* species. Clin. Infect. Dis. 20, 1526–1530.

Jarvis, W.R., L.A. Shaw and J.S. Traquair. 1989. Factors affecting antagonism of cucumber powdery mildew by *Stephanoascus flocculosus* and *S. rugulosus*. Mycol. Res. 92, 162–165.

Jarvis, W.R., J.A. Traquair and R.R. Bélanger. 2007. Perspectives on the development of Sporodex®: fungal biocontrol for powdery mildew in greenhouse crops. In: C. Vincent, M. Goettel and G. Lazarovits (Eds), Biological Control: A Global Perspective. CABI Publishing, Wallingford, pp. 224–233.

Jaspersen, S.L., and M. Winey. 2004. The budding yeast spindle pole body: structure, duplication, and function. Annu. Rev. Cell Dev. Biol. 20, 1–28.

Jedd, G., and N.H. Chua. 2000. A new self-assembled peroxisomal vesicle required for efficient resealing of the plasma membrane. Nat. Cell Biol. 2, 226–231.

Jeffery, J., J.L.F. Kock, A. Botha, D.J. Coetzee and P.J. Botes. 1997. The value of lipid composition in the taxonomy of the Schizosaccharomycetales. Antonie van Leeuwenhoek 72, 327–335.

Jeffries, T.W. 2006. Engineering yeasts for xylose metabolism. Curr. Opin. Biotechnol. 17, 320–326.

Jeffries, T.W., and C.P. Kurtzman. 1994. Strain selection, taxonomy, and genetics of xylose-fermenting yeasts. Enzyme Microb. Technol. 16, 922–932.

Jeffries, T.W., I.V. Grigoriev, J. Grimwood, J.M. Laplaza, A. Aerts, A. Salamov, J. Schmutz, E. Lindquist, P. Dehal, H. Shapiro, Y.S. Jin, V. Passoth and P.M. Richardson. 2007. Genome sequence of the lignocellulose-bioconverting and xylose-fermenting yeast *Pichia stipitis*. Nat. Biotechnol. 25, 319–326.

Jeffroy, O., H. Brinkmann, F. Delsuc and H. Philippe. 2006. Phylogenomics: the beginning of incongruence? Trends Genet. 22, 225–231.

Jenkins, A.E. 1938. A new species of *Taphrina* on sugar maple and black maple. J. Wash. Acad. Sci. 28, 353–358.

Jenkins, A.E. 1939. New species of *Taphrina* on red maple and sugar maple. J. Wash. Acad. Sci. 29, 222–230.

Jenkinson, H.F., and M.G. Shepherd. 1987. A mutant of *Candida albicans* deficient in beta-*N*-acetylglucosaminidase (chitobiase). J. Gen. Microbiol. 133, 2097–2106.

Jensen, V. 1967. Taxonomic studies on soil yeasts. 1. The genus *Saccharomyces* (Meyen) Reess. K. Vet. Landboh. Arsskr. 179–194.

Jespersen, L., and M. Jakobsen. 1996. Specific spoilage organisms in breweries and laboratory media for their detection. Int. J. Food Microbiol. 33, 139–155.

Jespersen, L., D.S. Nielsen, S. Honholt and M. Jakobsen. 2005. Occurrence and diversity of yeasts involved in fermentation of West African cocoa beans. FEMS Yeast Res. 5, 441–453.

Ji, Z.-H., and F.-Y. Bai. 2008. *Ogataea ganodermae* sp. nov., a methanol-assimilating yeast species isolated from basidiocarps of *Ganoderma* sp. Int. J. Syst. Evol. Microbiol. 58, 1502–1506.

Ji, Z.-H., J.-H. Jia and F.-Y. Bai. 2009. Four novel *Candida* species in the *Candida albicans*/*Lodderomyces elongisporus* clade isolated from the gut of flower beetles. Antonie van Leeuwenhoek 95, 23–32.

Jia, J., M. Tang, X. Chen, L. Qi and S. Dong. 2003. Co-immobilized microbial biosensor for BOD estimation based on sol-gel derived composite material. Biosens. Bioelectron. 18, 1023–1029.

Jiang, B., H. Bussey and T. Roemer. 2002. Novel strategies in antifungal lead discovery. Curr. Opin. Microbiol. 5, 466–471.

Jijakli, M.H., and P. Lepoivre. 1998. Characterization of an exo-beta-1,3-glucanase produced by *Pichia anomala* strain K, antagonist of *Botrytis cinerea* on apples. Phytopathology 88, 335–343.

Jijakli, M.H., P. Lepoivre, P. Tossut and P. Thonard. 1993. Biological control of *Botrytis cinerea* and *Penicillium* sp. on post-harvest apples by two antagonistic yeasts. Meded. Fac. Landbouwwet.-Rijksuniv. Gent. 58, 1349–1358.

Jindamorakot, S., S. Am-in, T.T. Thuy, N.D. Duy, H. Kawasaki, W. Potacharoen, S. Limtong, M. Tanticharoen

and T. Nakase. 2004. *Candida easanensis* sp. nov., *Candida pattaniensis* sp. nov. and *Candida nakhonratchasimensis* sp. nov., three new species of yeasts isolated from insect frass in Thailand. J. Gen. Appl. Microbiol. 50, 261–269.

Jindamorakot, S., W. Potacharoen, S. Limtong and T. Nakase. 2007a. Four new species of bipolar budding yeasts of genus *Hanseniaspora* and its anamorph *Kloeckera* isolated in Thailand. In: E. Stackebrandt, M. Wozniczka, V. Weihs, and J. Sikorski. (Eds), Eleventh International Conference on Culture Collections, ICCC 11. DSMZ Deutsche Sammlung von Mikroorganismen und Zellkulturen GmbH and World Federation of Culture Collections, Goslar, Germany, pp. 109–112.

Jindamorakot, S., S. Limtong, W. Yongmanitchai, M. Tuntirungkij, W. Potacharoen, H. Kawasaki and T. Nakase. 2007b. Two new anamorphic yeasts, *Candida thailandica* sp. nov. and *Candida lignicola* sp. nov., isolated from insect frass in Thailand. FEMS Yeast Res. 7, 1409–1414.

Jindamorakot, S., S. Limtong, W. Yongmanitchai, M. Tuntirungkij, W. Potacharoen, H. Kawasaki, M. Tanticharoen and T. Nakase. 2008. *Candida ratchasimensis* sp. nov. and *Candida khaoyaiensis* sp. nov., two anamorphic yeast species isolated from flowers in Thailand. FEMS Yeast Res. 8, 955–960.

Jindamorakot, S., S. Ninomiya, S. Limtong, W. Yongmanitchai, M. Tuntirungkij, W. Potacharoen, K. Tanaka, H. Kawasaki and T. Nakase. 2009. Three new species of bipolar budding yeasts of the genus *Hanseniaspora* and its anamorph *Kloeckera* isolated in Thailand. FEMS Yeast Res. 9, 1327–1337.

Jobb, G., A.v. Haeseler and K. Strimmer. 2004. TREEFINDER: a powerful graphical analysis environment for molecular phylogenetics. BMC Evol. Biol. 4, 18.

Johannsen, E. 1980. Hybridization studies within the genus *Kluyveromyces*. Antonie van Leeuwenhoek 46, 177–189.

Johannsen, E. 1981. Hybridization studies within the genus *Schizosaccharomyces* Lindner. Can. J. Microbiol. 27, 184–191.

Johannsen, E., and J.P. van der Walt. 1978. Interfertility as basis for the delimitation of *Kluyveromyces marxianus*. Arch. Microbiol. 118, 45–48.

Johanson, C.J. 1886. Om svampslagtet Taphrina och dithorande svenska arter. Ofvers of Kongl. Svensk Vetensk. Akad. Forhandl. 1885, 29–47.

Johnson, D.A., J.D. Rogers and K.M. Regnier. 1988. A soft rot of onion caused by the yeast *Kluyveromyces marxianus* var. *marxianus*. Plant Dis. 359–361.

Johnson, E.A. 1976. Astaxanthin production by the yeast *Phaffia rhodozyma* and its use as a pigment source in animal feeding. University of California, Davis.

Johnson, E.A. 1991. Microbiological safety of fermented foods. In: J.G. Zeikus and E.A. Johnson (Eds), Mixed Cultures in Biotechnology. McGraw-Hill, New York, pp. 135–169.

Johnson, E.A. 2003. *Phaffia rhodozyma*: colorful odyssey. Int. Microbiol. 6, 169–174.

Johnson, E.A., and G.H. An. 1991. Astaxanthin from microbial sources. Crit. Rev. Biotechnol. 11, 297–326.

Johnson, E.A., and M.J. Lewis. 1979. Astaxanthin formation by the yeast *Phaffia rhodozyma*. J. Gen. Microbiol. 115, 173–183.

Johnson, E.A., and H.J. Phaff. 1978. *Rhodotorula fujisanensis*, a new taxonomic combination. Curr. Microbiol. 1, 223–225.

Johnson, E.A., and W.A. Schroeder. 1995. Microbi. carotenoids. Adv. Biochem. Eng. 53, 119–177.

Johnson, E.A., M. Miranda and H.J. Phaff. 1977a. Yeasts associated with kelp wrack at Bodega Bay. Unpublished results.

Johnson, E.A., D.E. Conklin and M.J. Lewis. 1977b. The yeast *Phaffia rhodozyma* as a dietary pigment source for salmonids and crustaceans. J. Fish Res. Bd Can. 34, 2417–2421.

Johnson, E.A., T.G. Villa, M.J. Lewis and H.J. Phaff. 1978. Simple method for isolation of astaxanthin from basidiomycetous yeast *Phaffia rhodozyma*. Appl. Environ. Microbiol. 35, 1155–1159.

Johnson, E.A., M.J. Lewis and C.R. Grau. 1980a. Pigmentation of egg yolks with astaxanthin from the yeast *Phaffia rhodozyma*. Poultry Sci. 59, 1777–1782.

Johnson, E.A., T.G. Villa and M.J. Lewis. 1980b. *Phaffia rhodozyma* as an astaxanthin source in animal diets. Aquaculture 20, 123–134.

Johnson, E.F. (Ed.) 2002. Cytochrome P450. Part C. Methods in Enzymology, Vol. 357. Academic Press, San Diego, CA.

Johnson, E.M. 2009. Rare and emerging *Candida* species. Curr. Fungal Infect. Rep. 3, 152–159.

Johnson, G. 1905. *Saccharomyces thermantitonum*. J. Inst. Brewing 11, 466–490.

Johnson, L.B., S.F. Bradley and C.A. Kauffman. 1998. Fungaemia due to *Cryptococcus laurentii* and a review of *non-neoformans* cryptoccaemia. Mycoses 41, 277–280.

Johnson, N.C., J.H. Graham and F.A. Smith. 1997. Functioning of mycorrhizal associations along the mutualism–parasitism continuum. New Phytologist 135, 575–585.

Johnson-Reid, J.A., and R.T. Moore. 1972. Some ultrastructural features of *Rhodosporidium toruloides* Banno. Antonie van Leeuwenhoek 38, 417–435.

Johnston, J.C., and E.J. Trione. 1974. Cytokinin production by the fungi *Taphrina cerasi* and *T. deformans*. Can. J. Bot. 52, 1583–1589.

Johnston, J.R., and R.K. Mortimer. 1986. Electrophoretic karyotyping of laboratory and commercial strains of *Saccharomyces* and other yeasts. Int. J. Syst. Bacteriol. 36, 569–572.

Johnston, M., L. Hillier, L. Riles, K. Albermann, B. Andre, W. Ansorge, V. Benes, M. Bruckner, H. Delius, E. Dubois, A. Dusterhoft, K.D. Entian, M. Floeth, A. Goffeau, U. Hebling, K. Heumann, D. Heuss-Neitzel, H. Hilbert, F. Hilger, K. Kleine, P. Kotter, E.J. Louis, F. Messenguy, H.W. Mewes, T. Miosga, D. Mostl, S. Muller-Auer, U. Nentwich, B. Obermaier, E. Piravandi, T.M. Pohl, D. Portetelle, B. Purnelle, S. Rechmann, M. Rieger, M. Rinke, M. Rose, M. Scharfe, B. Scherens, P. Scholler, C. Schwager, S. Schwarz, A.P. Underwood, L.A. Urrestarazu, M. Vandenbol, P. Verhasselt, F. Vierendeels, M. Voet, G. Volckaert, H. Voss, R. Wambutt, E. Wedler, H. Wedler, F.K. Zimmermann, A. Zollner, J. Hani and J.D. Hoheisel. 1997. The nucleotide sequence of *Saccharomyces cerevisiae* chromosome XII. Nature 387 (Suppl.), 87–90.

Johri, B.N., and R.J. Bandoni. 1984. Taxonomy of the sporobolomycetous genus *Bullera*. In: Proc. Int. Symp. on Taxonomy of Fungi, Madras 1973. Part 2, pp. 536–547.

Joly, S., C. Pujol, M. Rysz, K. Vargas and D.R. Soll. 1999. Development and characterization of complex DNA

fingerprinting probes for the infectious yeast *Candida dubliniensis*. J. Clin. Microbiol. 37, 1035–1044.

Jones, C.P., and D.S. Martin. 1938. Identification of yeast-like organisms isolated from the vaginal tracts of pregnant and non-pregnant women. Am. J. Obstet. Gynecol. 35, 98–106.

Jones, D.T., W.R. Taylor and J.M. Thornton. 1992. The rapid generation of mutation data matrices from protein sequences. Comput. Appl. Biosci. 8, 275–282.

Jones, E.B.G., and W.Ch. Slooff. 1966. *Candida aquatica* sp. n. isolated from water scums. Antonie van Leeuwenhoek 32, 223–228.

Jones, J.L., D.L. Hanson, M.S. Dworkin, D.L. Alderton, P.L. Fleming, J.E. Kaplan and J. Ward. 1999. Surveillance for AIDS-defining opportunistic illnesses, 1992–1997. MMWR CDC Surveill. Summ. 48, 1–22.

Jones, K.G., and M. Blackwell. 1998. Phylogenetic analysis of ambrosia species in the genus *Raffaelea* based on 18S rDNA sequences. Mycol. Res. 102, 661–665.

Jones, K.G., P.F. Dowd and M. Blackwell. 1999. Polyphyletic origins of yeast-like endocytobionts from anobiid and cerambycid beetles. Mycol. Res. 103, 542–546.

Jones, M.G., and W.C. Noble. 1982. An electrophonetic study of enzymes as a tool in the taxonomy of the Dermatophytes. J. Gen. Microbiol. 128, 1101–1107.

Jones, R.W., and D. Prusky. 2002. Expression of an antifungal peptide in *Saccharomyces*: a new approach for biological control of the postharvest diseases caused by *Colletotrichum coccodes*. Phytopathology 92, 33–37.

Jones, T., N.A. Federspiel, H. Chibana, J. Dungan, S. Kalman, B. B. Magee, G. Newport, Y.R. Thorstenson, N. Agabian, P.T. Magee, R.W. Davis and S. Scherer. 2004. The diploid genome sequence of *Candida albicans*. Proc. Natl. Acad. Sci. USA 101, 7329–7334.

Jong, S.-C., and D.S. King. 1977. Identity of *Sterigmatomyces aphidis* and *Trichosporon oryzae*. Mycotaxon 6, 11–16.

Jong, S.-C., and F.-L. Lee. 1986. The new species *Dekkera naardenensis*, teleomorph of *Brettanomyces naardenensis*. Mycotaxon 25, 147–152.

Jordan, P.A., and J.M. Gibbins. 2006. Extracellular disulfide exchange and the regulation of cellular function. Antiox. Redox Signal. 8, 312–324.

Jörgensen, A. 1909. Die Mikroorganismen der Gärungsindustrie, 5te Aufl. P. Parey, Berlin.

Joshi, K.R., and J.B. Gavin. 1974. A simple laboratory method for the rapid identification of *Candida albicans*. Pathology 6, 231–233.

Jouve, J.L. 2000. Good manufacturing practice, HACCP and quality systems. In: B.M. Lund, T.C. Baird-Parker and G. W. Gould (Eds), The Microbiological Safety and Quality of Food, Vol. 2. Aspen Publishers, Maryland, pp. 1625–1655.

Jukes, T.H., and C.R. Cantor. 1969. Evolution of protein molecules. In: H.N. Munro (Ed.), Mammalian Protein Metabolism. Academic Press, New York, pp. 21–132.

Jülich, W. 1983. Parasitic heterobasidiomycetes on other fungi. A key to European taxa. Int. J. Mycol. I, 421–428.

Julsing, M.K., A. Koulman, H.J. Woerenbag, W.J. Quax and O. Kayser. 2006. Combinatorial synthesis of medicinal plant secondary metabolites. Biomolec. Eng. 23, 265–279.

Jung, U.S., and D.E. Levin. 1999. Genome-wide analysis of gene expression regulated by the yeast cell wall integrity signalling pathway. Mol. Microbiol. 34, 1049–1057.

Júnior, V.L., L.A. Maffia, R.S. Romeiro and E.S.G. Mizubuti. 2006. Biocontrol of tomato late blight with the combination of epiphytic antagonists and rhizobacteria. Biol. Control 38, 331–340.

Jurzitza, G. 1970. Über Isolierung, Kultur und Taxonomie einiger Anobiidensymbionten (Insecta, Coleoptera). Arch. Mikrobiol. 72, 203–222.

Jurzitza, G., C. Kühlwein and N.J.W. Kreger-van Rij. 1960. Zur Systematik einiger Cerambycidensymbionten. Arch. Mikrobiol. 36, 229–243.

Juvvadi, P.R., J. Maruyama and K. Kitamoto. 2007. Phosphorylation of the *Aspergillus oryzae* Woronin body protein, AoHex1, by protein kinase C: evidence for its role in the multimerization and proper localization of the Woronin body protein. Biochem. J. 405, 533–540.

Kaczowka, S.J., C.J. Reuter, L.A. Malarico and J.A. Maupin-Furlow. 2005. Recombinant production of *Zymomonas mobilis* pyruvate decarboxylase in the haloarchaeon *Haloferax volcanii*. Archaea 1, 327–334.

Kaeberlein, M., C.R. Burtner and B.K. Kennedy. 2007. Recent developments in yeast aging. PLoS Genet. 3, 655–660.

Kaelin, W.G. 2005. The concept of synthetic lethality in the context of anticancer therapy. Nat. Rev. Cancer 689–698.

Kaewwichian, R., W. Yongmanitchai, N. Srisuk, K. Fujjiyama and S. Limtong. 2010. *Geotrichum siamensis* sp. nov. and *Geotrichum phurueaensis* sp. nov., two asexual arthroconidial yeast species isolated in Thailand. FEMS Res. 10, 214–220.

Kagan, B.L. 1983. Mode of action of yeast killer toxins: channel formation in lipid bilayer membranes. Nature 302, 709–711.

Kaihara, S., Y. Osanai, K. Nishikawa, Y. Doi and S. Matsumura. 2005. Enzymatic transformation of bacterial polyhydroxyalkanoates into repolymerizable oligomers directed towards chemical recycling. Macromol. Biosci. 5, 644–652.

Kakugawa, K., M. Tamai, K. Imanura, K. Miyamoto, S. Miyoshi, S. Morinaga, O. Suzuki and T. Miyakawa. 2002. Isolation of yeast *Kurtzmanomyces* sp. I-11, novel producer of mannosylerythritol lipid. Biosci. Biotechnol. Biochem. 66, 188–191.

Kakuta, M., Y. Sone, T. Umeda and A. Misaki. 1979. Comparative structural studies on acidic heteropolysaccharides isolated from "Shirokikurage", fruit body of *Tremella fuciformis* Berk. and the growing culture of its yeast-like cells. Agric. Biol. Chem. 43, 1659–1668.

Kalathenos, P., J.P. Sutherland and T.A. Roberts. 1995. Resistance of some wine spoilage yeasts to combinations of ethanol and acids present in wine. J. Appl. Bacteriol. 78, 245–250.

Kalina, T., and M. Puncocharova. 1987. Taxonomy of the subfamily Scotiellocystoideae Fott 1976 (Chlorellaceae, Chlorophyceae). Algol. Stud. 45, 473–521.

Kalogiannis, S., S.E. Tjamos, A. Stergiou, P.P. Antoniou, B.N. Ziogas and E.C. Tjamos. 2006. Selection and evaluation of phyllosphere yeasts as biocontrol agents against grey mould of tomato. Eur. J. Plant Pathol. 116, 69–76.

Kals, M., K. Natter, G.G. Thallinger, Z. Trajanoski and S.D. Kohlwein. 2005. YPL.db2: the Yeast Protein Localization database, version 2.0. Yeast 22, 213–218.

Kamalan, A., and A.S. Thambiah. 1976. A study of 3891 cases of mycosis in the tropics. Sabouraudia 14, 129–148.

Kamalan, A., P. Yesudian and A.S. Thambiah. 1977. Cutaneous infection by *Cryptococcus laurentii*. Br. J. Dermatol. 97, 221–223.

Kamienski, T. 1899. Notice préliminaire sur l'espèce de *Metschnikowia* (*Monospora* Metschn.). Trav. Soc. Imp. Nat. St. Pétersbourg 30, 363–364.

Kamiyama, A., M. Niimi, M. Tokunaga and H. Nakayama. 1989. DNA homology between *Candida albicans* strains: evidence to justify the synonymous status of C. *stellatoidea*. Mycopathologia 107, 3–7.

Kämper, J., R. Kahmann, M. Bölker, L.J. Ma, T. Brefort, B.J. Saville, F. Banuett, J.W. Kronstad, S.E. Gold, O. Müller, M.H. Perlin, H.A. Wösten, R. de Vries, J. Ruiz-Herrera, C.G. Reynaga-Peña, K. Snetselaar, M. McCann, J. Pérez-Martín, M. Feldbrügge, C.W. Basse, G. Steinberg, J.I. Ibeas, W. Holloman, P. Guzman, M. Farman, J.E. Stajich, R. Sentandreu, J.M. González-Prieto, J.C. Kennell, L. Molina, J. Schirawski, A. Mendoza-Mendoza, D. Greilinger, K. Münch, N. Rössel, M. Scherer, M. Vranes, O. Ladendorf, V. Vincon, U. Fuchs, B. Sandrock, S. Meng, E.C. Ho, M.J. Cahill, K.J. Boyce, J. Klose, S.J. Klosterman, H.J. Deelstra, L. Ortiz-Castellanos, W. Li, P. Sanchez-Alonso, P.H. Schreier, I. Häuser-Hahn, M. Vaupel, E. Koopmann, G. Friedrich, H. Voss, T. Schlüter, J. Margolis, D. Platt, C. Swimmer, A. Gnirke, F. Chen, V. Vysotskaia, G. Mannhaupt, U. Güldener, M. Münsterkötter, D. Haase, M. Oesterheld, H.W. Mewes, E.W. Mauceli, D. DeCaprio, C.M. Wade, J. Butler, S. Young, D.B. Jaffe, S. Calvo, C. Nusbaum, J. Galagan and B.W. Birren. 2006. Insights from the genome of the biotrophic fungal plant pathogen *Ustilago maydis*. Nature 444, 97–101.

Kamzolova, S.V., T.V. Finogenova, IuN. Lunina, O.A. Perevoznikova, L.N. Minachova and I.G. Morgunov. 2007. Synthesis citric and isocitric acids by *Yarrowia lipolytica* during yeasts growth on rapeseed oils. Mikrobiologiia 76, 26–31.

Kaneko, T., K. Ishii, H. Kawaharada, K. Kagotani, Y. Shimada and K. Watanabe. 1977. Taxonomic studies of a hydrocarbon-assimilating *Candida* strain. Agric. Biol. Chem. 41, 2269–2275.

Kaneko, T., K. Makimura, M. Onozaki, K. Ueda, Y. Yamada, Y. Nishiyama and H. Yamaguchi. 2005. Vital growth factors of *Malassezia* species on modified CHROMagar *Candida*. Med. Mycol. 43, 699–704.

Kaneko, T., K. Makimura, T. Sugita and H. Yamaguchi. 2006. Tween 40-based precipitate production observed on chromogenic agar and development of biological identification kit for *Malassezia* species. Med. Mycol. 44, 227–231.

Kaneko, Y., and I. Banno. 1991. Reexamination of *Saccharomyces bayanus* by DNA–DNA hybridization and electrophoretic karyotyping. IFO Res. Commun. 15, 30–41.

Kaneko, Y., M. Kozaburo and I. Banno. 1989. Karyotyping of *Saccharomyces exiguus* by pulsed field gel electrophoresis. Inst. Ferment. Osaka Res. Commun. 14, 111–117.

Kaneshiro, E.S. 1998a. *Pneumocystis carinii* pneumonia: the status of *Pneumocystis* biochemistry. Int. J. Parasitol. 28, 65–84.

Kaneshiro, E.S. 1998b. The lipids of *Pneumocystis carinii*. Clin. Microbiol. Rev. 11, 27–41.

Kaneshiro, E.S. 2004. Sterol metabolism in the opportunistic pathogen *Pneumocystis*: advances and new insights. Lipids 39, 753–761.

Kaneshiro, E.S., and R.G. Sleight. 1994. Biochemistry and metabolism. In: P.D. Walzer (Ed.), *Pneumocystis carinii* Pneumonia. Marcel-Dekker, New York, pp. 45–71.

Kaneshiro, E.S., J.E. Ellis, K. Jayasimhulu and D.H. Beach. 1994. Evidence for the presence of "metabolic sterols" in *Pneumocystis*: identification and initial characterization of *Pneumocystis carinii* sterols. J. Eukaryot. Microbiol. 41, 78–85.

Kaneshiro, E.S., Z. Amit, J. Chandra, R.P. Baughman, C. Contini and B. Lundgren. 1999. Sterols of *Pneumocystis carinii* hominis organisms isolated from human lungs. Clin. Diagn. Lab. Immunol. 6, 970–976.

Kaneshiro, E.S., M.S. Collins and M.T. Cushion. 2000. Inhibitors of sterol biosynthesis and amphotericin B reduce the viability of *Pneumocystis carinii* f. sp. *carinii*. Antimicrob. Agents Chemother. 44, 1630–1638.

Kaneshiro, E.S., J.A. Rosenfeld, M. Basselin, S. Bradshaw, J.R. Stringer, A.G. Smulian and J.L. Giner. 2001. *Pneumocystis carinii* erg6 gene: sequencing and expression of recombinant SAM:sterol methyltransferase in heterologous systems. J. Eukaryot. Microbiol. (Suppl.) 144S–146S.

Kanetsuna, F., and L.M. Carbonell. 1970. Cell wall glucans of the yeast and mycelial forms of *Paracoccidioides brasiliensis*. J. Bacteriol. 101, 675–680.

Kanetsuna, F., and L.M. Carbonell. 1971. Cell wall composition of the yeastlike and mycelial forms of *Blastomyces dermatitidis*. J. Bacteriol. 106, 946–948.

Kanetsuna, F., L.M. Carbonell, R.E. Moreno and J. Rodriguez. 1969. Cell wall composition of the yeast and mycelial forms of *Paracoccidioides brasiliensis*. J. Bacteriol. 97, 1036–1041.

Kanetsuna, F., L.M. Carbonell, I. Azuma and Y. Yamamura. 1972. Biochemical studies thermal dimorphism of *Paracoccidioides brasiliensis*. J. Bacteriol. 110, 208–218.

Kanetsuna, F., L.M. Carbonell, F. Gil and I. Azuma. 1974. Chemical and ultrastructural studies on the cell walls of the yeastlike and mycelial forms of *Histoplasma capsulatum*. Mycopathol. Mycol. Appl. 54, 1–13.

Kang, H.-K., S.-H. Kim, J.-Y. Park, X.-J. Jin, D.-K. Oh, S.-S. Kang and D. Kim. 2005. Cloning and characterization of a dextranase gene from *Lipomyces starkeyi* and its expression in *Saccharomyces cerevisiae*. Yeast 22, 1239–1248.

Kang, H.-K., J.-Y. Park, J.-S. Ahn, S.-H. Kim and D. Kim. 2009. Cloning of a gene encoding dextranase from *Lipomyces starkeyi* and its expression in *Pichia pastoris*. J. Microbiol. Biotechnol. 19, 172–177.

Kang, N.-Y., J.-N. Park, J.-E. Chin, H.-B. Lee, S.-Y. Im. 2003. Construction of amylolytic industrial strain of *Saccharomyces cerevisiae* containing the *Schwanniomyces occidentalis* alpha-amylase gene. Biotechnol. Lett. 25, 1847–1851.

Kano, R., S. Hosaka and A. Hasegawa. 2004. First isolation of *Cryptococcus magnus* from a cat. Mycopathologia 157, 263–264.

Kantarcioglu, A.S., T. Boekhout, G.S. de Hoog, B. Theelen, A. Yucel, T.R. Ekmekci, B.C. Fries, R. Ikeda, A. Koslu and K. Altas. 2007. Subcutaneous cryptococcosis due to *Cryptococcus diffluens* in a patient with sporotrichoid

lesions: case report, features of the case isolate and *in vitro* antifungal susceptibilities. Med. Mycol. 45, 173–181.

Kanter, U., B. Usadel, F. Guerineau, Y. Li, M. Pauly and R. Tenhaken. 2005. The inositol oxygenase gene family of *Arabidiopsis* is involved in the biosynthesis of nucleotide sugar precursors for cell-wall matrix polysaccharides. Planta 221, 243–254.

Kaplan, L., and A.L. Demain. 1970. Nutritional studies on riboflavin overproduction by *Ashbya gossypii*. In: D.G. Ahearn (Ed.), Recent Trends in Yeast Research, Spectrum Monograph Series. Georgia State University, Atlanta, GA, USA, pp. 137–159.

Kapteyn, J.C., A.F. Ram, E.M. Groos, R. Kollar, R.C. Montijn, H. van Den Ende, A. Llobell, E. Cabib and F.M. Klis. 1997. Altered extent of cross-linking of beta1,6-glucosylated mannoproteins to chitin in *Saccharomyces cerevisiae* mutants with reduced cell wall beta1,3-glucan content. J. Bacteriol. 179, 6279–6284.

Kapteyn, J.C., P. van Egmond, E. Sievi, H. van den Ende, M. Makarow and F.M. Klis. 1999. The contribution of the O-glycosylated protein Pir2p/Hsp150 to the construction of the yeast cell wall in wild-type cells and b1,6-glucan-deficient mutants. Mol. Microbiol. 31, 1835–1844.

Kapteyn, J.C., L.L. Hoyer, J.E. Hecht, W.H. Muller, A. Andel, A.J. Verkleij, M. Makarow, H. van Den Ende and F.M. Klis. 2000. The cell wall architecture of *Candida albicans* wild-type cells and cell wall-defective mutants. Mol. Microbiol. 35, 601–611.

Karabulut, O.A., L. Cohen, B. Wiess, A. Daus, S. Lurie and S. Droby. 2002. Control of brown rot and blue mold of peach and nectarine by short hot water brushing and yeast antagonist. Postharvest Biol. Technol. 24, 103–111.

Karabulut, O.A., J.L. Smilanick, F.M. Gabler, M. Mansour and S. Droby. 2003. Near-harvest application of *Metschnikowia fructicola*, ethanol, and sodium bicarbonate to control-postharvest diseases of grape in central California. Plant Dis. 87, 1384–1389.

Karabulut, O.A., H. Tezcan, A. Daus, L. Cohen, B. Wiess and S. Droby. 2004. Control of preharvest and postharvest fruit rot in strawberry by *Metschnikowia fructicola*. Biocontrol Sci. Technol. 14, 513–521.

Karamboloff, N., and G. Krumbholz. 1931. Untersuchungen über osmophile Sprosspilze. IV *Zygosaccharomyces gracilis* sp. n. Arch. Mikrobiol. 3, 113–121.

Karatygin, I.V. 2003. Order Taphrinales: position in the class Taphrinomycetes and species identification key for the genus *Taphrina*. Mykol. Fitopatol. 37, 26–36. In Russian.

Karhumaa, K., R. Formanger, B. Hahn-Hagerdal and M.F. Gorwa-Grauslund. 2007. High activity of xylose reductase and xylitol dehydrogenase improves xylose fermentation by recombinant *Saccharomyces cerevisiae*. Appl. Microbiol. Biotechnol. 73, 1039–1046.

Karos, M., Y.C. Chang, C.M. McClelland, D.L. Clark, J. Fu, B.L. Wickes and K.J. Kwon-Chung. 2000. Mapping of the *Cryptococcus neoformans* MATalpha locus: presence of mating type-specific mitogen-activated protein kinase cascade homologs. J. Bacteriol. 182, 6222–6227.

Karube, I., S. Suzuki, T. Okada and M. Hikuma. 1980. Microbial sensors for volatile compounds. Biochimie 62, 567–573.

Kassur, S.B., A. Dobrzanska and T.K. Rowecka. 1998. Diagnostyka zarazenia grzybem *Pneumocystis carinii* specific form *hominis* (*Pneumocystis hominis*). Nowa Pediatria 2, 46–48.

Kastner, J.R., W.J. Jones and R.S. Roberts. 1999. Oxygen starvation induces cell death in *Candida shehatae* fermentations of D-xylose, but not D-glucose. Appl. Microbiol. Biotechnol. 51, 780–785.

Kataoka, M., M. Sasaki, A.R. Hidalgo, M. Nakano and S. Shimizu. 2001. Glycolic acid production using ethylene glycol-oxidizing microorganisms. Biosci. Biotechnol. Biochem. 65, 2265–2270.

Kato, K., Y. Kurimura, N. Makiguchi and Y. Asai. 1974. Determination of strongly methanol assimilating yeasts. J. Gen. Appl. Microbiol. 20, 123–127.

Kato, M., H. Iefuji, K. Miyake and Y. Iimura. 1997. Transformation system for a wastewater treatment yeast, *Hansenula fabianii* J640: isolation of the orotidine 5′phosphate decarboxylase gene (URA3) and uracil auxotrophic mutants. Appl. Microbiol. Biotechnol. 48, 621–625.

Kato, M., M. Ozeki, A. Kikuchi and T. Kanbe. 2001. Phylogenetic relationship and mode of evolution of yeast DNA topoisomerase II gene in the pathogenic *Candida* species. Gene 272, 275–281.

Kato, S., A. Shimizu-Ibuka, K. Mura, A. Takeuchi, C. Tokue and S. Arai. 2007. Molecular cloning and characterization of an alpha-amylase from *Pichia burtonii* 151. Biosci. Biotechnol. Biochem. 71, 3007–3013.

Katoh, K., K. Misawa, K. Kuma and T. Miyata. 2002. MAFFT: a novel method for rapid multiple sequence alignment based on fast Fourier transform. Nucl. Acids Res. 30, 3059–3066.

Katoh, K., K. Kuma, H. Toh and T. Miyata. 2005. MAFFT version 5: improvement in accuracy of multiple sequence alignment. Nucl. Acids Res. 33, 511–518.

Katz, S.H., and M.M. Voight. 1989. Bread and beer. Expedition 28, 23–24.

Kauffman, C.A. 2006a. Atlas of Fungal Infections, 2nd edn. Current Medicine, Philadelphia, PA.

Kauffman, C.A. 2006b. Endemic mycoses: blastomycosis, histoplasmosis, and sporotrichosis. Infect. Dis. Clin. North Am. 20, 645–662.

Kaur, N., and A.K. Gupta. 2002. Applications of inulin and oligofructose in health and nutrition. J. Biosci. 27, 703–714.

Kaur, P., G. Kunze and T. Satyanarayana. 2007. Yeast phytases: present scenario and future perspectives. Crit. Rev. Biotechnol. 27, 93–109.

Kaur, R., R. Domergue, M.L. Zupancic and B.P. Cormack. 2005. A yeast by any other name: *Candida glabrata* and its interaction with the host. Curr. Opin. Microbiol. 8, 378–384.

Kaur, R., A. Wadhwa and S.K. Agarwal. 2007. *Rhodotorula mucilaginosa*: an unusual cause of oral ulcers in HIV-infected patients. AIDS 21, 1068–1069.

Kavanagh, K.L., M. Klimacek, B. Nidetzky and D.K. Wilson. 2003. Structure of xylose reductase bound to NAD+ and the basis for single and dual co-substrate specificity in family 2 aldo-keto reductases. Biochem. J. 373, 319–326.

Kavanaugh, L.A., J.A. Fraser and F.S. Dietrich. 2006. Recent evolution of the human pathogen *Cryptococcus neoformans* by intervarietal transfer of a 14-gene fragment. Mol. Biol. Evol. 23, 1879–1890.

Kawaguchi, Y., H. Honda, J. Taniguchi-Morimura and S. Iwasaki. 1989. The codon CUG is read as serine in an asporogenic yeast *Candida cylindracea*. Nature 341, 164–166.

Kawai, F., D. Zhang and V. Sugimoto. 2000. Isolation and characterization of acid- and Al-tolerant microorganisms. FEMS Microbiol. Lett. 15, 143–147.

Kawakami, N. 1958. Electron-microscopy of fungi (V). The morphological study of the spore of non-pellicle group in the genus *Debaryomyces* and the classification of the genus *Debaryomyces*. Electron Microsc. 7, 235–237.

Kawakami, N., and T. Nehira. 1958. Electron microscopy of fungi. IV. The morphological study of the spore of pellicle group in the genus *Debaryomyces*. Electron Microsc. 7, 33–35.

Kawakami, N., T. Nehira and K. Kodama. 1961. Electron microscopy of fungi. X. Spore forms of the genus *Pichia*. Mem. Fac. Eng. Hiroshima Univ. 1, 407–414.

Kawamukai, M. 2002. Biosynthesis, bioproduction and novel roles of ubiquinone. J. Biosci. Bioeng. 94, 511–517.

Kawano, S., M. Horikawa, Y. Yasohara and J. Hasegawa. 2003. Microbial enantioselective reduction of acetylpyridine derivatives. J. Biosci. Biotechnol. Biochem. 67, 809–814.

Kawano, T., H. Kojima, H. Ohosawa and K. Morinaga. 1976. Feed and method of aquianimals cultivation. US Patent 3939279.

Kaygusuz, I., L. Mulazimoglu, N. Cerikcioglu, A. Toprak, A. Oktay and V. Korten. 2003. An unusual native tricuspid valve endocarditis caused by *Candida colliculosa*. Clin. Microbiol. Infect. 9, 319–322.

Kayser, E. 1892. Contribution à l'étude des levures de vin. Ann. Inst. Pasteur 6, 569–583.

Kazlauskas, R.J., and U.T. Bornscheuer. 1998. Biotransformations with lipases. In: H.J. Rehm, G. Reed, A. Pühler, P.J.W. Stadler and D.R. Kelly (Eds), Biotechnology-Series, Vol. 8a. Wiley-VCH, Weinheim, pp. 37–191.

Kealy, J.T., L. Liu, D.V. Santi, M.C. Betlach and P.J. Barr. 1998. Production of a polyketide natural product in nonpolyketide producing prokaryotic and eukaryotic hosts. Proc. Natl. Acad. Sci. USA 95, 505–509.

Keddie, F.M. 1966. Electron microscopy of *Malassezia furfur* in tinea versicolor. Sabouraudia 5, 134–137.

Keely, S.P., and J.R. Stringer. 2005. Nomenclature and genetic variation of *Pneumocystis*. In: P.D. Walzer and M.T. Cushion (Eds), *Pneumocystis* Pneumonia. Marcel-Dekker, New York, pp. 39–60.

Keely, S.P., M.T. Cushion and J.R. Stringer. 1996. Stability of four genetic loci in *Pneumocystis carinii* sp. f. *carinii*. J. Eukaryot. Microbiol. 43, 49S.

Keely, S.P., J.M. Fischer, M.T. Cushion and J.R. Stringer. 2004. Phylogenetic identification of *Pneumocystis murina* sp. nov., a new species in laboratory mice. Microbiology 150, 1153–1165.

Keilin, D. 1920. On a new Saccharomycete *Monosporella unicuspidata* gen. n. nom., n. sp., parasitic in the body cavity of a dipterous larva (*Dasyhelea obscura* Winnertz). Parasitology 12, 83–91.

Keller, B., P. Scheibl, E. Bleckmann and M. Hoedemaker. 2000. Differentiation of yeasts in mastitis milk. Mycoses 43 (Suppl. 1), 17–19.

Kellis, M., N. Patterson, M. Endrizzi, B. Birren and E.S. Lander. 2003. Sequencing and comparison of yeast species to identify genes and regulatory elements. Nature 423, 241–254.

Kellis, M., B.W. Birren and E.S. Lander. 2004. Proof and evolutionary analysis of ancient genome duplication in the yeast *Saccharomyces cerevisiae*. Nature 428, 617–624.

Kern, A., E. Tilley, I.S. Hunter, M. Ligisa and A. Glieder. 2007. Engineering metabolic pathways of industrial microorganisms. J. Biotechnol. 129, 6–29.

Kern, H., and S. Naef-Roth. 1975. Zur bildung von Auxinen und Cytokininen durch Taphrina-arten. Phytopathol. Z. 83, 193–222.

Kerrigan, J., M.Th. Smith, J.D. Rogers and G.A. Poot. 2001. *Ascobotryozyma americana* gen. nov. et sp. nov. and its anamorph *Botryozyma americana*, an unusual yeast from the surface of nematodes. Antonie van Leeuwenhoek 79, 716.

Kerrigan, J., M.Th. Smith, J.D. Rogers, G.A. Poot and G.W. Douhan. 2003. *Ascobotryozyma cognata* sp. nov, a new ascomycetous yeast associated with nematodes in wood-boring beetle galleries. Mycol. Res. 107, 1110–1120.

Kerrigan, J., M.Th. Smith, J.D. Rogers and G.A. Poot. 2004. *Botryozyma mucatilis* sp. nov., an anamorphic ascomycetous yeast associated with nematodes in poplar slime flux. FEMS Yeast Res. 4, 849–856.

Kerscher, S., G. Durstewitz, S. Casaregola, C. Gaillardin and U. Brandt. 2001. The complete mitochondrial genome of *Yarrowia lipolytica*. Comp. Funct. Genomics 2, 80–90.

Kessler, E. 1982. Physiological and biochemical contributions to the taxonomy of the genus *Prototheca*. III. Utilization of organic carbon and nitrogen compounds. Arch. Microbiol. 132, 103–106.

Kessler, E. 1992. *Chlorella*. Biochemisch Taxonomie einer fur Forschung und Biotechnologie wichtigen Gattung einzelliger Grunalgen. Naturwissenschaften 79, 260–265.

Keszthelyi, A., M. Ohkusu, K. Takeo, I. Pfeiffer, J. Litter and J. Kuscera. 2006. Characterization of the anticryptococcal effect of the FC-1 toxin produced by *Filobasidium capsuligenum*. Mycoses 49, 176–183.

Khachigian, L.M., and C.R. Parish. 2006. Phosphomannopentaose sulfate (PI-88): heparan sulfate mimetic with clinical potential in multiple vascular pathologies. Cardiovasc. Drug Rev. 22, 1–6.

Khale, A., and M.V. Deshpande. 1992. Dimorphism in *Benjaminiella poitrasii*: cell wall chemistry of parent and two stable yeast mutants. Antonie van Leeuwenhoek 62, 299–307.

Khan, N.I., D.A. Schisler, M.J. Boehm, P.J. Slininger and R.J. Bothast. 2001. Selection and evaluation of microorganisms for biocontrol of fusarium head blight of wheat incited by *Gibberella zeae*. Plant Dis. 85, 1253–1258.

Khan, N.I., D.A. Schisler, M.J. Boehm, P.E. Lipps and P.J. Slininger. 2004. Field testing of antagonists of fusarium head blight incited by *Gibberella zeae*. Biol. Control 29, 245–255.

Khan, S.R. 1976. Ultrastructure of the septal pore apparatus of *Tremella*. J. Gen. Microbiol. 97, 339–342.

Khan, S.R., and J.W. Kimbrough. 1980. Septal ultrastructure in some genera of Tremellaceaea. Can. J. Bot. 58, 55–60.

Khan, S.R., J.W. Kimbrough and K.J. Kwon-Chung. 1981. Ultrastructure of *Filobasidiella arachnophila*. Can. J. Bot. 59, 893–897.

Khan, Z.U., S. Ahmad, F. Hagen, J.W. Fell, T. Kowshik, R. Chandy and T. Boekhout. 2010. *Cryptococcus randhawai* sp. nov., a novel anamorphic basidiomycetous yeast isolated from tree trunk hollow of *Ficus religiosa* (peepal tree) from New Delhi, India. Antonie van Leeuwenhoek 97, 253–259.

Khawcharoenporn, T., A. Apisarnthanarak and L.M. Mundy. 2007. Non-*neoformans* cryptococcal infections: a systematic review. Infection 35, 51–58.

Khlif, M., C. Mary, H. Sellami, A. Sellami, H. Dumon, A. Ayadi and S. Ranque. 2009. Evaluation of nested and real-time PCR assays in the diagnosis of Candidaemia. Clin. Microbiol. Infect. 15, 656–661.

Khouri, J. 1932. Sur une *Monilia* isolée des crachats d'un malade atteint de blastomycose pulmonaire: *Monilia aegyptiaca*. C.R. Mem. Soc. Biol. 111, 419–420.

Kidd, K.K., and L.A. Sgaramella-Zonta. 1971. Phylogenetic analysis: concepts and methods. Am. J. Hum. Genet. 23, 235–252.

Kidd, S.E., F. Hagen, R.L. Tscharke, M. Huynh, K.H. Bartlett, M. Fyfe, L. MacDougall, T. Boekhout, K.J. Kwon-Chung and W. Meyer. 2004. A rare genotype of *Cryptococcus gattii* caused the cryptococcosis outbreak on Vancouver Island (British Columbia, Canada). Proc. Natl. Acad. Sci. USA 101, 17258–17263.

Kidd, S.E., H. Guo, K.H. Bartlett, J. Xu and J.W. Kronstad. 2005. Comparative gene genealogies indicate that two clonal lineages of *Cryptococcus gattii* in British Columbia resemble strains from other geographical areas. Eukaryot. Cell 4, 1629–1638.

Kidd, S.E., P.J. Bach, A.O. Hingston, S. Mak, Y. Chow, L. MacDougall, J.W. Kronstad and K.H. Bartlett. 2007a. *Cryptococcus gattii* dispersal mechanisms, British Columbia, Canada. Emerg. Infect. Dis. 13, 51–57.

Kidd, S.E., Y. Chow, S. Mak, P.J. Bach, H. Chen, A.O. Hingston, J.W. Kronstad and K.H. Bartlett. 2007b. Characterization of environmental sources of the human and animal pathogen *Cryptococcus gattii* in British Columbia, Canada, and the Pacific Northwest of the United States. Appl. Environ. Microbiol. 73, 1433–1443.

Kiel, J.A., M. Veenhuis and I.J. van der Klei. 2006. PEX genes in fungal genomes: common, rare or redundant. Traffic 7, 1291–1303.

Kiesecker, J.M., D.K. Skelly, K.H. Beard and E. Preisser. 1999. Behavioral reduction of infection risk. Proc. Natl. Acad. Sci. USA 96, 9165–9168.

Kiesling, T., M.R. Diaz, A. Statzell-Tallman and J.W. Fell. 2002. Field identification of marine yeast using DNA hybridization macroarrays. In: K.D. Hyde, S.T. Moss and L.L.P. Vrijmoed (Eds), Fungi in Marine Environments. Fungal Diversity Press, Hong Kong, pp. 69–80.

Kiho, T., Y. Tsujimura, M. Sakashima, S. Usui and S. Ukai. 1994. Polysaccharides in fungi. XXXIII. Hypoglycemic activity of an acidic polysaccharide (AC) from *Tremella fuciformis*. Yakagaku Zasshi 114, 308–315.

Kiho, T., H. Morimoto, M. Sakashima, S. Usui and S. Ukai. 1995. Polysaccharides in fungi. XXXV. Anti-diabetic activity of an acidic polysaccharide from the fruiting bodies of *Tremella aurantia*. Biol. Pharm. Bull. 18, 1627–1629.

Kiho, T., H. Morimoto, T. Kobayashi, S. Usui, S. Ukai, K. Aizawa and T. Inakuma. 2000. Effect of a polysaccharide (TAP) from the fruiting bodies of *Tremella aurantia* on glucose metabolism in mouse liver. Biosci. Biotechnol. Biochem. 64, 417–419.

Kijima, K., and H. Suzuki. 2007. Improving the umami taste of soy sauce by the addition of bacterial gamma-glutamyltranspeptidase as a glutaminase to the fermentation mixture. Enzyme Microb. Technol. 41, 80–84.

Kiken, D.A., A. Sekaran, R.J. Antaya, A. Davis, S. Imaeda and N. B. Silverberg. 2006. White piedra in children. J. Am. Acad. Dermatol. 55, 956–961.

Kim, J.H., B.C. Campbell, N.E. Mahoney, K.L. Chan and R.J. Molyneux. 2004. Identification of phenolics for control of *Aspergillus flavus* using *Saccharomyces* in a model target-gene bioassay. J. Agric. Food Chem. 52, 7814–7821.

Kim, J.W., YS. Kim and K.H. Kyung. 2004. Inhibitory activity of essential oils of garlic and onion against bacteria and yeasts. J. Food Prot. 67, 499–504.

Kim, K., D. Yoo, Y. Kim, B. Lee, D. Shin and E.K. Kim. 2002. Characteristics of sophorolipid as an antimicrobial agent. J. Microbiol. Biotechnol. 12, 235–241.

Kimbrough, J.W. 1994. Septal ultrastructure and ascomycete systematics. In: D.L. Hawksworth (Ed.), Ascomycete Systematics. Plenum Press, New York, pp. 127–141.

Kimura, M. 1980. A simple method for estimating evolutionary rate of base substitutions through comparative studies of nucleotide sequences. J. Mol. Evol. 16, 111–120.

Kimura, M. 1981. Estimation of evolutionary distances between homologous nucleotide sequences. Proc. Natl. Acad. Sci. USA 78, 454–458.

King, D.S., and S.-C. Jong. 1975. *Sarcinosporon*: a new genus to accommodate *Trichosporon inkin* and *Prototheca filamenta*. Mycotaxon 3, 89–94.

King, D.S., and S.-C. Jong. 1976. *Aciculoconidium*: a new hyphomycetous genus to accommodate *Trichosporon aculeatum*. Mycotaxon 3, 401–408.

King, D.S., and S.-C. Jong. 1977. A contribution to the genus *Trichosporon*. Mycotaxon 6, 391–417.

Kinkel, L.L., J.H. Andrews, F.M. Berbee and E.V. Nordheim. 1987. Leaves as islands for microbes. Oecologia 71, 405–408.

Kinkel, L.L., J.H. Andrews and E.V. Nordheim. 1989a. Fungal immigration dynamics and community development on apple leaves. Microb. Ecol. 18, 45–48.

Kinkel, L.L., J.H. Andrews and E.V. Nordheim. 1989b. Microbial introductions to apple leaves: influences of altered immigration on fungal community dynamics. Microb. Ecol. 18, 161–173.

Kircher, H.W. 1982. Chemical composition of cacti and its relationship to Sonoran Desert *Drosophila*. In: J.S.F. Barker and W.T. Starmer (Eds), Ecological Genetics and Evolution: The Cactus–*Drosophila* Model System. Academic Press, Australia, Sydney, pp. 143–158.

Kirk, B.T., and J.B. Sinclair. 1966. Plasmodesmata between hyphal cells of *Geotrichum candidum*. Science 153, 16–46.

Kirk, O., and M.W. Christensen. 2002. Lipases from *Candida antarctica*: unique biocatalysts from a unique origin. Org. Process Res. Dev. 6, 446–451.

Kirk, O., T.V. Borchert and C.C. Fugisang. 2002. Industrial enzyme applications. Curr. Opin. Biotechnol. 13, 345–351.

Kirk, P.M., P.F. Cannon, J.C. David and J.A. Stalpers. 2001. Ainsworth & Bisby's Dictionary of the Fungi, 9th edn. CAB, Egham.

Kirk, P.M., P.F. Cannon, D.W. Minter and J.A. Stalpers. 2008. Ainsworth & Bisby's Dictionary of the Fungi, 10th edn. CAB International, Wallingford.

Kirschner, R., and F. Oberwinkler. 2000. A new species of *Colacogloea* with zygoconidia. Sydowia 52, 195–203.

Kirschner, R., J.P. Sampaio, M. Gadanho, M. Weiβ and F. Oberwinkler. 2001a. *Cuniculitrema polymorpha* (Tremellales, gen. nov. and sp. nov.), a heterobasidiomycete vectored by bark beetles, which is the teleomorph of *Sterigmatosporidium polymorphum*. Antonie van Leeuwenhoek 80, 149–161.

Kirschner, R., D. Begerow and F. Oberwinkler. 2001b. A new *Chionosphaera* species associated with conifer inhabiting bark beetles. Mycol. Res. 105, 1404–1405.

Kirschner, R., J.P. Sampaio, D. Begerow, Z.-C. Chen and F. Oberwinkler. 2003. *Mycogloea nippon*ica – the first known teleomorph in the heterobasidiomycetous yeast genus *Kurtzmanomyces*. Antonie van Leeuwenhoek 84, 109–114.

Kirsop, B.E. and C.P. Kurtzman (Eds). 1988. Living Resources for Biotechnology. Yeasts. Cambridge University Press, Cambridge, 234pp.

Kitamoto, D., S. Akiba, C. Hioki and T. Tabuchi. 1990a. Extracellular accumulation of mannosylerythritol lipids by a strain of *Candida antarctica*. Agric. Biol. Chem. 54, 31–36.

Kitamoto, D., K. Haneishi, T. Nakahara and I. Tabuchi. 1990b. Production of mannosylerythritol lipids by *Candida antarctica* from vegetable oils. Agric. Biol. Chem. 54, 37–40.

Klassen, R., and F. Meinhardt. 2002. Linear plasmids pWR1A and pWR1B of the yeast *Wingea robertsiae* are associated with a killer phenotype. Plasmid 48, 142–148.

Klassen, R., and F. Meinhardt. 2003. Structural and functional analysis of the killer element pPin1-3 from *Pichia inositovora*. Mol. Genet. Genomics 290, 190–199.

Klassen, R., L. Tontsidou, M. Larsen and F. Meinhardt. 2001. Genome organization of the linear cytoplasmic element pPEIB from *Pichia etchellsii*. Yeast 18, 953–961.

Klassen, R., D. Jablonowski, M.J.R. Stark, R. Schaffrath and F. Meinhardt. 2006. Mating-type locus control of killer toxins from *Kluyveromyces lactis* and *Pichia acaciae*. FEMS Yeast Res. 6, 404–413.

Klecan, A.L., S. Hippe and S.C. Somerville. 1990. Reduced growth of *Erysiphe graminis* f. sp. *hordei* induced by *Tilletiopsis pallescens*. Phytopathology 80, 325–331.

Klein, R.D., and M.A. Favreau. 1995. The *Candida* species: biochemistry, molecular biology, and industrial applications. In: Y.H. Hui and G.G. Khachatourians (Eds), Food Biotechnology. Microorganisms. VCH Publishers, New York, pp. 297–371.

Kleinkauf, H., and H. von Döhren. 1997. Products of secondary metabolism. In: H.-J. Rehm and G. Reed (Eds), Biotechnology, 2nd, completely revised edn Vol. 7. VCH-Wiley, Weinheim.

Kleyn, J.G. 1954. A study of some environmental factors controlling sporulation of yeast using a new sporulation medium. Wallerstein Lab. Commun. 17, 91–104.

Klibanov, A.M. 2001. Improving enzymes by using them in organic solvents. Nature 409, 241–246.

Klimpel, K.R., and W.E. Goldman. 1988. Cell walls from avirulent variants of *Histoplasma capsulatum* lack α-(1,3)-glucan. Infect. Immun. 56, 2997–3000.

Klingenberg, A., and E. Sprecher. 1985. Production of monoterpenes in liquid cultures by the yeast *Ambrosiozyma monospora*. Planta Med. 51, 264–265.

Klingspor, L., and S. Jalal. 2006. Molecular detection and identification of *Candida* and *Aspergillus* spp. from clinical samples using real-time PCR. Clin. Microbiol. Infect. 12, 745–753.

Klis, F.M., A. Boorsma and P.W. de Groot. 2006. Cell wall construction in *Saccharomyces cerevisiae*. Yeast 23, 185–202.

Klis, F.M., M. de Jong, S. Brul and P.W. de Groot. 2007. Extraction of cell surface-asociated proteins from living yeast cells. Yeast 24, 253–258.

Klöcker, A. 1902. Eine neue *Saccharomyces* art (*Saccharomyces saturnus mihi*) mit eigentümlichen Sporen. Zentralbl. Bakteriol. Parasitenkd., Abt. II, 8, 129–130.

Klöcker, A. 1924. Die Gärungsorganismen in der Theorie und Praxis der Alkoholgärungsgewerbe, 3te Aufl. Urban & Schwarzenberg, Berlin.

Klöcker, A. 1909a. Deux nouveaux genres de la famille des Saccharomycètes. C.R. Trav. Lab. Carlsberg 7, 273–278.

Klöcker, A. 1909b. *Endomyces javanensis* nov. sp. C.R. Trav. Lab. Carlsberg 7, 267–272.

Klöcker, A. 1912a. Untersuchungen über einige neue *Pichia*-Arten. Zentralbl. Bakteriol. Parasitenkd., Abt. II, 35, 369–375.

Klöcker, A. 1912b. Beschreibungen von 17 *Saccharomyces apiculatus* Formen. Zentralbl. Bakteriol. Parasitenkd., Abt. II, 35, 375–388.

Kluge, A.G., and J.S. Farris. 1969. Quantitative phyletics and the evolution of anurans. Syst. Zool. 18, 1–32.

Kluyver, A.J. 1914. Biochemische suikerbepalingen. Thesis, Technische Hoogeschool Delft.

Kluyver, A.J., and C.B. van Niel. 1924. Über Spiegelbilder erzeugende Hefenarten und die neue Hefengattung *Sporobolomyces*. Zentralbl. Bakteriol. Parasitenkd., Abt. II, 63, 1–20.

Kluyver, A.J., and C.B. van Niel. 1927a. A comparative study of the cell wall structure of basidiomycetous and related yeasts. J. Gen. Microbiol. 68, 87–95.

Kluyver, A.J., and C.B. van Niel. 1927b. *Sporobolomyces*: ein Basidiomyzet? Ann. Mycol. 25, 389–394.

Knauf, U., and W. Hachtel. 2002. The genes encoding subunits of ATP synthase are conserved in the reduced plastid genome of the heterotrophic alga *Prototheca wickerhamii*. Mol. Genet. Genomics 267, 492–497.

Knutsen, A.K., V. Robert, G.A. Poot, W. Epping, M. Figge, A. Holst-Jensen, I. Skaar and M.Th. Smith. 2007. Polyphasic re-examination of *Yarrowia lipolytica* strains and the description of three novel *Candida* species: *Candida oslonensis* sp. nov., *Candida alimentaria* sp. nov. and *Candida hollandica* sp. nov. Int. J. Syst. Evol. Microbiol. 57, 2426–2435.

Kobayashi, H., N. Shibata, T. Yonezu and S. Suzuki. 1987. Structural study of phosphor–mannan–protein complex of *Citeromyces matritensis* containing beta-1,-2 linkage. Application of partial acid degradation and acetolysis techniques under mild conditions. Arch. Biochem. Biophys. 256, 381–396.

Kobayashi, T. 1953. Studies on the yeasts and yeast-like fungi which grow well on wood hydrolysate medium. Rep. Wood Saccharification Discussion Committee 2, 1–93.

Kobayasi, Y. 1937. On the genus *Holtermannia* of Tremellaceae. Sci. Rep. Tokyo Bunr. Daig. B 3, 75–81.

Kobayasi, Y. 1939. The genus *Tremella* and its allies from Japan (Fungorum Ordinis Tremellales, Studia Monographica II). Sci. Rep. Tokyo Bunr. Daig. 4, 1–26.

Kobayasi, Y. 1962. Revision of *Sirobasidium* with description of a new species found in Japan. Trans. Mycol. Soc. Jpn 4, 29–34.

Kobayasi, Y., and K. Tubaki. 1965. Studies on cultural characters and asexual reproduction of Heterobasidiomycetes. Trans. Mycol. Soc. Jpn 6, 29–36.

Kock, J.L.F., and J.P. van der Walt. 1986. Fatty acid composition of *Schizosaccharomyces* Lindner. Syst. Appl. Microbiol. 8, 163–165.

Kock, J.L.F., and A. Botha. 1998. Fatty acids in fungal taxonomy. In: J.C. Frisvad, P.D. Bridge and D.K. Arora (Eds), Chemical Fungal Taxonomy. Academic Press, London, pp. 219–246.

Kock, J.L.F., S.C. Erasmus and P.M. Lategan. 1986. A rapid method to identify some species of the Dipodascaceae and Endomycetaceae. J. Microbiol. Methods 5, 199–203.

Kock, J.L.F., D.J. Coetzee, M.S. van Dijk, M. Truscott, A. Botha and P.H. Ockert. 1992. Evidence for, and taxonomic value of, an arachidonic acid cascade in the Lipomycetaceae. Antonie van Leeuwenhoek 62, 251–259.

Kock, J.L.F., J.P. van der Walt and Y. Yamada. 1995. *Smithiozyma* gen. nov. (Lipomycetaceae). S. Afr. J. Bot. 61, 232–233.

Kock, J.L.F., P. Venter, D. Linke, T. Schewe and S. Nigam. 1998. Biological dynamics and distribution of 3-hydroxy fatty acids in the yeast *Dipodascopsis uninucleata* as investigated by immunofluorescence microscopy. Evidence for putative regulatory role in the sexual reproductive cycle. FEBS Lett. 427, 345–348.

Kock, J.L.F., P.W.J. van Wyk, P. Venter, D.J. Coetzee, D.P. Smith, B.C. Viljoen and S. Nigam. 1999. An acetylsalicylic acid-sensitive aggregation phenomenon in *Dipodascopsis uninucleata*. Antonie van Leeuwenhoek 75, 261–266.

Kock, J.L.F., P. Venter, D.P. Smith, P.W.J. van Wyk, P.J. Botes, D. J. Coetzee, C.H. Pohl, A. Botha, K.-H. Riedel and S. Nigam. 2000. A novel oxylipin-associated "ghosting" phenomenon in yeast flocculation. Antonie van Leeuwenhoek 77, 401–406.

Kock, J.L.F., C.J. Strauss, C.H. Pohl and S. Nigam. 2003. The distribution of 3-OH oxylipins in fungi. Prostaglandins Other Lipid Mediat. 71, 85–96.

Kock, J.L.F., C.J. Strauss, E.E. Pretorius, C.H. Pohl, A.S. Bareetseng, P.J. Botes, P.W.J. van Wyk, S.W. Schoombie and S. Nigam. 2004. Revealing yeast spore movement in confined space. S. Afr. J. Sci. 100, 237–241.

Kocková-Kratochvílová, A., and M. Havelkova. 1974. *Prototheca hydrocarbonea* n. sp. Lebenszyklus, Metabolismus, und Feinstruktur. Z. Allgem. Mikrobiol. 14, 123–134.

Kocková-Kratochvílová, A., and D. Ondrušová. 1971. *Torulopsis*arten aus den Oberflachen höherer Pilze. *Torulopsis kruisii* n. sp. und *Torulopsis schatavii* n. sp. Biologia (Bratislava) 26, 477–485.

Kocková-Kratochvílová, A., and E. Sláviková. 1988. *Candida mucifera* n. sp. J. Basic Microbiol. 28, 613–618.

Kocková-Kratochvílová, A., and Y. Svobodová-Poláková. 1959. *Nadsonia slovaca* n. sp. isolated in Slovakia. J. Gen. Microbiol. 20, 24–26.

Kocková-Kratochvílová, A., E. Sláviková and J. Beránek. 1977a. *Torulopsis armenti* n. sp. Z. Allg. Mikrobiol. 17, 429–431.

Kocková-Kratochvílová, A., E. Sláviková, J. Zemek and L. Kuniak. 1977b. The heterogeneity of the genus *Trichosporon*. Proc. 5th Int. Spec. Symposium Yeasts, p. 9.

Kocková-Kratochvílová, A., M. Simordová and S. Sternbersky. 1987. *Moniliella suaveolens* var. *nigra.* Mykosen 30, 544–547.

Kodama, K. 1974. Ascosporogenous yeasts isolated from tree exudates in Japan. Ann. Microbiol. Milano 24, 215–231.

Kodama, K. 1975. New species of *Pichia* isolated from tree exudates in Japan. J. Ferment. Technol. 53, 626–630.

Kodama, K., and T. Kyono. 1974a. Ascosporogenous yeasts isolated from tree exudates in Japan. J. Ferment. Technol. 52, 1–9.

Kodama, K., and T. Kyono. 1974b. Ascosporogenous yeasts isolated from tree exudates in Japan (continued). J. Ferment. Technol. 52, 605–613.

Kodama, K., T. Kyono and S. Kodama. 1955. A study of film-forming yeasts (II). Genus *Pichia* (2). J. Ferment. Technol. 33, 317–324.

Kodama, K., T. Kyono and S. Kodama. 1957. Studies on the film yeasts (XIII). *Hansenula* (7). J. Ferment. Technol. 35, 328–331. In Japanese.

Kodama, K., T. Kyono and S. Kodama. 1962. Taxonomic study on the genus *Pichia* Hansen (2). J. Gen. Appl. Microbiol. 8, 52–55.

Kodama, K., T. Kyono, K. Iida and N. Onoyama. 1964a. Studies on wild yeasts which thrive in "sake-moto". J. Ferment. Technol. 42, 739–745.

Kodama, K., T. Kyono, H. Naganishi and Y. Takahara. 1964b. *Debaryomyces franciscae* (Capriotti) nov. comb. J. Ferment. Technol. 42, 1–6.

Kodama, K., T. Kyono, H. Naganishi and Y. Takahara. 1964c. Taxonomic studies on the genus *Debaryomyces*. (IV) *Debaryomyces nilssoni* (Capriotti) nov. comb. J. Ferment. Technol. 42, 655–660.

Kodama, K., H. Iino and M. Kozaki. 1978. Serological relationships of ascomycetous yeasts. Hakkokogaku 56, 701–707. In Japanese.

Koeller, K.M., and C.-H. Wong. 2001. Enzymes for chemical synthesis. Nature 409, 232–240.

Koenig, D.W., and D.F. Day. 1989. Induction of *Lipomyces starkeyi* dextranase. Appl. Environ. Microbiol. 55, 2079–2081.

Köhler, G., and C. Mistein. 1975. Continuous culture of fused cells secreting antibody of predefined specificity. Nature 256, 487–495.

Kohlwein, S.D. 2000. The beauty of the yeast: live cell microscopy at the limits of optical resolution. Microsc. Res. Tech. 51, 511–529.

Kolfschoten, G.A., and D. Yarrow. 1970. *Brettanomyces naardenensis*, a new yeast from soft drinks. Antonie van Leeuwenhoek 36, 458–460.

Kollar, R., E. Petrakova, G. Ashwell, P.W. Robbins and E. Cabib. 1995. Architecture of the yeast cell wall. The linkage between chitin and β(1→3)-glucan. J. Biol. Chem. 270, 1170–1178.

Kollar, R., B.B. Reinhold, E. Petrakova, H.J. Yeh, G. Ashwell, J. Drgonova, J.C. Kapteyn, F.M. Klis and E. Cabib. 1997. Architecture of the yeast cell wall. β(1→6)-glucan

interconnects mannoprotein, β(1→)3-glucan, and chitin. J. Biol. Chem. 272, 17762–17775.
Kolombet, L.V., A.A. Starshov and D. Schisler. 2005. Biological efficiency *Trichoderma asperellum* GJS 03-35 and yeast *Cryptococcus nadoensis* OH 182.9 as biocontrol agents against fusarium head blight of wheat. Mikologiya I Fitopatologiya 39, 80–88.
Koltin, Y., and D.R. Day. 1975. Specificity of *Ustilago maydis* killer proteins. Appl. Microbiol. 30, 694–696.
Koltin, Y., and D.R. Day. 1976. Inheritance of killer phenotypes and double-stranded RNA in *Ustilago maydis*. Proc. Natl. Acad. Sci. USA 73, 594–598.
Komagata, K. 1992. Value of chemosystematic data for predicting anamorph–teleomorph relationships between the genera *Rhodotorula* and *Rhodosporidium*. FEMS Microbiol. Lett. 100, 503–508.
Komagata, K., and T. Nakase. 1965. New species of the genus *Candida* isolated from frozen foods. J. Gen. Appl. Microbiol. 11, 255–267.
Komagata, K., T. Nakase and N. Katsua. 1964a. Assimilation of hydrocarbons by yeasts. I. Preliminary screening. J. Gen. Appl. Microbiol. 10, 313–321.
Komagata, K., T. Nakase and N. Katsuya. 1964b. Assimilation of hydrocarbons by yeast. II. Determination of hydrocarbon–assimilating yeasts. J. Gen. Appl. Microbiol. 10, 323–331.
Komeda, T., H. Yurimoto, N. Kato, Y. Sakai and K. Kondo. 2003. Cis-acting elements sufficient for induction of FDH1 expression by formate in the methylotrophic yeast *Candida boidinii*. Mol. Gen. Genomics 270, 273–280.
Komiyama, T., T. Shirai, T. Ohta, H. Urakami, Y. Furuichi, Y. Ohta and Y. Tsukada. 1998. Action properties of HYI killer toxin from *Williopsis saturnus* var. *saturnus*, and antibiotics, aculeacin A and papulacandin B. Biol. Pharm. Bull. 21, 1013–1019.
Kondo, K., T. Saito, S. Kajiwara, M. Takagi and N. Misawa. 1995. A transformation system for the yeast *Candida utilis*: use of a modified endogenous ribosomal protein gene as a drug-resistant marker and ribosomal DNA as an integration target for vector DNA. J. Bacteriol. 177, 7171–7177.
Konishi, M., and T. Morita. 2008. Efficient production of mannosylerythritol lipids with high hydrophilicity by *Pseudozyma hubeiensis* KM-59. Appl. Microbiol. Biotechnol. 78, 37–46.
Kono, I., and K. Himeno. 1997. A novel killer yeast effective on *Schizosaccharomyces pombe*. Biosci. Biotechnol. Biochem. 61, 563–564.
Konokotina, A.G. 1913. Über die neuen Hefepilze mit heterogamer Kopulation – *Nadsonia* (*Guilliermondia*) *elongata* und *Debaryomyces tyrocola*. Bull. Jard. Imp. Bot. St. Pétersbourg. 13, 32–44. In Russian. (Rev. in: Zentralbl. Bakteriol. Parasitenkd., Abt. II, 40, 177).
Koopmans, A. 1977. A cytological study of *Nematospora coryli* Pegl. Genet. 47, 187–195.
Kopecká, M., G.H. Fleet and H.J. Phaff. 1995. Ultrastructure of the cell wall of *Schizosaccharomyces pombe* following treatment with various glucanases. J. Struct. Biol. 114, 140–152.
Kopecká, M., M. Gabriel, K. Takeo, M. Yamaguchi, A. Svoboda, M. Ohkusu, K. Hata and S. Yoshida. 2001. Microtubules and actin cytoskeleton in *Cryptococcus neoformans* compared with ascomycetous budding and fission yeasts. Eur. J. Cell Biol. 80, 303–311.
Korbel, J.O., B. Snel, M.A. Huynen and P. Bork. 2002. SHOT: a web server for the construction of genome phylogenies. Trends Genet. 18, 158–162.
Kordossis, T., A. Avlami, A. Velegraki, I. Stefanou, G. Georgakopoulos, C. Papalambrou and N.J. Legakis. 1998. First report of *Cryptococcus laurentii* meningitis and a fatal case of *Cryptococcus albidus* cryptococcaemia in AIDS patients. Med. Mycol. 36, 335–339.
Korf, R.P. 1957. *Dipodascus albidus* forma *minor*. Sydowia Beih 1, 285–288.
Kosíková, B., and E. Sláviková. 2004. Biotransformation of lignin polymers derived from beech wood pulping by *Sporobolomyces roseus* isolated from leafy material. Biotechnol. Lett. 26, 517–519.
Kossikov, K.V., and A.A. Medvedeva. 1977. Isolation of hybrids of *Schizosaccharomyces pombe* and *Octosporomyces japonicus*. Mikrobiologiia 46, 61–65.
Kostka, G. 1927. Über *Nadsonia richteri* nov. spec., eine interessante Schleimflusshefe aus Mähren. Verh. Naturforsch. Ver. Brunn 59, 14–22 (Rev. in: Wochenschr. Brau. 44, 128).
Kottom, T.J., and A.H. Limper. 1999. Assembly of cell wall glucans by *Pneumocystis carinii*: characterization of the Gsc-1 subunit mediating beta-glucan synthesis. J. Eukaryot. Microbiol. 46, 131S.
Kottom, T.J., and A.H. Limper. 2000. Cell wall assembly by *Pneumocystis carinii*. Evidence for a unique gsc-1 subunit mediating beta-1,3-glucan deposition. J. Biol. Chem. 275, 40628–40634.
Koufopanou, V., J. Hughes, G. Bell and A. Burt. 2006. The spatial scale of genetic differentiation in a model organism, the wild yeast *Saccharomyces paradoxus*. Philos. Trans. R. Soc. Lond. B. Biol. Sci. 361, 1941–1946.
Koul, S., J.L. Koul, B. Singh, M. Kapoor, R. Parshad, K.S. Manhas, S.C. Taneja and G.N. Qazi. 2005. *Trichosporon beigelli* esterase (TBE): a versatile esterase for the resolution of economically important racemates. Tetrahedron Asymmetry 16, 2575–2591.
Kraepelin, G., and U. Schulze. 1982. *Sterigmatosporidium* gen. n., a new heterothallic basidiomycetous yeast, the perfect state of a new species of *Sterigmatomyces* Fell. Antonie van Leeuwenhoek 48, 471–483.
Krajden, S., R.C. Summerbell, J. Kane, I.F. Salkin, M.E. Kemna, M.G. Rinaldi, M. Fuksa, E. Spratt, C. Rodrigues and J. Choe. 1991. Normally saprobic cryptococci isolated from *Cryptococcus neoformans* infections. J. Clin. Microbiol. 29, 1883–1887.
Krallish, I., S. Gonta, L. Savenkova, P. Bergauer and R. Margesin. 2006. Phenol degradation by immobilized cold-adapted yeast strains of *Cryptococcus terreus* and *Rhodotorula creatinivora*. Extremophiles 10, 441–449.
Kramer, C.L. 1959. A new genus in the Protomycetaceae. Mycologia 50, 916–926.
Kramer, C.L. 1960. Morphological development and nuclear behavior in the genus *Taphrina*. Mycologia 52, 295–320.
Kramer, C.L. 1973. Protomycetales and Taphrinales. In: G.C. Ainsworth, F.K. Sparrow and A.S. Sussman (Eds), The Fungi – An Advanced Treatise, Vol. IVA. Academic Press, New York, pp. 33–41.

Kramer, C.L. 1987. The Taphrinales. In: G.S. de Hoog, M.Th. Smith and A.C.M. Weijman (Eds), The Expanding Realm of Yeast-like Fungi. Elsevier, Amsterdam, pp. 151–166. (Stud. Mycol. 30, 151–166).

Kramer, H.-J., D. Kessler, U.-C. Hipler, B. Irlinger, W. Hort, R.-H. Bodeker, W. Steglich and P. Mayser. 2005a. Pityriarubins, novel highly selective inhibitors of respiratory burst from cultures of the yeast *Malassezia furfur*: comparison with the bisindolylmaleimide arcyriarubin A. Chembiochem 6, 2290–2297.

Kramer, H.-J., M. Podobinska, A. Bartsch, A. Battmann, W. Thoma, A. Bernd, W. Kummer, B. Irlinger, W. Steglich and P. Mayser. 2005b. Malassezin, a novel agonist of the aryl hydrocarbon receptor from the yeast *Malassezia furfur*, induces apoptosis in primary human melanocytes. Chembiochem 6, 860–865.

Krasil'nikov, N.A. 1927. *Selenotila intestinalis* nov. sp. – Novyi gribok iz kishechnika babochki *Brenthis pales* Schiff. Mikrobiol. Zh. 4, 134–137. In Russian.

Krasil'nikov, N.A. 1933. Rassenbildung bei *Sporobolomyces philippovi* n. sp. Izv. Akad. Nauk, VII Ser., Otd. Mat. Estest. Nauk [Bull. Acad. Sci. URSS, Ser. VII, Classe Sci. Math. Natur.]. 10, 1469–1491. In Russian.

Krasil'nikov, N.A. 1954a. Semejstvo Saccharomycetaceae. In: L.I. Kursanova (Ed.), Opredelitel' Nizshih Rastenij, Vol. 3, Griby. Gosudarstvennoe Iztatel'stvo "Sovetskaya Nauka", Moscow, pp. 108–129. In Russian.

Krasil'nikov, N.A. 1954b. Semejstvo Chromotorulaceae. In: L.I. Kursanova (Ed.), Opredelitel Nizshih Rastenij, Vol. 3. Griby. Gosudarstvennoe Iztatelstvo "Sovetskaya Nauka", Moscow, pp. 129–136. In Russian.

Krasil'nikov, N.A. 1954c. Semejstvo Torulopsidaceae. In: L.I. Kursanova (Ed.), Opredelitel' Nizshih Rastenij, Vol. 3. Griby. Gosudarstvennoe Iztatel'stvo "Sovetskaya Nauka", Moscow, pp. 136–148. In Russian.

Krasil'nikov, N.A., I.P. Bab'eva and K. Meavahd. 1967. A new genus of soil yeast *Zygolipomyces* nov. gen. Mikrobiologiia 36, 923–931. In Russian.

Krcméry, V., A. Kunova and J. Mardiak. 1997. Nosocomial *Cryptococcus laurentii* fungemia in a bone marrow transplant patient after prophylaxis with ketoconazole successfully treated with oral fluconazole. Infection 2, 130.

Krcméry, V.J., F. Mateika, A. Kunova, S. Spanik, J. Giarfas, Z. Sycova and J. Trupl. 1999. Hematogenous *Trichosporono*sis in cancer patients: report of 12 cases including 5 during prophylaxis with itraconazol. Support Care Cancer 7, 39–43.

Kreger-van Rij, N.J.W. 1958. The relationship between *Saccharomyces tellustris* and *Candida bovina*. Antonie van Leeuwenhoek 24, 137–144.

Kreger-van Rij, N.J.W. 1961. Taxonomy of *Cryptococcus neoformans* and its variety *uniguttulatus*. Antonie van Leeuwenhoek 17, 59–64.

Kreger-van Rij, N.J.W. 1964a. *Endomycopsis vini* and *Pichia etchellsii*, spp. n. Antonie van Leeuwenhoek 30, 428–432.

Kreger-van Rij, N.J.W. 1964b. A taxonomic study of the yeast genera *Endomycopsis*, *Pichia* and *Debaryomyces*. Thesis, University of Leiden.

Kreger-van Rij, N.J.W. 1965. *Candida ciferrii*, a new yeast species. Mycopathol. Mycol. Appl. 26, 49–52.

Kreger-van Rij, N.J.W. 1966. *Kluyveromyces osmophilus*, a new yeast species. Mycopathol. Mycol. Appl. 29, 137–141.

Kreger-van Rij, N.J.W. 1969a. Taxonomy and systematics of yeasts. In: A.H. Rose and J.S. Harrison (Eds), The Yeasts, Vol. 1. Academic Press, New York, pp. 5–78.

Kreger-van Rij, N.J.W. 1969b. A new feature of the ascospores of *Saccharomycodes ludwigii* Hansen. Can. J. Microbiol. 15, 823–825.

Kreger-van Rij, N.J.W. 1969c. Some features of yeast ascospores observed under the electron microscope. In: A. Kocková-Kratochvílová (Ed.), Proc. 2nd Symp. Yeasts, Bratislava, 1966, pp. 169–176.

Kreger-van Rij, N.J.W. 1970a. *Debaryomyces* Lodder et Kreger-van Rij nom. conserv. In: J. Lodder (Ed.), The Yeasts, A Taxonomic Study, 2nd edn. North-Holland, Amsterdam, pp. 129–156.

Kreger-van Rij, N.J.W. 1970b. *Endomycopsis* Dekker. In: J. Lodder (Ed.), The Yeasts, A Taxonomic Study, 2nd edn. North-Holland, Amsterdam, pp. 166–208.

Kreger-van Rij, N.J.W. 1970c. *Pichia* Hansen. In: J. Lodder (Ed.), The Yeasts, A Taxonomic Study, 2nd edn. North-Holland, Amsterdam, pp. 455–554.

Kreger-van Rij, N.J.W. 1970d. *Schizoblastosporion* Ciferri. In: J. Lodder (Ed.), The Yeasts, A Taxonomic Study, 2nd edn. North Holland Publishing Co., Amsterdam, pp. 1224–1228.

Kreger-van Rij, N.J.W. 1974. The species *Dipodascopsis uninucleata* (Biggs) Batra & Millner. Persoonia 8, 105–109.

Kreger-van Rij, N.J.W. 1977a. Electron microscopy of sporulation in *Schwanniomyces alluvius*. Antonie van Leeuwenhoek 43, 55–64.

Kreger-van Rij, N.J.W. 1977b. Ultrastructure of *Hanseniaspora* ascospores. Antonie van Leeuwenhoek 43, 225–232.

Kreger-van Rij, N.J.W. 1984a. *Ambrosiozyma* van der Walt. In: N.J.W. Kreger–van Rij (Ed.), The Yeasts, A Taxonomic Study, 3rd edn. Elsevier, Amsterdam, pp. 106–113.

Kreger-van Rij, N.J.W. 1984b. *Arthroascus* von Arx. In: N.J.W. Kreger-van Rij (Ed.), The Yeasts, A Taxonomic Study, 3rd edn. Elsevier, Amsterdam, pp. 114–116.

Kreger-van Rij, N.J.W. 1984c. *Debaryomyces* Lodder et Kreger-van Rij nom. cons. In: N.J.W. Kreger-van Rij (Ed.), The Yeasts, A Taxonomic Study, 3rd edn. Elsevier, Amsterdam, pp. 130–145.

Kreger-van Rij, N.J.W. 1984d. *Guilliermondella* Nadson et Krassilnikov. In: N.J.W. Kreger-van Rij (Ed.), The Yeasts, A Taxonomic Study, 3rd edn. Elsevier, Amsterdam, pp. 151–153.

Kreger-van Rij, N.J.W. 1984e. *Saccharomycopsis* Schiönning. In: N.J.W. Kreger-van Rij (Ed.), The Yeasts, A Taxonomic Study, 3rd edn. Elsevier, Amsterdam, pp. 399–413.

Kreger-van Rij, N.J.W. 1984f. *Trichosporon* Behrend. In: N.J.W. Kreger-van Rij (Ed.), The Yeasts, A Taxonomic Study, 3rd edn. Elsevier, Amsterdam, pp. 933–962.

Kreger-van Rij, N.J.W., and D.G. Ahearn. 1968. Shape and structure of the ascospores of *Hanseniaspora uvarum*. Mycologia 60, 604–612.

Kreger-van Rij, N.J.W., and J.P. van der Walt. 1963. Ascospores of *Endomycopsis selenospora* (Nadson et Krassilnikov) Dekker. Nature 199, 1012–1013.

Kreger-van Rij, N.J., and M. Veenhuis. 1970. An electron microscope study of the yeast *Pityrosporum ovale*. Arch. Mikrobiol. 71, 123–131.

Kreger van Rij, N J.W., and M. Veenhuis. 1971a. A comparative study of the cell wall structure of basidiomycetous and related yeasts. J. Gen. Microbiol. 68, 87–95.

Kreger-van Rij, N.J.W., and M. Veenhuis. 1971b. Septal pores in *Trichosporon cutaneum*. Sabouraudia 9, 36–38.

Kreger-van Rij, N.J.W., and M. Veenhuis. 1971c. Bipolar budding yeasts – an electron microscopic study. Antonie van Leeuwenhoek 37, 125–136.

Kreger-van Rij, N.J.W., and M. Veenhuis. 1973a. Electron microscopy of septa in ascomycetous yeasts. Antonie van Leeuwenhoek 39, 481–490.

Kreger-van Rij, N.J.W., and M. Veenhuis. 1973b. Electron microscopy of some special cell contacts in yeasts. J. Bacteriol. 113, 350–356.

Kreger-van Rij, N.J.W., and M. Veenhuis. 1974. Spores and septa in the genus *Dipodascus*. Can. J. Bot. 52, 1335–1338.

Kreger-van Rij, N.J.W., and M. Veenhuis. 1975a. Electron microscopy of ascus formation in the yeast *Debaryomyces hansenii*. J. Gen. Microbiol. 89, 256–264.

Kreger-van Rij, N.J.W., and M. Veenhuis. 1975b. Conjugation in the yeast *Saccharomycopsis capsularis* Schiönning. Arch. Microbiol. 104, 263–269.

Kreger-van Rij, N.J.W., and M. Veenhuis. 1976a. Conjugation in the yeast *Guilliermondella selenospora* Nadson et Krassilnikov. Can. J. Microbiol. 22, 960–966.

Kreger-van Rij, N.J.W., and M. Veenhuis. 1976b. Ultrastructure of the ascospores of some species of the *Torulaspora* group. Antonie van Leeuwenhoek 42, 445–455.

Kriegs, J.O., G. Churakov, M. Kiefmann, U. Jordan, J. Brosius and J. Schmitz. 2006. Retroposed elements as archives for the evolutionary history of placental mammals. PLoS Biol. 4, e91.

Krisman, C.R. 1962. A method for the colorimetric estimation of glycogen with iodine. Anal. Biochem. 4, 17–23.

Kritzinger, S.M., S.G. Kilian, M.A. Potgieter and J.C. du Preez. 2003. The effect of production parameters on the synthesis of the prebiotic trisaccharide, neokestose, by *Xanthophyllomyces dendrorhous* (*Phaffia rhodozyma*). Enzyme Microb. Technol 32, 728–737.

Kroemer, K., and F. Heinrich. 1922. Über eine in überschwefelten Mosten auftretende Hefe der Gattung *Saccharomycodes*. Festschr. Staatl. Lehr. Forschungsanstalt Wein-, Obst- und Gartenbau. Geisenheim, pp. 258–294.

Kroemer, K., and G. Krumbholz. 1931. Untersuchungen über osmophile Sprosspilze. I. Beiträge zur Kenntnis der Gärungsvorgänge und der Gärungserreger der Trockenbeerenauslesen. Arch. Mikrobiol. 2, 352–410.

Krüger, W. 1894a. Kurze Charakteristik einiger niederer Organismen im Saftflusse der Laubbäume. Hedwigia 33, 241–266.

Krüger, W. 1894b. Beiträge zur Kenntniss der Organismen des Saftflusses (sog. Schleimflusses) der Laubbäume. Parts I and II. Zopf's Beiträge Physiologie zat Morphologie niedaren der Organismen (Leipzig) 4, 69–116.

Krukowski, H., M. Tietze, T. Majewski and P. Rózański. 2001. Survey of yeast mastitis in dairy herds of small-type farms in the Lublin region, Poland. Mycopathologia 150, 5–7.

Krukowski, H., A. Lisowski, P. Rózański and A. Skórka. 2006. Yeasts and algae isolated from cows with mastitis in the south-eastern part of Poland. Pol. J. Vet. Sci. 9, 181–184.

Krumbholz, G. 1931. Untersuchungen über osmophile Sprosspilze. II. Beiträge zur Kenntnis der Gattung *Zygosaccharomyces*. Arch. Mikrobiol. 2, 411–492.

Krumbholz, G. 1932. Über eine pastoriane Hefe von Weinbeeren, *Saccharomyces elongatus* sp. n. Zentralbl. Bakteriol. Parasitenkd., Abt. II, 86, 206–214.

Krumbholz, G. 1933. Ist die Beibehaltung einer Gattung *Torulaspora* berechtigt? Arch. Mikrobiol. 4, 167–169.

Krumbholz, G., and W. Tauschanoff. 1933. *Mycotorula intermedia* n. sp., ein Beitrag zur Kenntnis der Gärungserreger im Wein. Zentralbl. Bakteriol. Parasitenkd., Abt. II, 88, 366–373.

Krzemecki, A. 1913. Über eine Aroma bildende *Oidium-Art, Oidium suavolens*. Zentralbl. Bakteriol. Parasitenkd., Abt. II, 38, 577–584.

Kubatoba, A. 1993. New records of micromycetes from Czechoslovakis. II. *Filobasidiella depauperata* (Petch) Samson, Staplers & Weijman. Ceska Mykol. 46, 126–130.

Kubicek-Pranz, E.M., and M. Röhr. 1985. D-Amino acid oxidase from the yeast *Trigonopsis variabilis*. Appl. Biochem. 7, 104–113.

Kucsera, J., I. Pfeiffer and L. Ferenczy. 1998. Homothallic life cycle in the diploid red yeast *Xanthophyllomyces dendrorhous* (*Phaffia rhodozyma*). Antonie van Leeuwenhoek 73, 163–168.

Kudryavtsev, V.I. 1954. Yeast Systematics. USSR Academy of Sciences, Moscow. In Russian.

Kudryavtsev, V.I. 1960. Die Systematik der Hefen. Akademie Verlag, Berlin.

Kufferath, H. 1920. Peut-on obtenir du moût de bière alcalin? Ann. Bull. Soc. R. Sci. Méd. Nat. Bruxelles 74, 16–46.

Kufferath, H. 1925. Études sur les levures du lambic. Isolement, caractères de culture et biologie. Ann. Soc. Zymol. 1, 7–17.

Kufferath, H., and M.H. van Laer. 1921. Études sur les levures de lambic. Leur action chimique sur les milieux de culture. Bull. Soc. Chim. Belge 30, 270–276.

Kulakovskaia, E.V., T.V. Kulakovskaia, V.I. Golubev, A.S. Shashkov, A.A. Grachev and N.E. Nifant'ev. 2007. Fungicidal activity of cellobiose lipids from cultural fluid of yeast *Cryptococcus humicola* and *Pseudozyma fusiformata*. Bioorg. Khim. 33, 167–171. In Russian.

Kulakovskaya, T.V., E.V. Kulakovskaya and W.I. Golubev. 2003. ATP leakage from yeast cells treated by extracellular glycolipids of *Pseudozyma fusiformata*. FEMS Yeast Res. 3, 401–404.

Kulakovskaya, T., A.S. Shashkov, E.V. Kulakovskaya and W.I. Golubev. 2004. Characterization of an antifungal glycolipid secreted by the yeast *Sympodiomycopsis paphiopedili*. FEMS Yeast Res. 5, 247–252.

Kulakovskaya, T.V., A.S. Shashkov, E.V. Kulakovskaya and W.I. Golubev. 2005. Ustilagic acid secretion by *Pseudozyma fusiformata* strains. FEMS Yeast Res. 5, 919–923.

Kumamoto, T., M. Yamamoto, Y. Seriu, K. Kouno, R. Okamoto, T. Ishikura and A. Takamatsu. 1986. Four new species of methanol-assimilating yeasts: *Candida methanolophaga*, *Candida ovalis*, *Candida ooitensis* and *Pichia methylovora*. Trans. Mycol. Soc. Jpn 27, 387–397.

Kumar, S., and T. Satyanarayana. 2001. Medium optimization for glucoamylase production by a yeast, *Pichia subpelliculosa* ABWF-64, in submerged cultivation. World J. Microbiol. Biotechnol. 17, 83–87.

Kumar, A., S. Agarwal, J.A. Heyman, S. Matson, M. Heidtman, S. Piccirillo, L. Umansky, A. Drawid, R. Jansen, Y. Liu, K.H. Cheung, P. Miller, M. Gerstein, G.S. Roeder and M. Snyder. 2002. Subcellular localization of the yeast proteome. Genes Dev. 16, 707–719.

Kumbhojkar, M.S. 1972. *Schizosaccharomyces slooffiae* Kumbhojkar, a new species of osmophilic yeasts from India. Curr. Sci. 41, 151–152.

Kundalkar, B.D., and M.S. Patil. 1986. Study of Sirobasidiaceous fungi from India. Indian Phytopathol. 39, 356–360.

Kung, H.F., Y.H. Tsai and C.I. Wei. 2007. Histamine and other biogenic amines and histamine forming bacteria in miso products. Food Chem. 101, 351–356.

Kunova, A., and V. Krcméry. 1999. Fungaemia due to thermophilic cryptococci: 3 cases of *Cryptococcus laurentii* bloodstream infections in cancer patients receiving antifungals. Scand. J. Infect Dis. 31, 328.

Künsch, H.R. 1989. The jackknife and the bootstrap for general stationary observations. Ann. Stat. 17, 1217–1241.

Kunz, S. 2006. Fire blight control in organic fruit growing – systematic investigation of the mode of action of potential control agents. Mitt. Biol. Bundesanst. Land-Forstwirtsch. 408, 249–253.

Kunze, G., and I. Kunze. 1994. Characterization of *Arxula adeninivorans* strains from different habitats. Antonie van Leeuwenhoek 65, 29–34.

Kuraishi, H. 1958. *Pichia megalospora* nov. spec., a new yeast from decomposing mushrooms. Sci. Rep. Tôhoku Univ., IV Ser. Biol. 24, 109–111.

Kuraishi, H., K. Katayama-Fujimura, J. Sugiyama and T. Yokoyama. 1985. Ubiquinone systems in fungi. 1. Distribution of ubiquinones in the major families of ascomycetus, basidiomycetes and deuteromycetes, and their taxonomic implications. Trans. Mycol. Soc. Jpn 26, 383–395.

Kuramae, E.E., V. Robert, B. Snel and T. Boekhout. 2006a. Conflicting phylogenetic position of *Schizosaccharomyces pombe*. Genomics 88, 387–393.

Kuramae, E.E., V. Robert, B. Snel, M. Weiss and T. Boekhout. 2006b. Phylogenomics reveal a robust fungal tree of life. FEMS Yeast Res. 6, 1213–1220.

Kuramoto, T., Y. Ito, M. Ota, Y. Tamura and S. Kitahata. 1994. Microbial production of glycyrrhetic acid 3-O-mono-beta-D-glucuronide from glycyrrhizin by *Cryptococcus magnus* MG-27. Biosci. Biotechnol. Biochem. 58, 455–458.

Kuroda, K., K. Kobayashi, H. Tsumura, T. Komeda, Y. Chiba and Y. Jigami. 2006. Production of Man5GlcNAc2-type sugar chain by the methylotrophic yeast *Ogataea minuta*. FEMS Yeast Res. 6, 1052–1062.

Kursanov, L.I. 1954. Opredelitel'nizshikh Rastenii, Tom 3. Sovetskaya Nauka, Griby.

Kurtz, A.M., and S.A. Crow. 1997. Transformation of chlororesorcinol by the hydrocarbonoclastic yeasts *Candida maltosa*, *Candida tropicalis*, and *Trichosporon olivide*. Curr. Microbiol. 35, 165–168.

Kurtzman, C.P. 1973. Formation of hyphae and chlamydospores by *Cryptococcus laurentii*. Mycologia 65, 388–395.

Kurtzman, C.P. 1977. *Cephaloascus albidus*, a new heterothallic yeast-like fungus. Mycologia 69, 547–555.

Kurtzman, C.P. 1984a. Synonymy of the yeast genera *Hansenula* and *Pichia* demonstrated through comparisons of deoxyribonucleic acid relatedness. Antonie van Leeuwenhoek 50, 209–217.

Kurtzman, C.P. 1984b. Resolution of varietal relationships within the species *Hansenula anomala*, *Hansenula bimundalis*, and *Pichia nakazawae* through comparisons of DNA relatedness. Mycotaxon 19, 271–279.

Kurtzman, C.P. 1984c. *Hansenula* H. et P. Sydow. In: N.J.W. Kreger-van Rij (Ed.), The Yeasts, A Taxonomic Study, 3rd edn. Elsevier, Amsterdam, pp. 165–213.

Kurtzman, C.P. 1984d. *Pichia* Hansen. In: N.J.W. Kreger-van Rij (Ed.), The Yeasts, A Taxonomic Study, 3rd edn. Elsevier, Amsterdam, pp. 295–378.

Kurtzman, C.P. 1987a. Two new species of *Pichia* from arboreal habitats. Mycologia 79, 410–417.

Kurtzman, C.P. 1987b. Prediction of biological relatedness among yeasts from comparisons of nuclear DNA complementarity. In: G.S. de Hoog, M.Th. Smith and A.C.M. Weijman (Eds), The Expanding Realm of Yeast-like Fungi. Elsevier, Amsterdam, pp. 459–468. (Stud. Mycol. 30, 459–468).

Kurtzman, C.P. 1990a. DNA relatedness among species of *Sterigmatomyces* and *Fellomyces*. Int. J. Syst. Bacteriol. 40, 56–59.

Kurtzman, C.P. 1990b. *Candida shehatae* – genetic diversity and phylogenetic relationships with other xylose-fermenting yeasts. Antonie van Leeuwenhoek 57, 215–222.

Kurtzman, C.P. 1990c. DNA relatedness among species of the genus *Zygosaccharomyces*. Yeast 6, 213–219.

Kurtzman, C.P. 1991a. DNA relatedness among saturn-spored yeasts assigned to the genera *Williopsis* and *Pichia*. Antonie van Leeuwenhoek 60, 13–19.

Kurtzman, C.P. 1991b. *Saturnospora ahearnii*, a new salt marsh yeast from Louisiana. Antonie van Leeuwenhoek 60, 31–34.

Kurtzman, C.P. 1992. DNA relatedness among phenotypically similar species of *Pichia*. Mycologia 84, 72–76.

Kurtzman, C.P. 1993a. Systematics of the ascomycetous yeasts assessed from ribosomal RNA sequence divergence. Antonie van Leeuwenhoek 63, 165–174.

Kurtzman, C.P. 1993b. DNA-DNA hybridization approaches to species identification in small genome organisms. In: E.A. Zimmer, T.J. White, R.L. Cann and A.C. Wilson (Eds), Methods in Enzymology, Vol. 224. Academic Press, New York, pp. 335–348.

Kurtzman, C.P. 1993c. The systematics of ascomycetous yeasts defined from ribosomal RNA sequence divergence: theoretical and practical aspects. In: D.R. Reynolds and J.W. Taylor (Eds), The Fungal Holomorph: Mitotic, Meiotic and Pleomorphic Speciation in Fungal Systematics. CAB International, Wallingford, pp. 271–279.

Kurtzman, C.P. 1995. Relationships among the genera *Ashbya*, *Eremothecium*, *Holleya* and *Nematospora* determined from rDNA sequence divergence. J. Ind. Microbiol. 14, 523–530.

Kurtzman, C.P. 1996. Transfer of *Hansenula ofunaensis* to the genus *Pichia*. Mycotaxon 59, 85–88.

Kurtzman, C.P. 1998a. *Yarrowia* van der Walt & von Arx. In: C.P. Kurtzman and J.W. Fell (Eds), The Yeasts, A Taxonomic Study, 4th edn. Elsevier, Amsterdam, pp. 420–421.

Kurtzman, C.P. 1998b. *Myxozyma* van der Walt, Weijman & von Arx. In: C.P. Kurtzman and J.W. Fell (Eds), The Yeasts, A Taxonomic Study, 4th edn. Elsevier, Amsterdam, pp. 592–597.

Kurtzman, C.P. 1998c. *Pichia* E.C. Hansen emend. Kurtzman. In: C.P. Kurtzman and J.W. Fell (Eds), The Yeasts, A Taxonomic Study. Elsevier, Amsterdam, pp. 273–352.

Kurtzman, C.P. 1998d. Discussion of teleomorphic and anamorphic ascomycetous yeasts and a key to genera. In: C.P. Kurtzman and J.W. Fell (Eds), The Yeasts, A Taxonomic Study, 4th edn. Elsevier, Amsterdam, pp. 111–121.

Kurtzman, C.P. 1999. Two new members of the *Saccharomycopsis* clade: *Saccharomycopsis microspora* comb. nov. and *Candida lassenensis*, sp. nov. Mycotaxon 71, 241–250.

Kurtzman, C.P. 2000a. Four new yeasts in the *Pichia anomala* clade. Int. J. Syst. Evol. Microbiol. 50, 395–404.

Kurtzman, C.P. 2000b. Three new ascomycetous yeasts from insect-associated arboreal habitats. Can. J. Microbiol. 46, 50–58.

Kurtzman, C.P. 2001a. Four new *Candida* species from geographically diverse locations. Antonie van Leeuwenhoek 79, 353–361.

Kurtzman, C.P. 2001b. Six new anamorphic ascomycetous yeasts near *Candida tanzawaensis*. FEMS Yeast Res. 1, 177–185.

Kurtzman, C.P. 2003. Phylogenetic circumscription of *Saccharomyces*, *Kluyveromyces* and other members of the Saccharomycetaceae, and the proposal of the new genera *Lachancea*, *Nakaseomyces, Naumovia, Vanderwaltozyma* and *Zygotorulaspora*. FEMS Yeast Res. 4, 233–245.

Kurtzman, C.P. 2004. *Trichomonascus petasosporus* sp. nov. and *Sympodiomyces indianaensis* sp. nov., two new members of the Saccharomycetales. Antonie van Leeuwenhoek 85, 297–304.

Kurtzman, C.P. 2005a. Description of *Komagataella phaffii* sp. nov. and the transfer of *Pichia pseudopastoris* to the methylotrophic yeast genus *Komagataella*. Int. J. Syst. Evol. Microbiol. 55, 973–976.

Kurtzman, C.P. 2005b. New species and a new combination in the *Hyphopichia* and *Yarrowia* yeast clades. Antonie van Leeuwenhoek 88, 121–130.

Kurtzman, C.P. 2006a. Detection, identification and enumeration methods for spoilage yeasts. In: C. De and W. Blackburn (Eds), Food Spoilage Microorganisms. Woodhead Publishing, Cambridge, pp. 28–54.

Kurtzman, C.P. 2006b. New species and new combinations in the yeast genera *Kregervanrija* gen. nov., *Saturnispora* and *Candida*. FEMS Yeast Res. 6, 288–297.

Kurtzman, C.P. 2007a. Eleven new species of *Sugiyamaella* and *Candida* from forest habitats. FEMS Yeast Res. 7, 1046–1063.

Kurtzman, C.P. 2007b. New anamorphic yeast species: *Candida infanticola* sp. nov., *Candida polysorbophila* sp. nov., *Candida transvaalensis* sp. nov. and *Trigonopsis californica* sp. nov. Antonie van Leeuwenhoek 92, 221–231.

Kurtzman, C.P. 2007c. Six new species of the anamorphic yeast genus *Blastobotrys*. Int. J. Syst. Evol. Microbiol. 57, 1154–1162.

Kurtzman, C.P. 2008. *Naumovozyma* Kurtzman, nom. nov. Myconet ISSN 4813 (http://www.fieldmuseum.org/myconet/newnotes.asp).

Kurtzman, C.P. 2009. Biotechnological strains of *Komagataella* (*Pichia*) *pastoris* are *Komagataella phaffii* as determined from multigene sequence analysis. J. Ind. Microbiol. Biotechnol. 36, 1435–1438.

Kurtzman, C.P., and D.G. Ahearn. 1976. Sporulation in *Pichia spartinae*. Mycologia 68, 682–685.

Kurtzman, C.P., and B.S. Dien. 1998. *Candida arabinofermentans*, a new L-arabinose fermenting yeast. Antonie van Leeuwenhoek 74, 237–243.

Kurtzman, C.P., and S. Droby. 2001. *Metschnikowia fructicola*, a new ascosporic yeast with potential for biocontrol of postharvest fruit rots. Syst. Appl. Microbiol. 24, 395–399.

Kurtzman, C.P., and J.W. Fell. 1991. Molecular relatedness between the basidiomycetous yeasts *Sporidiobolus ruinenii* and *Sporobolomyces coprophilus*. Mycologia 83, 107–110.

Kurtzman, C.P. and J.W. Fell (Eds). 1998. The Yeasts. A Taxonomic Study. 4th edn. Elsevier Science, B.V., The Netherlands.

Kurtzman, C.P., and J.W. Fell. 2006. Yeast systematics and phylogeny – implications of molecular identification methods for studies in ecology. In: C. Rosa and G. Peter (Eds), Biodiversity and Ecophysiology of Yeasts. Springer-Verlag, Berlin, pp. 11–30.

Kurtzman, C.P., and S.A. James. 2006. *Zygosaccharomyces* and related genera. In: C. de W. Blackburn (Ed.), Food Spoilage Microorganisms. Woodhead Publishing, Cambridge, pp. 289–305.

Kurtzman, C.P., and N.J.W. Kreger-van Rij. 1976. Ultrastructure of ascospores from *Debaryomyces melissophilus*, a new taxonomic combination. Mycologia 68, 422–425.

Kurtzman, C.P., and Z. Liu. 1990. Evolutionary affinities of species assigned to *Lipomyces* and *Myxozyma* estimated from ribosomal RNA sequence divergence. Curr. Microbiol. 21, 387–393.

Kurtzman, C.P., and C.J. Robnett. 1991. Phylogenetic relationships among species of *Saccharomyces*, *Schizosaccharomyces*, *Debaryomyces* and *Schwanniomyces* determined from partial ribosomal RNA sequences. Yeast 7, 61–72.

Kurtzman, C.P., and C.J. Robnett. 1994a. Orders and families of ascosporogenous yeasts and yeast-like taxa compared from ribosomal RNA sequence similarities. In: D.L. Hawksworth (Ed.), Ascomycete Systematics: Problems and Perspectives in the Nineties. Plenum Press, New York, pp. 249–258.

Kurtzman, C.P., and C.J. Robnett. 1994b. Synonymy of the yeast genera *Wingea* and *Debaryomyces*. Antonie van Leeuwenhoek 66, 337–342.

Kurtzman, C.P., and C.J. Robnett. 1995. Molecular relationships among hyphal ascomycetous yeasts and yeastlike taxa. Can. J. Bot. 73, S824–S830.

Kurtzman, C.P., and C.J. Robnett. 1997. Identification of clinically important ascomycetous yeasts based on nucleotide divergence in the 5′ end of the large-subunit (26S) ribosomal DNA gene. J. Clin. Microbiol. 35, 1216–1223.

Kurtzman, C.P., and C.J. Robnett. 1998a. Identification and phylogeny of ascomycetous yeasts from analysis of nuclear large subunit (26S) ribosomal DNA partial sequences. Antonie van Leeuwenhoek 73, 331–371.

Kurtzman, C.P., and C.J. Robnett. 1998b. Three new insect-associated species of the yeast genus *Candida*. Can. J. Microbiol. 44, 965–973.

Kurtzman, C.P., and C.J. Robnett. 2003. Phylogenetic relationships among yeasts of the "*Saccharomyces* complex"

determined from multigene sequence analyses. FEMS Yeast Res. 3, 417–432.
Kurtzman, C.P., and C.J. Robnett. 2007. Multigene phylogenetic analysis of the *Trichomonascus*, *Wickerhamiella* and *Zygoascus* yeast clades, and the proposal of *Sugiyamaella* gen. nov. and fourteen new species combinations. FEMS Yeast Res. 7, 141–151.
Kurtzman, C.P., and C.J. Robnett. 2010. Systematics of methanol assimilating yeasts and neighboring taxa from multigene sequence analysis and the proposal of *Peterozyma* gen. nov. FEMS Yeast Res. 10, 353–360.
Kurtzman, C.P., and M.J. Smiley. 1974. A taxonomic re-evaluation of the round-spored species of *Pichia*. In: H. Klaushofer and U.B. Sleytr (Eds), Proc. IV. Int. Symp. on Yeasts, Vienna, Austria. I. Hochschürulerschaft an der Hochschule für Bodenkultur, Vienna, pp. 231–232.
Kurtzman, C.P., and M.J. Smiley. 1976. Heterothallism in *Pichia kudriavzevii* and *Pichia terricola*. Antonie van Leeuwenhoek 42, 355–363.
Kurtzman, C.P., and M.J. Smiley. 1979. Taxonomy of *Pichia carsonii* and its synonyms *P. vini* and *P. vini* var. *melibiosi*: comparison by DNA reassociation. Mycologia 71, 658–662.
Kurtzman, C.P., and M.Th. Smith. 1998. *Saccharomycopsis* Schiönning. In: C.P. Kurtzman and J.W. Fell (Eds), The Yeasts, A Taxonomic Study. Elsevier, Amsterdam, pp. 374–386.
Kurtzman, C.P., and J. Sugiyama. 2001. Ascomycetous yeasts and yeastlike taxa. In: D.J. McLaughlin, E.G. McLaughlin and P.A. Lemke (Eds), The Mycota. Vol. VII Part A Systematics and Evolution. Springer-Verlag, Berlin, pp. 179–200.
Kurtzman, C.P., and M. Suzuki. 2010. Phylogenetic analysis of ascomycete yeasts that form coenzyme Q-9 and the proposal of the new genera *Babjeviella, Meyerozyma, Millerozyma, Priceomyces* and *Scheffersomyces*. Mycoscience 51, 2–14.
Kurtzman, C.P., and L.J. Wickerham. 1972. *Pichia besseyi* sp. n. Antonie van Leeuwenhoek 38, 49–52.
Kurtzman, C.P., and L.J. Wickerham. 1973. *Saccharomycopsis crataegensis*, a new heterothallic yeast. Antonie van Leeuwenhoek 39, 81–87.
Kurtzman, C.P., L.J. Wickerham and C.W. Hesseltine. 1970. Yeasts from wheat and flour. Mycologia 62, 542–547.
Kurtzman, C.P., M.J. Smiley and F.L. Baker. 1972. Scanning electron microscopy of ascospores of *Schwanniomyces*. J. Bacteriol. 112, 1380–1382.
Kurtzman, C.P., J.C. Gentles, E.G.V. Evans, M.E. Slodki and R.M. Ward. 1973a. Growth of *Hansenula holstii* on cadavers. Appl. Microbiol. 25, 184–186.
Kurtzman, C.P., R.F. Vesonder and M.J. Smiley. 1973b. Formation of extracellular C14–C18 2-D-hydroxy fatty acids by species of *Saccharomycopsis*. Appl. Microbiol. 26, 650–652.
Kurtzman, C.P., R.F. Vesonder and M.J. Smiley. 1974. Formation of extracellular 3-D-hydroxypalmitic acid by *Saccharomycopsis malanga* comb. nov. Mycologia 66, 580–587.
Kurtzman, C.P., M.J. Smiley and F.L. Baker. 1975. Scanning electron microscopy of ascospores of *Debaryomyces* and *Saccharomyces*. Mycopathol. Mycol. Appl. 55, 29–34.
Kurtzman, C.P., C.J. Johnson and M.J. Smiley. 1979. Determination of conspecificity of *Candida utilis* and *Hansenula jadinii* through DNA reassociation. Mycologia 71, 844–847.
Kurtzman, C.P., M.J. Smiley, C.J. Johnson, L.J. Wickerham and G.B. Fuson. 1980a. Two new and closely related heterothallic species, *Pichia amylophila* and *Pichia mississippiensis*: characterization by hybridization and deoxyribonucleic acid reassociation. Int. J. Syst. Bacteriol. 30, 208–216.
Kurtzman, C.P., M.J. Smiley and C.J. Johnson. 1980b. Emendation of the genus *Issatchenkia* Kudriavzev and comparison of species by deoxyribonucleic acid reassociation, mating reaction, and ascospore ultrastructure. Int. J. Syst. Bacteriol. 30, 503–513.
Kurtzman, C.P., R.J. Bothast and J.E. VanCauwenberge. 1982. Conversion of D-xylose to ethanol by the yeast *Pachysolen tannophilus*. US Patent 4359534.
Kurtzman, C.P., C.J. Robnett and D. Yarrow. 2001a. Three new species of *Candida* from apple cider: *C. anglica, C. cidri and C. pomicola*. Antonie van Leeuwenhoek 80, 237–244.
Kurtzman, C.P., C.J. Robnett and D. Yarrow. 2001b. Two new anamorphic yeasts: *Candida germanica* and *Candida neerlandica*. Antonie van Leeuwenhoek 80, 77–83.
Kurtzman, C.P., M.A. Lachance, H.V. Nguyen and H. Prillinger. 2001c. Proposal to conserve the name *Kluyveromyces* with a conserved type (Ascomycota: Hemiascomycetes, Saccharomycetaceae). Taxon 50, 907–908.
Kurtzman, C.P., C.J. Robnett and E. Basehoar-Power. 2001d. *Zygosaccharomyces kombuchaensis*, a new ascosporogenous yeast from "kombucha tea". FEMS Yeast Res. 1, 133–138.
Kurtzman, C.P., T. Boekhout, V. Robert, J. Fell and T. Deak. 2003. Methods to identify yeasts. In: T. Boekhout and V. Robert (Eds), Yeasts in Food: Beneficial and Detrimental Aspects. Behrs-Verlag, Hamburg, pp. 69–121.
Kurtzman, C.P., A. Statzell-Tallman and J.W. Fell. 2004. *Tetrapisispora fleetii* sp. nov., a new member of the Saccharomycetaceae. Studies in Mycol. 50, 397–400.
Kurtzman, C.P., C.J. Robnett, J.N. Ward, C. Brayton, P. Gorelick and T.J. Walsh. 2005. Multigene phylogenetic analysis of pathogenic *Candida* species in the *Kazachstania* (*Arxiozyma*) *telluris* complex and description of their ascosporic states as *Kazachstania bovina* sp. nov., K. *heterogenica* sp. nov., *K. pintolopesii* sp. nov., and *K. slooffiae* sp. nov. J. Clin. Microbiol. 43, 101–111.
Kurtzman, C.P., J. Albertyn and E. Basehoar-Powers. 2007. Multigene phylogenetic analysis of the Lipomycetaceae and proposed transfer of *Zygozyma* species to *Lipomyces* and *Babjevia anomala* to *Dipodascopsis*. FEMS Yeast Res. 7, 1027–1034.
Kurtzman, C.P., C.J. Robnett and E. Basehoar-Powers. 2008. Phylogenetic relationships among species of *Pichia, Issatchenkia* and *Williopsis* determined from multigene phylogenetic analysis, and the proposal of *Barnettozyma* gen. nov., *Lindnera* gen. nov. and *Wickerhamomyces* gen. nov. FEMS Yeast Res. 8, 939–954.
Kurz, M., C. Eder, D. Isert, Z. Li, E.F. Paulus, M. Schiell, L. Toti, L. Vertesy, J. Wink and G. Seibert. 2003. Ustilipids, acylated beta-D-mannopyranosyl D-erythritols from *Ustilago maydis* and *Geotrichum candidum*. J. Antibiot. (Tokyo) 56, 91–101.
Kurzai, O., W.J. Heinz, D.J. Sullivan, D.C. Coleman, M. Frosch and F.A. Mühlschlegel. 1999. Rapid PCR test for discriminating between *Candida albicans* and *Candida dubliniensis*

isolates using primers derived from the pH-regulated PHR1 and PHR2 genes of C. *albicans*. J. Clin. Microbiol. 37, 1587–1590.

Kustimur, S., A. Kalkanci, K. Cagla, M. Dizbay, F. Aktas and T. Sugita. 2002. Nosocomial fungemia due to *Trichosporon asteroides*: firstly described bloodstream infection. Diagn. Microbiol. Infect. Dis. 43, 167–170.

Kuttin, E.S., and J. Müller. 1981. *Trichosporon beemeri* sp. nov. Antonie van Leeuwenhoek 47, 255–265.

Kützing, F.T. 1833. Algarum aquae dulcis Germanicarum, Decas III.

Kvasnikov, E.I., S.S. Nagornaya and J.F. Shchelokova. 1975a. Distribution of the yeast *Rhodosporidium diobovatum* in soil and plants. Mikrobiologiia 44, 753–756. In Russian. (English translation in: Microbiology 44, 679–681).

Kvasnikov, E.I., S.S. Nagornaia and I.F. Shchelokova. 1975b. Yeast flora of plant rhizosphere and phyllosphere. Mikrobiologiia 44, 339–346.

Kvasnikov, E.I., S.S. Nagornaya and I.F. Shchelokova. 1979a. *Schwanniomyces ukrainicus* nov. sp. Mikrobiol. Zh. (Kiev) 41, 3–5.

Kvasnikov, E.I., S.S. Nagornaya and I.F. Shchelokova. 1979b. *Hansenula ukrainica* nov. sp. Mikrobiol. Zh. 41, 107–109.

Kwon, H.-K., S.-H. Woo and J.-M. Park. 2002. Degradation of tetracyanonickelate (II) by *Cryptococcus humicolus* MCN2. FEMS Microbiol. Lett. 214, 211–216.

Kwon-Chung, K.J. 1975. A new genus, *Filobasidiella*, the perfect state of *Cryptococcus neoformans*. Mycologia 67, 1197–1200.

Kwon-Chung, K.J. 1976a. A new species of *Filobasidiella*, the sexual state of *Cryptococcus neoformans* B and C serotypes. Mycologia 68, 942–946.

Kwon-Chung, K.J. 1976b. Morphogenesis of *Filobasidiella neoformans*, the sexual state of *Cryptococcus neoformans*. Mycologia 68, 821–833.

Kwon-Chung, K.J. 1977a. Heterothallism vs. self-fertile isolates of *Filobasidiella neoformans* (*Cryptococcus neoformans*). Proc. 4th Int. Conf. on the Mycoses. PAHO, Scientific Publication No. 356, pp. 204–213.

Kwon-Chung, K.J. 1977b. Perfect state of *Cryptococcus uniguttulatus*. Int. J. Syst. Bacteriol. 27, 293–299.

Kwon-Chung, K.J. 1980. Nuclear genotypes of spore chains in *Filobasidiella neoformans* (*Cryptococcus neoformans*). Mycologia 72, 418–422.

Kwon-Chung, K.J. 1987. Filobasidiaceae – a taxonomic survey. In: G.S. de Hoog, M.Th. Smith and A.C.M. Weijman (Eds), The Expanding Realm of Yeast-like Fungi. Elsevier, Amsterdam, pp. 75–85. (Stud. Mycol. 30, 75–85).

Kwon-Chung, K.J. 1998a. *Chionosphaera* Cox. In: C.P. Kurtzman and J.W. Fell (Eds), The Yeasts, A Taxonomic Study, 4th edn. Elsevier, Amsterdam, pp. 643–645.

Kwon-Chung, K.J. 1998b. *Filobasidiella*. In: C.P. Kurtzman and J.W. Fell (Eds), The Yeasts, A Taxonomic Study, 4th edn. Elsevier, Amsterdam, pp. 656–662.

Kwon-Chung, K.J., and J.E. Bennett. 1978. Distribution of α and *a* mating types of *Cryptococcus neoformans* among natural and clinical isolates. Am. J. Epidemiol. 108, 337–340.

Kwon-Chung, K.J., and J.E. Bennett. 1984. Epidemiologic differences between the two varieties of *Cryptococcus neoformans*. Am. J. Epidemiol. 120, 123–130.

Kwon-Chung, K.J., and J.E. Bennett. 1992. Medical Mycology. Lea and Febiger, Philadelphia, PA, 866pp.

Kwon-Chung, K.J., and J.W. Fell. 1984. *Filobasidiella* Kwon-Chung. In: N.J.W. Kreger-van Rij (Ed.), The Yeasts, A Taxonomic Study, 3rd edn. Elsevier, Amsterdam, pp. 472–482.

Kwon-Chung, K.J., and C.K. Kennedy. 1986. Intrageneric effect of killer toxin produced by *Cryptococcus laurentii*. Mycologia 78, 287–289.

Kwon-Chung, K.J., and T.J. Popkin. 1976. Ultrastructure of the septal complex in *Filobasidiella neoformans* (*Cryptococcus neoformans*). J. Bacteriol. 126, 524–528.

Kwon-Chung, K.J., and J.C. Rhodes. 1986. Encapsulation and melanin formation as indicators of virulence in *Cryptococcus neoformans*. Infect. Immun. 51, 218–223.

Kwon-Chung, K.J., and A. Varma. 2006. Do major species concepts support one, two or more species within *Cryptococcus neoformans*? FEMS Yeast Res. 6, 574–587.

Kwon-Chung, K.J., J.E. Bennett and T.S. Theodore. 1978. *Cryptococcus bacillisporus* sp. nov.: serotype B-C of *Cryptococcus neoformans*. Int. J. Syst. Bacteriol. 28, 616–620.

Kwon-Chung, K.J., J.E. Bennett and J.C. Rhodes. 1982a. Taxonomic studies on *Filobasidiella* species and their anamorphs. Antonie van Leeuwenhoek 48, 25–38.

Kwon-Chung, K.J., I. Polacheck and J.E. Bennett. 1982b. An improved diagnostic medium for separation of *Cryptococcus neoformans* var. *neoformans* (serotypes A and D) and *Cryptococcus neoformans* var. *gattii* (serotypes B and C). J. Clin. Microbiol. 15, 535–537.

Kwon-Chung, K.J., B.L. Wickes, J.L. Booth, H.S. Vishniac and J.E. Bennett. 1987. Urease inhibition by ethylene-diamine-tetra-acetate in two varieties of *Cryptococcus neoformans*. Infect. Immun. 55, 1751–1754.

Kwon-Chung, K.J., B.L. Wickes and W.G. Merz. 1988. Association of electrophoretic karyotypes of *Candida stellatoidea* with virulence for mice. Infect. Immun. 56, 1814–1819.

Kwon-Chung, K.J., J.C. Edman and B.L. Wickes. 1992. Genetic association of mating types and virulence in *Cryptococcus neoformans*. Infect. Immun. 60, 602–605.

Kwon-Chung, K.J., Y.C. Chang, R. Bauer, E.C. Swann, J.W. Taylor and R. Goel. 1995. The characteristics that differentiate *Filobasidiella depauperata* from *Filobasidiella neoformans*. Stud. Mycol. 38, 67–79.

Kwon-Chung, K.J., Y.C. Chang and L. Penoyer. 1997. Species of the genus *Filobasidiella* differ in the organization of their 5S rRNA genes. Mycologia 89, 244–249.

Kwon-Chung, K.J., T. Boekhout, J.W. Fell and M.R. Diaz. 2002. Proposal to conserve the name *Cryptococcus gattii* against *C. hondurianus* and *C. bacillisporus* (Basidiomycota, Hymenomycetes, Tremellomycetidae). Taxon 51, 804–806.

La Carbona, S., C. Le Goff and X. Le Goff. 2006. Fission yeast cytoskeletons and cell polarity factors: connecting at the cortex. Biol. Cell 98, 619–631.

La Fage, J.P., and R.F. Hou. 1978. Nutrient dynamics of termites. In: M.V. Brian (Ed.), Production Ecology of Ants and Termites. Cambridge University Press, Cambridge, pp. 165–232.

Laaser, G. 1989. Vergleichende systematische Studien an Basidiomycetenhefen unter besonderer Berücksichtigung der Hefestadien. Biblioth. Mycol. 130, 1–325. In German.

Laaser, G., K.D. Jahnke, H.J. Prillinger, R. Bauer, P. Hoffmann, G. Deml and F. Oberwinkler. 1988. A new-tremelloid yeast isolated from *Asterophora lycoperdoides* (Bull.: Fr.) Ditm. Antonie van Leeuwenhoek 54, 57–74.

Labarre, C., H. van Tilbeurgh and K. Blodeau. 2007. *Pichia pastoris* is a valuable host for the expression of genes encoding membrane proteins from the hyperthermophilic Archeon *Pyrococcus abyssi*. Extremophiles 11, 403–413.

Labows, J.N., K.J. McGinley, J.J. Leyden and G.F. Webster. 1979. Characteristic gamma-lactone odor production of the genus *Pityrosporum*. Appl. Environ. Microbiol. 38, 412–415.

Labrecque, O., D. Sylvestre and S. Messier. 2005. Systemic *Cryptococcus albidus* infection in a Doberman Pinscher. J. Vet. Diagn. Invest. 17, 598–600.

Labuschagne, M., and J. Albertyn. 2007. Cloning of an epoxide hydrolase-encoding gene from *Rhodotorula mucilaginosa* and functional expression in *Yarrowia lipolytica*. Yeast 24, 69–78.

Lachaise, D., M.C. Pignal and J. Rouault. 1979. Yeast flora partitioning by drosophilid species inhabiting a tropical African savanna of the Ivory Coast (Diptera). Ann. Soc. Entomol. Fr. 15, 659–680.

Lachance, M.-A. 1981. *Hanseniaspora nodinigri*, a new yeast species found in black knots (*Dibotryon morbosum*) of *Prunus virginiana*. Can. J. Microbiol. 27, 651–653.

Lachance, M.-A. 1982a. *Sporopachydermia quercuum*, a new yeast species found in exudates of *Quercus rubra*. Can. J. Microbiol. 28, 567–571.

Lachance, M.-A. 1982b. Reaction of an ascomycetous yeast with diazonium blue B. Can. J. Microbiol. 28, 1194–1195.

Lachance, M.-A. 1993a. *Kluyveromyces*-systematics since 1970. Antonie van Leeuwenhoek. 63, 95–104.

Lachance, M.-A. 1993b. *Metschnikowia agaveae* sp. nov., a heterothallic haploid yeast from blue agave. Can. J. Microbiol. 39, 562–566.

Lachance, M.-A. 1995. Yeast communities in a natural tequila fermentation. Antonie van Leeuwenhoek 68, 151–160.

Lachance, M.-A. 1998. *Kluyveromyces* van der Walt. In: C.P. Kurtzman and J.W. Fell (Eds), The Yeasts, A Taxonomic Study, 4th edn. Elsevier, Amsterdam, pp. 227–247.

Lachance, M.-A. (Ed.) 2001. Yeast Newslett. 50.

Lachance, M.-A. 2003. The Phaff school of yeast ecology. Int. Microbiol. 6, 163–167.

Lachance, M.-A. 2007. Current status of *Kluyveromyces* systematics. FEMS Yeast Res. 7, 642–645.

Lachance, M.-A. 1990. Ribosomal DNA spacer variation in the cactophilic yeast *Clavispora opuntiae*. Mol. Biol. Evol. 7, 178–193.

Lachance, M.-A., and J.M. Bowles. 2002. *Metschnikowia arizonensis* and *Metschnikowia dekortorum*, two new large-spored yeast species associated with floricolous beetles. FEMS Yeast Res. 2, 81–86.

Lachance, M.-A., and J.M. Bowles. 2004. *Metschnikowia similis* sp. nov. and *Metschnikowia colocasiae* sp. nov., two ascomycetous yeasts isolated from *Conotelus* spp. (Coleoptera: Nitidulidae) in Costa Rica. Stud. Mycol. 50, 69–76.

Lachance, M.-A., and W.M. Pang. 1997. Predacious yeasts. Yeast 13, 225–232.

Lachance, M.-A., and H.J. Phaff. 1998a. *Clavispora* Rodrigues de Miranda. In: C.P. Kurtzman and J.W. Fell (Eds), The Yeasts, A Taxonomic Study, 4th edn. Elsevier, Amsterdam, pp. 148–152.

Lachance, M.-A., and H.J. Phaff. 1998b. *Sporopachydermia* Rodrigues de Miranda. In: C.P. Kurtzman and J.W. Fell (Eds), The Yeasts, A Taxonomic Study, 4th edn. Elsevier, Amsterdam, pp. 395–399.

Lachance, M.-A., and W.T. Starmer. 1998. Ecology and yeasts. In: C.P. Kurtzman and J.W. Fell (Eds), The Yeasts, A Taxonomy Study, 4th Edn. Elsevier, Amsterdam, pp. 21–30.

Lachance, M.-A., and W.T. Starmer. 2008. The yeast genus *Kurtzmaniella* gen. nov. and description of the heterothallic, haplontic species *Kurtzmaniella cleridarum* sp. nov., the teleomorph of *Candida cleridarum*. Int. J. Syst. Evol. Microbiol. 58, 520–524.

Lachance, M.-A., M. Miranda, M.W. Miller and H.J. Phaff. 1976. Dehiscence and active spore release in pathogenic strains of the yeast *Metschnikowia bicuspidata* var. *australis*: possible predatory implication. Can. J. Microbiol. 22, 1756–1761.

Lachance, M.-A., H.J. Phaff, W.T. Starmer, A. Moffitt and L.G. Olson. 1986. Interspecific discontinuity in the genus *Clavispora* Rodrigues de Miranda by phenetic analysis, genomic deoxyribonucleic acid reassociation, and restriction mapping of ribosomal deoxyribonucleic acid. Int. J. Syst. Bacteriol. 36, 524–530.

Lachance, M.-A., W.T. Starmer and J.M. Bowles. 1988a. The yeast community of morning glory and associated drosophilids in a Hawaiian kipuka. Yeast 5, Special Issue, S501–S504.

Lachance, M.-A., W.T. Starmer and H.J. Phaff. 1988b. Identification of yeasts found in decaying cactus tissue. Can. J. Microbiol. 34, l025–l036.

Lachance, M.-A., C.A. Rosa, W.T. Starmer, B. Schlag-Edler, J.S.F. Barker and J.M. Bowles. 1988c. *Wickerhamiella australiensis*, *Wickerhamiella cacticola*, *Wickerhamiella occidentalis*, *Candida drosophilae*, and *Candida lipophila*, five new related yeast species from flowers and associated insects. Int. J. Syst. Bacteriol. 48, 1431–1443.

Lachance, M.-A., W.T. Starmer and H.J. Phaff. 1990. *Metschnikowia hawaiiensis* sp. nov., a heterothallic haploid yeast from Hawaiian morning glory and associated drosophilids. Int. J. Syst. Bacteriol. 40, 415–420.

Lachance, M.-A., H.J. Phaff and W.T. Starmer. 1993. *Kluyveromyces bacillisporus* sp. nov., a yeast from Emory oak exudate. Int. J. Syst. Bacteriol. 43, 115–119.

Lachance, M.-A., P. Nair and P. Lo. 1994. Mating in the heterothallic haploid yeast *Clavispora opuntiae*, with special reference to mating type imbalances in local populations. Yeast 10, 895–906.

Lachance, M.-A., D.G. Gilbert and W.T. Starmer. 1995. Yeast communities associated with *Drosophila* species and related flies in an eastern oak–pine forest: a comparison with western communities. J. Ind. Microbiol. 14, 484–494.

Lachance, M.-A., C.A. Rosa, W.T. Starmer and J.M. Bowles. 1998a. *Candida ipomoeae*, a new yeast species related to large-spored *Metschnikowia* species. Can. J. Microbiol. 44, 718–722.

Lachance, M.-A., C.A. Rosa, W.T. Starmer, B. Schlag-Edler, J.S.F. Barker and J.M. Bowles. 1998b. *Metschnikowia continentalis* var. *continentalis*, *Metschnikowia continentalis* var. *borealis*, and *Metschnikowia hibisci*, new heterothallic haploid

yeasts from ephemeral flowers and associated insects. Can. J. Microbiol. 44, 279–288.
Lachance, M.-A., J.M. Bowles, W.T. Starmer and J.S.F. Barker. 1999. *Kodamaea kakaduensis* and *Candida tolerans*, two new yeast species from Australian hibiscus flowers. Can. J. Microbiol. 45, 172–177.
Lachance, M.-A., J.M. Bowles, C. Mueller and W.T. Starmer. 2000a. On the biogeography of yeasts in the *Wickerhamiella* clade and description of *Wickerhamiella lipophila* sp. nov., the teleomorph of *Candida lipophila*. Can. J. Microbiol. 46, 1145–1148.
Lachance, M.-A., A. Pupovac-Velikonja, S. Natarajan and B. Schlag-Edler. 2000b. Nutrition and phylogeny of predacious yeasts. Can. J. Microbiol. 46, 495–505.
Lachance, M.-A., W.T. Starmer, J.M. Bowles, H.J. Phaff and C.A. Rosa. 2000c. Ribosomal DNA, species structure, and biogeography of the cactophilic yeast *Clavispora opuntiae*. Can. J. Microbiol. 46, 195–210.
Lachance, M.-A., J.M. Bowles, M.M. Chavarria Diaz and D.H. Janzen. 2001a. *Candida cleridarum*, *Candida tilneyi*, and *Candida powellii*, three new yeast species isolated from insects associated with flowers. Int. J. Syst. Evol. Microbiol. 51, 1201–1207.
Lachance, M.-A., J.M. Bowles, S. Kwon, G. Marinoni, W.T. Starmer and D.H. Janzen. 2001b. *Metschnikowia lochheadii* and *Metschnikowia drosophilae*, two new yeast species isolated from insects associated with flowers. Can. J. Microbiol. 47, 103–109.
Lachance, M.-A., J.E. Kaden, H.J. Phaff and W.Y. Starmer. 2001c. Phylogenetic structure of the *Sporopachydermia cereana* species complex. Int. J. Syst. Evol. Microbiol. 51, 237–247.
Lachance, M.-A., J.A. Klemens, J.M. Bowles and D.H. Janzen. 2001d. The yeast community of sap fluxes of Costa Rican *Maclura* (*Chlorophora*) *tinctoria* and description of two new yeast species, *Candida galis* and *Candida ortonii*. FEMS Yeast Res. 1, 87–92.
Lachance, M.-A., W.T. Starmer, C.A. Rosa, J.M. Bowles, J.S.F. Barker and D.H. Janzen. 2001e. Biogeography of the yeasts of ephemeral flowers and their insects. FEMS Yeast Res. 1, 18.
Lachance, M.-A., J.M. Bowles and W.T. Starmer. 2003a. Geography and niche occupancy as determinants of yeast biodiversity: the yeast–insect–morning glory ecosystem of Kipuka Puaulu, Hawai'i. FEMS Yeast Res. 4, 104–111.
Lachance, M.-A., J.M. Bowles and W.T. Starmer. 2003b. *Metschnikowia santaceciliae*, *Candida hawaiiana*, and *Candida kipukae*, three new yeast species associated with insects of tropical morning glory. FEMS Yeast Res. 3, 97–103.
Lachance, M.-A., H.M. Daniel, W. Meyer, G.S. Prasad, S.P. Gautam and K. Boundy-Mills. 2003c. The D1/D2 domain of the large-subunit rDNA of the yeast species *Clavispora lusitaniae* is unusually polymorphic. FEMS Yeast Res. 4, 253–258.
Lachance, M.A.,J. Dobson, D.N. Wijayanayaka and A.M. Smith. 2010. The use of parsimony network analysis for the formal delineation of phylogenetic species of yeasts: Candida apicola, Candida azyma, and Candida parazyma sp. nov., cosmopolitan yeasts associated with floricolous insects. Antonie Van Leeuwenhoek 97, 155–170.
Lachance, M.-A., C.P. Ewing, J.M. Bowles and W.T. Starmer. 2005. *Metschnikowia hamakuensis* sp. nov., *Metschnikowia kamakouana* sp. nov. and *Metschnikowia mauinuiana* sp. nov., three endemic yeasts from Hawaiian nitidulid beetles. Int. J. Syst. Evol. Microbiol. 55, 1369–1377.
Lachance, M.-A., T.M. Anderson and W.T. Starmer. 2006a. A new subclade of haplontic *Metschnikowia* species associated with insects of morning glory flowers in Africa and description of the yeast *Metschnikowia aberdeeniae* sp. nov. Int. J. Syst. Evol. Microbiol. 56, 1141–1145.
Lachance, M.-A., J.M. Bowles, F. Wiens, J. Dobson and C.P. Ewing. 2006b. *Metschnikowia orientalis* sp. nov., an Australasian yeast from nitidulid beetles. Int. J. Syst. Evol. Microbiol. 56, 2489–2493.
Lachance, M.-A., J.M. Bowles, T.M. Anderson and W.T. Starmer. 2008a. *Metschnikowia shivogae* sp. nov., a yeast species associated with insects of morning glory flowers in East Africa. Int. J. Syst. Evol. Microbiol. 58, 2241–2244.
Lachance, M.-A., D. Lawrie, J. Dobson and J. Piggott. 2008b. Biogeography and population structure of the neotropical endemic yeast species *Metschnikowia lochheadii*. Antonie van Leeuwenhoek 94, 403–414.
Lachance, M.-A., J. Dobson, D.N. Wijayanayaka and A.M.E. Smith. 2009. The use of parsimony network analysis for the formal delineation of phylogenetic species of yeasts: *Candida apicola, Candida azyma*, and *Candida parazyma* sp. nov., cosmopolitan yeasts associated with floricolous insects. Antonie van Leeuwenhoek 97, 155–170.
Laconi, S., and R. Pompei. 2007. Study and characterization of intestinal yeasts of mullet (*Mugil* spp.) for potential probiotic use. J. Food Agric. Environ. 5, 475–480.
Ladisch, M.R., and K.L. Kohlmann. 1992. Recombinant human insulin. Biotechnol. Prog. 8, 469–478.
Laffin, R.J., and V.M. Cutter. 1959a. Investigations on the life cycle of *Sporidiobolus johnsonii*. I. Irradiation and cytological studies. J. Elisha Mitchell Sci. Soc. 75, 89–96.
Laffin, R.J., and V.M. Cutter. 1959b. Investigations on the life cycle of *Sporidiobolus johnsonii*. II. Mutants and micromanipulation. J. Elisha Mitchell Sci. Soc. 75, 97–100.
Lagerheim, G. 1898. Mykologische studien I. Beiträge zur Kenntnis der parasitischen Pilze 1–3. Beih. K. Svenska Vet.-Akad. Handl 24, 1–21.
Lagerheim, N.G., de, and N. Patouillard. 1892. *Sirobasidium*, nouveau genre d'Hyménomycètes Heterobasidiés. J. Bot. 6, 465–469.
Lages, F., M. Silva-Gracia and C. Lucas. 1999. Active glycerol uptake is a mechanism underlying halotolerance in yeasts: a study of 42 species. Microbiology 145, 2577–2585.
Lagorce, A., V. Le Berre-Anton, B. Aguilar-Uscanga, H. Martin-Yken, A. Dagkessamanskaia and J. Francois. 2002. Involvement of GFA1, which encodes glutamine-fructose-6-phosphate amidotransferase, in the activation of the chitin synthesis pathway in response to cell-wall defects in *Saccharomyces cerevisiae*. Eur. J. Biochem. 269, 1697–1707.
Lagorce, A., N.C. Hauser, D. Labourdette, C. Rodriguez, H. Martin-Yken, J. Arroyo, J.D. Hoheisel and J. Francois. 2003. Genome-wide analysis of the response to cell wall mutations in the yeast *Saccharomyces cerevisiae*. J. Biol. Chem. 278, 20345–20357.
Lahav, R., P. Fareleira, A. Nejidat and A. Abeliovich. 2002. The identification and characterization of osmotolerant yeast

isolates from chemical wastewater evaporation ponds. Microb. Ecol. 43, 388–396.
Laitila, A., A. Wilhelmson, E. Kotaviita, J. Olkku, S. Home and R. Juvonen. 2006. Yeasts in an industrial malting ecosystem. J. Ind. Microbiol. Biotechnol. 33, 953–966.
Lake, J.A. 1994. Reconstructing evolutionary trees from DNA and protein sequences: paralinear distances. Proc. Natl. Acad. Sci. USA 91, 1455–1459.
Laluce, C. 1991. Current aspects of fuel ethanol-production in Brazil. Crit. Rev. Biotechnol. 11, 149–161.
Lambrechts, M.G., and I.S. Pretorius. 2000. Yeasts and its importance to wine aroma – a review. South Afr. J. Enol. Viticult. 21, 97–129.
Lanave, C., G. Preparata, C. Saccone and G. Serio. 1984. A new method for calculating evolutionary substitution rates. J. Mol. Evol. 20, 86–93.
Lanciotti, R., M. Sinigaglia, F. Gardini and M.E. Guerzoni. 1998. *Hansenula anomala* as spoilage agent of cream-filled cakes. Microbiol. Res. 153, 145–148.
Landell, M.F., J. Inácio, Á. Fonseca, M.H. Vainstein and P. Valente. 2009. *Cryptococcus bromeliarum* sp. nov., an orange-coloured basidiomycetous yeast isolated from bromeliads in Brazil. Int. J. Syst. Evol. Microbiol. 59, 910–913.
Landell, M.F., R. Billodre, J.P. Ramos, O. Leoncini, M.H. Vainstein and P. Valente. 2010. *Candida aechmeae* sp. nov. and *Candida vrieseae* sp. nov., novel yeast species isolated from the phylloplane of bromeliads in southern Brazil. Int. J. Syst. Evol. Microbiol. 60, 244–248.
Landrieu, M. 1912. Les Mycoses Oculaires. Thèse, Faculté de Médecine de Paris. Poinat, Paris.
Landvik, S. 1996. *Neolecta*, a fruit-body-producing genus of the basal ascomycetes, as shown by SSU and LSU rDNA sequences. Mycol. Res. 100, 199–202.
Landvik, S., O.E. Eriksson, A. Gargas and P. Gustafsson. 1993. Relationships of the genus *Neolecta* (Neolectales ordo nov., Ascomycotina) inferred from 18S rDNA sequences. Syst. Ascomyc. 11, 107–118.
Lang, S. 2002. Biological amphiphiles (microbial biosurfactants). Curr. Opin. Colloid Interface Sci. 7, 12–20.
Langer, G. 1994. Die Gattung *Botryobasidium* Donk (Corticiaceae, Basidiomycetes). Bibl. Mycol. 158, 1–459.
Langeron, M. 1922. Un nouveau *Sporotrichum* malgache, *S. carougeaui* Langeron 1913 et remarques sur loes Sporotriches. Bull Soc. Pathol. Exot. 15, 453–459.
Langeron, M., and P. Guerra. 1935. Bases morphologiques et biologiques de la classification des champignons levuriformes anascospores. Proc. 6th Int. Bot. Congress Amsterdam 2, 165–167.
Langeron, M., and P. Guerra. 1938. Nouvelles recherches de zymologie médicale. 2me Partie. Études monographiques sur les Mycotoruloidées. Le genre *Candida* Berkhout 1923. Ann. Parasitol. Hum. Comp. 16, 36–179, 429–476, 481–525.
Langeron, M., and P. Guerra. 1939. Remarques sur le *Candida stellatoidea* (Jones et Martin 1938.). Ann. Parasitol. Hum. Comp. 17, 257–260.
Langeron, M., and P. Guerra. 1940. Valeur et nature des variations et dissociations de colonies chez les champignons levuriformes. Ann. Parasitol. Hum. Comp. 17, 447–469.
Langeron, M., and P. Guerra. 1941. Les secteurs clairs et sombres des colonies de levures. Ann. Parasitol. Hum. Comp. 18, 95–111.
Langeron, M., and R.-V. Talice. 1932. Nouvelles méthodes d'étude et essai de classification des champignons levuriformes. Ann. Parasitol. Hum. Comp. 10, 1–80.
Lanzafame, M., G. Checchi, A. Parinello, M. Trevenzoli and A.M. Cattelan. 2001. *Rhodotorula glutinis*-related meningitis. J. Clin. Microbiol. 39, 410.
Lapointe, F.-J., and G. Cucumel. 1997. The average consensus procedure: combination of weighted trees containing identical or overlapping sets of taxa. Syst. Biol. 46, 306–312.
Larabell, C.A., and M.A. Le Gros. 2004. X-ray tomography generates 3-D reconstructions of the yeast, *Saccharomyces cerevisiae*, at 60-nm resolution. Mol. Biol. Cell 15, 957–962.
Larios, A., H.S. Garcia, R.M. Oliart and G. Valerio-Alfaro. 2004. Synthesis of flavor and fragrance esters using *Candida antarctica* lipase. Appl. Microbiol. Biotechnol. 65, 373–376.
Larocco, M., A. Dorenbaun, A. Robinson and L.K. Pickering. 1988. Recovery of *Malassezia pachydermatis* from eight infants in a neonatal intensive care nursery: clinical and laboratory features. Pediatr. Infect. Dis. J. 7, 398–401.
Larsson, K.H., E. Larsson and U. Kõljalg. 2004. High phylogenetic diversity among corticioid homobasidiomycetes. Mycol. Res. 108, 983–1002.
Las Heras-Vazquez, F.J., L. Mingorance-Cazoria, J.M. Clemente-Jimenez and F. Rodriguez-Vico. 2003. Identification of yeast species from orange fruit and juice by RFLP and sequence analysis of the 5.8S rRNA gene and the two internal transcribed spacers. FEMS Yeast Res. 3, 3–9.
Last, F.T. 1955. Seasonal incidence of *Sporobolomyces* on cereal leaves. Trans. Br. Mycol. Soc. 38, 221–239.
Last, F.T., and D. Price. 1969. Yeasts associated with living plants and their environs. In: A.H. Rose and J.S. Harrison (Eds), The Yeasts, 1st edn. Vol. 1. Academic Press, London, pp. 183–218.
Latham, B.P. 1998. Yeast community persistence in a spatially structure environment. Microb. Ecol. 36, 60–65.
Laufenberg, G., P. Rosato and B. Kunz. 2004. Adding value to vegetable waste: oil press cakes as substrates for microbial decalactone production. Eur. J. Lipid Sci. Technol. 106, 207–217.
Laurent, E. 1889. Observations sur le champignon du muguet. Bull. Soc. Belge Microscop. 16, 14–18.
Lautenbach, E., I. Nachamkin, M.G. Schuster, P.M. Groshek, T.J. Lester, H.J. Chang, C.F. von Reyn, W.R. Jarvis, L.C. Marcus and E. Marcus. 1998. *Malassezia pachydermatis* infections. N. Engl. J. Med. 339, 270–271.
Lavie, P. 1950. Sur un organisme énigmatique *Acaromyces laviae*, qui semble s'attaquer à l'*Acarapis woodi*. L'Apiculteur 3, 41–45.
Lavie, P. 1954. Essais de lutte biologique contre l'*Acarapis woodii*, agent de l'acariose de l'abeille. C.R. Acad. Sci. 238, 947–948.
Lazera, M.S., F.D.A. Pires, L. Camillo-Coura, M.M. Nishikawa, C.C.F. Bezzerra, L. Trilles and B. Wanke. 1996. Natural habitat of *Cryptococcus neoformans* var. *neoformans* in decaying wood forming hollows in living trees. J. Med. Vet. 34, 127–131.
Le Jeune, C., M. Lollier, C.C. Demuyter, J.-L. Erny Legras, M. Aigle and I. Masneuf-Pomarède. 2007. Characterization of natural hybrids of *Saccharomyces cerevisiae* and *Saccharomyces bayanus* var. *uvarum*. FEMS Yeast Res. 7, 540–549.

Le Quesne, W.J. 1974. The uniquely evolved character concept and its cladistic application. Syst. Zool. 23, 513–517.

Leask, B.G.S., and D. Yarrow. 1976. *Pichia norvegensis* sp. nov. Sabouraudia 14, 61–63.

Leathers, T.D. 2003. Bioconversions of maize residues to value-added coproducts using yeast-like fungi. FEMS Yeast Res. 3, 133–140.

Leathers, T.D., and S.C. Gupta. 1997. Xylitol and riboflavin accumulation in xylose-grown cultures of *Pichia guilliermondoii*. Appl. Microbiol. Biotech. 47, 58–61.

Leberle, H. 1909. Beiträge zur Kenntnis der Gattung *Mycoderma*. Kastner u. Callway, München.

Lederberg, J., R.E. Shope and S.C. Oaks. 1992. Emerging Infections: Microbial Threats to Health in the United States. National Academy Press, Washington, DC.

Lee, B.-K., and J.-K. Kim. 2001. Production of *Candida utilis* biomass on molasses in different culture types. Aquacult. Eng. 25, 111–124.

Lee, C.-F., F.-L. Lee, W.-H. Hsu and W.-H. Hsu. 1993. DNA reassociation and electrokaryotype study of some *Candida* species and synonymy of *Candida terebra*, *Candida entomaea*, and *Candida veronae*. Can. J. Microbiol. 39, 864–867.

Lee, C.-F., F.-L. Lee, W.-H. Hsu and H.J. Phaff. 1994a. *Arthroascus fermentans*, a new yeast species isolated from soil in Taiwan. Int. J. Syst. Bacteriol. 44, 303–307.

Lee, C.-F., F.-L. Lee and W.-H. Hsu. 1994b. Synonymy of *Candida methylica* with *Candida boidinii* and of *Candida methanolophaga* with *Candida succiphila*. Int. J. Syst. Bacteriol. 44, 839–841.

Lee, C., C. Grasso and M. Sharlow. 2002. Multiple sequence alignment using partial order graphs. Bioinformatics 18, 452–464.

Lee, C.-F., C.-H. Liu, S.-S. Young and K.-S. Chang. 2008. *Kazachstania jiainicus* sp. nov., an ascomycetous yeast species isolated from soil in Taiwan. FEMS Yeast Res. 8, 114–118.

Lee, C.-F., C.-H. Yao, Y.-R. Liu, S.-S. Young and K.-S. Chang. 2009a. *Kazachstania wufongensis* sp. nov., an ascosporogenous yeast isolated from soil in Taiwan. Antonie van Leeuwenhoek 95, 335–341.

Lee, C.-F., C.-H. Yao, Y.-R. Liu, C.-W. Hsieh and S.-S. Young. 2009b. *Lachancea dasienssis* sp. nov., an ascosporogenous yeast isolated from soil and leaves in Taiwan. Int. J. Syst. Evol. Microbiol. 59, 1818–1822.

Lee, D., M.-K. Lee, K.-J. Kang, C.-S. Shin, J.-H. Yun, D.-Y. Yum, J.-K. Lee, K.-D. Park, J.-D. Choi and B.T. Koo. 2000. Novel strain for decomposing TMAH, and method of wastewater treatment using the same. US Patent 20030008377.

Lee, F.-L., and S.-C. Jong. 1985. *Dekkera claussenii* sp. nov., the perfect state of *Brettanomyces claussenii*. Mycotaxon 23, 275–278.

Lee, F.-L., and S.-C. Jong. 1986a. New species of *Dekkera custersiana* and *D. lambica*, teleomorphs of *Brettanomyces*. Mycotaxon 25, 455–460.

Lee, F.-L., and S.-C. Jong. 1986b. The new species *Dekkera abstinens*, teleomorph of *Brettanomyces abstinens*. Mycologia 78, 150–151.

Lee, F.-L., H.-M. Fu and W.-H. Hsu. 1998. DNA hydribization and electrokaryotype study of some *Candida* species. Int. J. Syst. Bacteriol. 48, 1463–1466.

Lee, F.-L., C.-F. Lee, S. Okada, W.-H. Hsu and M. Kozaki. 1992. Chemotaxonomic comparison of osmotolerant yeasts isolated from "Inyu" (black soybean sauce) mash in Taiwan and "Shoyu" (soybean sauce) mash in Japan. Bull. Jpn. Fed. Cult. Coll. 8, 11–17.

Lee, F.-L., C.-F. Lee, S. Okada, T. Uchimura, K. Komagata and M. Kozaki. 1993. *Candida galacta* comb. nov., a new combination for *Candida apis* var. *galacta*. Int. J. Syst. Bacteriol. 43, 183–184.

Lee, H., and H. Schneider. 1987. Ethanol production from xylitol and some other polyols. Biotechnol. Lett. 9, 581–584.

Lee, J.-D., and K. Komagata. 1980a. Taxonomic study of methanol-assimilating yeasts. J. Gen. Appl. Microbiol. 26, 133–158.

Lee, J.-D., and K. Komagata. 1980b. *Pichia cellobiosa*, *Candida cariosilignicola* and *Candida succiphila*, new species of methanol-assimilating yeasts. Int. J. Syst. Bacteriol. 30, 514–519.

Lee, J.-D., and K. Komagata. 1983. Further taxonomic study of methanol-assimilating yeasts with special reference to electrophoretic comparison of enzymes. J. Gen. Appl. Microbiol. 29, 395–416.

Lee, M.G., and P. Nurse. 1987. Complementation used to clone a human homologue of the fission yeast cell cycle control gene cdc2. Nature 327, 31–35.

Lee, M.-H. 1974. A new species of yeast: *Rhodotorula sinensis* Lee sp. nov. Acta Microbiol. Sin. 14, 143–156.

Lee, M.S.Y. 2001. Unalignable sequences and molecular evolution. Trends Ecol. Evol. 16, 681–685.

Lee, N., G. Bakkeren, K. Wong, J.E. Sherwood and J.W. Kronstad. 1999. The mating-type and pathogenicity locus of the fungus *Ustilago hordei* spans a 500-kb region. Proc. Natl. Acad. Sci. USA 96, 15026–15031.

Leeming, J.P., and F.H. Notman. 1987. Improved methods for isolation and enumeration of *Malassezia furfur* from human skin. J. Clin. Microbiol. 25, 2017–2019.

Leeuw, N.J., J.L.F. Kock, C.H. Pohl, A.S. Bareetseng, O.M. Sebolai, M. Joseph, C.J. Strauss, P.J. Botes, P.W.J. van Wyk and S. Nigam. 2006. Oxylipin covered ascospores of *Eremothecium coryli*. Antonie van Leeuwenhoek 89, 91–97.

Legakis, Ph.A. 1961. A contribution to the study of the yeast flora of apples and apple wine. Thesis, University of Athens. In Greek.

Legan, J.D., and P.A. Voysey. 1991. Yeast spoilage of bakery products and ingredients. J. Appl. Bacteriol. 70, 361–371.

Legras, J.L., O. Ruh, D. Merdinoglu and F. Karst. 2005. Selection of hypervariable microsatellite loci for the characterization of *Saccharomyces cerevisiae* strains. Int. J. Food Microbiol. 102, 73–83.

Legras, J.-L., D. Medinoglu, J.-M. Cornuet and F. Karst. 2007. Bread beer and wine: *Saccharomyces* diversity reflects human history. Mol. Ecol. 16, 2091–2102.

Leher, S.B., W.E. Horner and G. Reese. 1996. Why are some proteins allergenic? Implications for biotechnology. Crit. Rev. Food Sci. Nutr. 36, 553–564.

Lehmann, P.F., L.E. Cowan, R.M. Jones and W.J. Ferencak III. 1987. Use of killer fungi and antifungal chemicals in characterization of yeast species and biotypes. Trans. Br. Mycol. Soc. 88, 199–206.

Lehmann, P.F., L.-C. Wu, W.R. Pruitt, S.A. Meyer and D.G. Ahearn. 1993. Unrelatedness of groups of yeasts within the *Candida haemulonii* complex. J. Clin. Microbiol. 31, 1683–1687.

Leibinger, W., B. Breuker, M. Hahn and K. Mendgen. 1997. Control of postharvest pathogens and colonization of the

apple surface by antagonistic microorganisms in the field. Phytopathology 87, 1103–1110.

Leisola, M., and O. Turunen. 2007. Protein engineering: opportunities and challenges. Appl. Microbiol. Biotechnol. 75, 1225–1232.

Lelieveld, H.L.M. 2000. Hygienic design of factories and equipment. In: B.M. Lund, T.C. Baird-Parker and G.W. Gould (Eds), The Microbiological Safety and Quality of Food, Vol. 2. Aspen Publishers, Maryland, pp. 1656–1690.

Lembke, A. 1943. Ergebnisse der Theoretischen und Angewandten Mikrobiologie. Bd. I. Systematik der Schimmelpilze. Verlag J. Neumann, Neudamm.

Lemmon, A.R., and M.C. Milinkovitch. 2002. The metapopulation genetic algorithm: an efficient solution for the problem of large phylogeny estimation. Proc. Natl. Acad. Sci. USA 99, 10516–10521.

Lengeler, K.B., G.M. Cox and J. Heitman. 2001. Serotype AD strains of *Cryptococcus neoformans* are diploid or aneuploid and are heterozygous at the mating-type locus. Infect. Immun. 69, 115–122.

Lengeler, K.B., D.S. Fox, J.A. Fraser, A. Allen, K. Forrester, F.S. Dietrich and J. Heitman. 2002. Mating-type locus of *Cryptococcus neoformans*: a step in the evolution of sex chromosomes. Eukaryot. Cell 1, 704–718.

Leonard, E., Y. Yan, K.H. Lim and M A.G. Koffas. 2005. Investigation of two distinct flavone synthases for plant-specific flavone biosynthesis in *Saccharomyces cerevisiae*. Appl. Environ. Microbiol. 71, 8241–8248.

Lepingle, A., S. Casaregola, C. Neuveglise, E. Bon, H. Nguyen, F. Artiguenave, P. Wincker and C. Gaillardin. 2000. Genomic exploration of the hemiascomycetous yeasts: 14 *Debaryomyces hansenii* var. *hansenii*. FEBS Lett. 487, 82–86.

Lesage, G., and H. Bussey. 2006. Cell wall assembly in *Saccharomyces cerevisiae*. Microbiol. Mol. Biol. Rev. 70, 317–343.

Lestini, B.J., and J.A. Church. 2006. *Trichosporon pullulans* as a complication of chronic granulomatous disease in a patient undergoing immunosuppressive therapy for inflammatory bowel disease. Pediatr. Infect. Dis. J. 1, 87–89.

Lettieri, T. 2006. Recent applications of DNA microarray technology to toxicology and ecotoxicology. Environ. Health Perspect. 114, 4–9.

Leufven, A., G. Berstrom and E. Falsen. 1984. Interconversion of verbenols and verbenone by identified yeasts isolated from the spruce bark beetle, *Ips typographus*. J. Chem. Ecol. 10, 1349–1361.

Leupold, U. 1950. Die Vererbung von Homothallic und Heterothallic bei *Schizosaccharomyces pombe*. C.R. Trav. Lab. Carlsberg, Ser. Physiol. 24, 381–480.

Leverentz, B., W.J. Janisiewicz, W.S. Conway, R.A. Saftner, Y. Fuchs, C.E. Sams and M.J. Camp. 2000. Combining yeasts or a bacterial biocontrol agent and heat treatment to reduce postharvest decay of "Gala" apples. Postharvest Biol. Technol. 21, 87–94.

Levin, D.E. 2005. Cell wall integrity signaling in *Saccharomyces cerevisiae*. Microbiol. Mol. Biol. Rev. 69, 262–291.

Levine, B. 2005. Eating oneself and uninvited guests: autophagy-related pathways in cellular defense. Cell 120, 159–162.

Levinson, W.E., C.P. Kurtzman and T.M. Kuo. 2006. Production of itaconic acid by *Pseudozyma antarctica* NRRL Y-7808 under nitrogen-limited growth conditions. Enzyme Microb. Technol. 39, 824–827.

Levinson, W.E., C.P. Kurtzman and T.M. Kuo. 2007. Characterization of *Yarrowia lipolytica* and related species for citric acid production from glycerol. Enzyme Microb. Technol. 41, 292–295.

Levitz, S.M., S. Nong, M.K. Mansour, C. Huang and C.A. Specht. 2001. Molecular characterization of a mammoprotein with homology to chitin deacetylases that stimulates T cell responses to *Cryptococcus neoformans*. Proc. Natl. Acad. Sci. USA 98, 10422–10427.

Levy, J., D. Benharroch, N. Peled and T. Lifshitz. 2006. *Blastoschizomyces capitatus* keratitis and melting in a corneal graft. Can. J. Ophthalmol. 41, 772–774.

Lewis, D.F.V. 2001. Guide to cytochromes P450: structure and function. Taylor and Francis, London.

Lewis, H., M.D. McCurdy and J.D. Morrow. 2001. Ventriculitis due to *Cryptococcus uniguttulatus*. South. Med. J. 94, 65–66.

Lewis, Y.S., and D.S. Johar. 1955. An acid tolerant yeast from tamarind. Sci. Cult. 21, 220–222.

Li, B.Q., and S.P. Tian. 2006. Efficacy of threhalose on stress tolerance and biocontrol efficacy of *Cryptococcus laurentii*. J. Appl. Microbiol. 100, 854–861.

Li, B.Q., and S.P. Tian. 2007. Effect of intracellular trehalose in *Cryptococcus laurentii* and exogenous lyoprotectants on its viability and biocontrol efficacy on *Penicillium expansum* in apple fruit. Lett. Appl. Microbiol. 44, 437–442.

Li, M. 1982. Studies on Sporobolomycetaceae 1. Taxonomy of *Bullera*. Acta Microbiol. Sin. 22, 17–25.

Li, M., X. Fu and X.R. Tang. 1990. The yeasts in Shennongjia, China, and a new species of *Kluyveromyces*. Acta Microbiol. Sin. 30, 94–97.

Li, M., J.H. Badger, X. Chen, S. Kwong, P. Kearney and H.Y. Zhang. 2001. An information-based sequence distance and its application to whole mitochondrial genome phylogeny. Bioinformatics 17, 149–154.

Li, P.Z., A. Anumanthan, X.G. Gao, K. Ilangovan, V.V. Suzara, N. Duzgunes and V. Renugopalakrishan. 2007. Expression of recombinant proteins in *Pichia pastoris*. Appl. Biochem. Biotechnol. 142, 105–124.

Li, S., D.K. Pearl and H. Doss. 2000. Phylogenetic tree construction using Markov Chain Monte Carlo. J. Am. Stat. Assoc. 95, 493–508.

Li, W.-H., and A. Zharkikh. 1994. What is the bootstrap technique? Syst. Biol. 43, 424–430.

Liao, W., J. Shao, S. Wu, J. Zhang and S. Li. 1983. *Cryptococcus neoformans* var. *shanghaiensis* caused meningitis. Chin. Med. J. (English Edn) 96, 287–290.

Libkind, D., and M.R. van Broock. 2006. Biomass and carotenoid pigments production by Patagonian native yeasts. World J. Microbiol. Biotechnol. 22, 687–692.

Libkind, D., S. Brizzio, A. Ruffini, M. Gadanho, M. van Broock and J.P. Sampaio. 2003. Molecular characterization of carotenogenic yeasts from aquatic environments in Patagonia, Argentina. Antonie van Leeuwenhoek 84, 313–322.

Libkind, D., R. Sommaruga, H. Zagarese and M.R. van Broock. 2005a. Mycosporines in carotenogenic yeasts. Syst. Appl. Microbiol. 28, 749–754.

Libkind, D., M. Gadanho, M. van Broock and J.P. Sampaio. 2005b. *Sporidiobolus longiusculus* sp. nov. and *Sporobolomyces patagonicus* sp. nov., two novel yeasts of the Sporidiobolales isolated from aquatic environments in Patagonia, Argentina. Int. J. Syst. Evol. Microbiol. 55, 503–509.

Libkind, D., M. Diéguez, M. Moliné, P. Pérez, H. Zagarese and M. van Broock. 2006. Occurrence of photoprotective compounds in yeasts from freshwater ecosystems of northwestern Patagonia (Argentina). Photochem. Photobiol. 82, 972–980.

Libkind, D., A. Ruffin, A. van Brook, L. Alves and J.P. Sampaio. 2007. Biogeography, host specificity and molecular phylogeny of the basidiomycetous yeast *Phaffia rhodozyma* and its sexual form, *Xanthophyllomyces dendrorhous*. Appl. Environ. Microbiol. 73, 1120–1125.

Libkind, D., M. Gadanho, M. van Broock and J.P. Sampaio. 2009. *Cystofilobasidium lacus-mascardii* sp. nov., a new teleomorphic basidiomycetous yeast species isolated from aquatic environments in the Patagonian Andes, and *Cystofilobasidium macerans* sp. nov., the sexual stage of *Cryptococcus macerans*. Int. J. Syst. Evol. Microbiol. 59, 622–630.

Liese, A., K. Weelbach and C. Wandrey. 2000. Industrial BioTransformations, 2nd edn. WileyVCH Verlag, Weinheim.

Ligon, J.M., P.L. Bolen, D.S. Hill, R.J. Bothast and C.P. Kurtzman. 1989. Physical and biological characterization of linear DNA plasmids of the yeast *Pichia inositovora*. Plasmid 21, 185–194.

Liljeqvist, S., and S. Stahl. 1999. Production of recombinant subunit vaccines: protein immunogens, live delivery systems and nucleic acid vaccines. J. Biotechnol. 73, 1–33.

Lilly, M., F.F. Bauer, M.G. Lambrechts, J.H. Swiegers, D. Cozzolino and I.S. Pretorius. 2006. The effect of increased alcohol acetyltransferase and esterase activity on the flavour profiles of wine and distillates. Yeast 23, 641–659.

Lim, J., T. Kim and S. Hwang. 2003. Treatment of fish-processing wastewater by co-culture of *Candida rugopelliculosa* and *Brachionus plicatilis*. Water Res. 37, 2228–2232.

Lima, G., A. Ippolito, F. Nigro and M. Salerno. 1997. Effectiveness of *Aureobasidium pullulans* and *Candida oleophila* against postharvest strawberry rots. Postharvest Biol. Technol. 10, 169–178.

Lima, G., F. de Curtis, R. Castoria and V. de Cicco. 1998. Activity of the yeast *Cryptococcus laurentii* and *Rhodororula glutinis* against post-harvest rots on different fruits. Biocontrol Sci. Technol. 8, 257–267.

Limper, A.H., F. Lebron, S.E. Evans and R.Y. Hahn. 2003. *Pneumocystis carinii*: cell wall beta-glucan-mediated pulmonary inflammation. J. Eukaryot. Microbiol. 50 (Suppl.), 646.

Limtong, S., N. Srisuk, W. Yongmanitchai, H. Kawasaki, H. Yurimoto, T. Nakase and N. Kato. 2004. Three new thermotolerant methylotrophic yeasts, *Candida, krabiensis* sp. nov., *Candida sithepensis* sp. nov., and *Pichia siamensis* sp. nov., isolated in Thailand. J. Gen. Appl. Microbiol. 50, 119–127.

Limtong, S., N. Srisuk, W. Yongmanitchai, H. Yurimoto, T. Nakase and N. Kato. 2005. *Pichia thermomethanolica* sp. nov., a novel thermotolerant methylotrophic yeast isolated in Thailand. Int. J. Syst. Evol. Microbiol. 55, 2225–2229.

Limtong, S., W. Yongmanitchai, H. Kawasaki and T. Seki. 2007a. *Candida thaimueangensis* sp. nov., an anamorphic yeast species from estuarine water in a mangrove forest in Thailand. Int. J. Syst. Evol. Microbiol. 57, 650–653.

Limtong, S., W. Yongmanitchai, M.M. Tun, H. Kawasaki and T. Seki. 2007b. *Kazachstania siamensis* sp. nov., an ascomycetous yeast species from forest soil in Thailand. Int. J. Syst. Evol. Microbiol. 57, 419–422.

Limtong, S., N. Srisuk, W. Yongmanitchai, H. Yurimoto and T. Nakase. 2008a. *Ogataea chonburiensis* sp. nov. and *Ogataea nakhonphanomensis* sp. nov., thermotolerant, methylotrophic yeast species isolated in Thailand, and transfer of *Pichia siamensis* and *Pichia thermomethanolica* to the genus *Ogataea*. Int. J. Syst. Evol. Microbiol. 58, 302–307.

Limtong, S., Y. Imanishi, S. Jindamorakot, S. Ninomiya, W. Yongmanitchai and T. Nakase. 2008b. *Torulaspora maleeae* sp. nov., a novel ascomycetous yeast species from Japan and Thailand. FEMS Yeast Res. 8, 337–343.

Limtong, S., W. Youngmanitchai, H. Kawasaki and T. Seki. 2008c. *Candida phangngensis* sp. nov., an anamorphic yeast species in the *Yarrowia* clade, isolated from water in mangrove forests in Phang-Nga Province, Thailand. Int. J. Syst. Evol. Microbiol. 58, 515–519.

Limtong, S., and W. Yongmanitchai. 2010. *Candida chanthaburiensis* sp. nov., *Candida kungkrabaensis* sp. nov. and *Candida suratensis* sp. nov., three novel yeast species from decaying plant materials submerged in water of mangrove forests. Antonie van Leeuwenhoek 98, 379–388.

Limtong, S., R. Kaewwichian, S. Am-In, C. Boonmak, S. Jindamorakot, W. Yongmanitchai, N. Srisuk, H. Kawasaki and T. Nakase. 2010a. Three anamorphic yeast species, *Candida sanitii* sp. nov., *Candida sekii* sp. nov. and *Candida suwanaritii*, three novel yeasts in the *Saturnispora* clade isolated in Thailand. FEMS Yeast Res. 10, 114–122.

Limtong, S., R. Kaewwichian, S. Am-In, T. Nakase, C.F. Lee and W. Yongmanitchai. 2010b. *Candida asiatica* sp. nov., an anamorphic ascomycetous yeast species isolated from natural samples from Thailand, Taiwan, and Japan. Antonie van Leeuwenhoek doi: 10.1007/s10482-010-9463-z.

Lin, D., L.-C. Wu, M.G. Rinaldi and P.F. Lehmann. 1995. Three distinct genotypes within *Candida parapsilosis* from clinical sources. J. Clin. Microbiol. 33, 1815–1821.

Lin, X., and J. Heitman. 2005. Chlamydospore formation during hyphal growth in *Cryptococcus neoformans*. Eukaryot. Cell 4, 1746–1754.

Lin, X., and J. Heitman. 2006. The biology of the *Cryptococcus neoformans* species complex. Annu. Rev. Microbiol. 60, 69–105.

Lin, X., C.M. Hull and J. Heitman. 2005. Sexual reproduction between partners of the same mating type in *Cryptococcus neoformans*. Nature 434, 1017–1021.

Lin, X., A.P. Litvintseva, N. Kristen, S. Patel, A. Floyd, T.G. Mitchell and J. Heitman. 2007. Alpha AD alpha hybrids of *Cryptococcus neoformans*: evidence of same-sex mating in nature and hybrid fitness. PLoS Genet. 3, 1975–1990.

Lin, Y.H., F.-L. Lee and W.-H. Hsu. 1996. Molecular and chemical taxonomic differentiation of *Candida boidinii* Ramírez strains. Int. J. Syst. Bacteriol. 46, 352–355.

Lindahl, A.L., M.E. Olsson, P. Mercke, O. Tollbom, J. Schelin, M. Brodelius and P.E. Brodelius. 2006. Production of the artemisinin precursor amorpha-4,11-diene by engineered *Saccharomyces cerevisiae*. Biotechnol. Lett. 28, 571–580.

Lindau, G. 1907. Fungi imperfecti: Hyphomycetes. In: L. Rabenhorst (Ed.), Kryptogamen-Flora von Deutschland, Österreich und der Schweiz, 1 Pilze, VIII Abt. Ed. Kummer, Leipzig.

Lindberg, J., F. Hagen, A. Laursen, J. Stenderup and T. Boekhout. 2007. *Cryptococcus gattii* risk for tourists visiting Vancouver Island, Canada. Emerg. Infect. Dis. 13, 178–179.

Lindegren, C.C., and G. Lindegren. 1943. Selecting, inbreeding, recombining, and hybridizing commercial yeasts. J. Bacteriol. 46, 405–419.

Lindner, P. 1893. *Schizosaccharomyces pombe* n. sp. neuer Gärungserreger. Wochenschr. Brau. 10, 1298–1300.

Lindner, P. 1894. *Saccharomyces farinosus* und *Saccharomyces bailii*. Zwei neue Hefenarten aus Danziger Jopenbier. Wochenschr. Brau. 11, 153–156.

Lindner, P. 1895. Mikroskopische Betriebskontrolle in den Gärungsgewerben mit einer Einführung in die Hefenreinkultur, Infektionslehre und Hefenkunde. P. Parey, Berlin.

Lindner, P. 1898a. Mikroskopische Betriebskontrolle in den Gärungsgewerben, 2te Aufl. P. Parey, Berlin.

Lindner, P. 1898b. *Monilia variabilis*, eine formenreiche und rassenhaltige neue Pilzart. Wochenschr. Brau. 15, 209–213.

Lindner, P. 1901. Mikroskopische Betriebskontrolle in den Gärungsgewerben, 3te Aufl. P. Parey, Berlin.

Lindner, P. 1904. Neue Erfahrungen aus dem letzten Jahre in Bezug der Hefen und Gärung. Jahrb. Vers. Lehranst. Brau. Berlin 7, 441–464.

Lindner, P. 1905a. Die Assimilierbarkeit der Selbstverdauungsprodukte der Bierhefe durch verschiedene Heferassen und Pilze. Mitteilung 1. Wochenschr. Brau. 22, 528–530.

Lindner, P. 1905b. Mikroskopische Betriebskontrolle in den Gärungsgewerben, 5te Aufl. P. Parey, Berlin.

Lindner, P. 1906. Einiges über den Weinbukettschimmel (*Sachsia suaveolens*). Wochenschr. Brauerei 21, 1–3.

Lindner, P. 1907. *Endomyces fibuliger* n. sp., ein neuer Gärungspilz und Erzeuger der sog. Kreidekrankheit des Brotes. Wochenschr. Brau. 24, 469–474.

Lindner, P., and E.G. Genoud. 1913. Zur Charakteristik der *Willia belgica* und einiger Hefen aus belgischem Lambicbier. Wochenschr. Brau. 30, 363–367.

Lindsberg, P.J., I. Pieninkeroinen and M. Valtonen. 1997. Meningoencephalitis caused by *Cryptococcus macerans*. Scand. J. Infect. Dis. 29, 430–433.

Link, H.F. 1809. Observationes in ordines plantarum naturales. Mag. Ges. Naturf. Freunde 3, 3–23.

Link, H.F. 1824. Species Plantarum, Vol. 6, Berolini.

Linko, M., A. Haikara, A. Ritala and M. Penttilä. 1998. Recent advances in the malting and brewing industry. J. Biotechnol. 65, 85–95.

Linster, C.L., and E. van Schaftingen. 2007. Vitamin C. Biosynthesis, recycling and degradation in mammals. FEBS J. 274, 1–22.

Linton, C.J., A.M. Borman, G. Cheung, A.D. Holmes, A. Szekely, M.D. Palmer, P.D. Bridge, C.K. Campbell and E.M. Johnson. 2007. Molecular identification of unusual pathogenic yeast isolates by large ribosomal subunit gene sequencing: 2 years of experience at the United Kingdom Mycology Reference Laboratory. J. Clin. Microbiol. 45, 1152–1158.

Liou, G.-Y., Y.-H. Wei, S.-J. Lin, C.-Y. Wen and F.-L. Lee. 2009. *Pseudozyma pruni* sp. nov., a novel ustilaginomycetous anamorphic fungus from flowers in Taiwan. Int. J. Syst. Evol. Microbiol. 59, 1813–1817.

Lisichkina, G.A., I.P. Bab'eva and D.Iu. Sorokin. 2003. Alkalitolerant yeasts from natural biotopes. Mikrobiologiia 72, 695–698. In Russian.

Liti, G., D.B. Barton and E.J. Louis. 2006. Sequence diversity, reproductive isolation and species concepts in *Saccharomyces*. Genetics 174, 839–850.

Litvintseva, A.P., R.E. Marra, K. Nielsen, J. Heitman, R. Vilgalys and T.G. Mitchell. 2003. Evidence of sexual recombination among *Cryptococcus neoformans* serotype A isolates in sub-Saharan Africa. Eukaryot. Cell 2, 1162–1168.

Litvintseva, A.P., L. Kestenbaum, R. Vilgalys and T.G. Mitchell. 2005a. Comparative analysis of environmental and clinical populations of *Cryptococcus neoformans*. J. Clin. Microbiol. 43, 556–564.

Litvintseva, A.P., R. Thakur, L.B. Reller and T.G. Mitchell. 2005b. Prevalence of clinical isolates of *Cryptococcus gattii* serotype C among patients with AIDS in sub-Saharan Africa. J. Infect. Dis. 192, 888–892.

Litvintseva, A.P., R. Thakur, R. Vilgalys and T.G. Mitchell. 2006. Multilocus sequence typing reveals three genetic subpopulations of *Cryptococcus neoformans* var. *grubii* (serotype A), including a unique population in Botswana. Genetics 172, 2223–2238.

Litvintseva, A.P., X. Lin, I. Templeton, J. Heitman and T.G. Mitchell. 2007. Many globally isolated AD hybrid strains of *Cryptococcus neoformans* originated in Africa. PloS Pathog. 3, 8, e114.

Liu, C.H., S.S. Young, T.C. Chang and C.F. Lee. 2008. *Candida dajiaensis* sp. nov., *Candida yuanshanicus* sp. nov., *Candida jianshihensis* sp. nov., and *Candida sanyiensis* sp. nov., four anamorphic, ascomycetous yeast species isolated from soil in Taiwan. FEMS Yeast Res. 8, 815–822.

Liu, L., Q. Xu, Y. Li, Z. Shi, Y. Zhu, G. Du and J. Chen. 2007. Enhancement of pyruvate production by osmotic-tolerant mutant of *Torulopsis glabrata*. Biotechnol. Bioeng. 97, 825–832.

Liu, Y.J., and B.D. Hall. 2004. Body plan evolution of ascomycetes, as inferred from an RNA polymerase II phylogeny. Proc. Natl. Acad. Sci. USA 101, 4507–4512.

Liu, Z., and C.P. Kurtzman. 1991. Phylogenetic relationships among species of *Williopsis* and *Saturnospora* gen. nov. as determined from partial rRNA sequences. Antonie van Leeuwenhoek 60, 21–30.

Liu, Z., G. Zhang and S. Liu. 2004. Constructing an amylolytic brewing yeast *Saccharomyces pastorianus* suitable for accelerated brewing. J. Biosci. Bioeng. 98, 414–419.

Llorente, B., A. Malpertuy, G. Blandin, F. Artiguenave, P. Wincker and B. Dujon. 2000. Genomic exploration of the hemiascomycetous yeasts: 12. *Kluyveromyces marxianus* var. *marxianus*. FEBS Lett. 487, 71–75.

Lloyd C.G. (as "McGinty") 1922. *Tremella cinnabarina* (Mont.) Lloyd. Mycol. Writ. 7, 1150.

Lloyd, C.G. 1919. *Tremella samoensis* fig. 1495. Mycol. Writ. 5, 875.

LoBuglio, K.F., and J.W. Taylor. 1995. Phylogeny and PCR identification of the human pathogenic fungus *Penicillium marneffei*. J. Clin. Microbiol. 33, 85–89.

Lochhead, A.G. 1942. *Zygosaccharomyces nectarophilus* n. sp. and *Zygosaccharomyces rugosus* n. sp. Can. J. Res. 20, 89–91.

Lochhead, A.G., and D.A. Heron. 1929. Microbiological studies of honey. Bull. 116 – New Series. Dept. Agric. Dom., Canada.

Lockhart, P.J., and D. Penny. 2005. The place of *Amborella* within the radiation of angiosperms. Trends Plant Sci. 10, 201–202.

Lockhart, P.J., M.A. Steel, M.D. Hendy and D. Penny. 1994. Recovering evolutionary trees under a more realistic model of sequence evolution. Mol. Biol. Evol. 11, 605–612.

Lockhart, S.R., K.J. Daniels, R. Zhao, D. Wessels and D.R. Soll. 2003. Cell biology of mating in *Candida albicans*. Eukaryot. Cell 2, 49–61.

Lockhart, S.R., S.A. Messer, M.A. Pfaller and D.J. Diekema. 2008a. *Lodderomyces elongisporus* masquerading as *Candida parapsilosis* as a cause of bloodstream infections. J. Clin. Microbiol. 46, 374–376.

Lockhart, S.R., S.A. Messer, M.A. Pfaller and D.J. Diekema. 2008b. Geographic distribution and antifungal susceptibility of the newly described species *Candida orthopsilosis* and *Candida metapsilosis* in comparison to the closely related species *Candida parapsilosis*. J. Clin. Microbiol. 46, 2659–2664.

Lockhart, S.R., S.A. Messer, M. Gherna, J.A. Bishop, W.G. Merz, M.A. Pfaller and D.J. Diekema. 2009. Identification of *Candida nivariensis* and *Candida bracarensis* in a large global collection of *Candida glabrata* isolates: comparison to the literature. J. Clin. Microbiol. 47, 1216–1217.

Lockwood, J.C. 1992. Exploitation competition. In: G.C. Carroll and D.T. Wicklow (Eds), The Fungal Community, Its Organization and Role in the Ecosystem, 2nd edn. Marcel Dekker, New York, pp. 243–274.

Lockwood, S.F., and G.J. Gross. 2005. Disodium disuccinate astaxanthin (Cardax): antioxidant and antiinflammatory cardioprotection. Cardiovasc. Drug Rev. 23, 199–216.

Locquin, M. 1984. Mycologie Générale et Structurale. Masson, Paris, 551pp.

Lodder, J. 1932. Über einige durch das "Centraalbureau voor Schimmelcultures" neuerworbene sporogene Hefearten. Zentralbl. Bakteriol. Parasitenkd., Abt. II, 86, 227–253.

Lodder, J. 1934. Die anaskosporogenen Hefen, I. Halfte. Verh. K. Ned. Akad. Wet., Afd. Natuurk., Sect. II, 32, 1–256.

Lodder, J. 1938. *Torulopsis* or *Cryptococcus*? Mycopathol. Mycol. Appl. 1, 62–67.

Lodder, J. 1970. General classification of the yeasts. In: J. Lodder (Ed.), The Yeasts, A Taxonomic Study, 2nd edn. North-Holland, Amsterdam, pp. 1–33.

Lodder, J., and N.F. de Vries. 1938. Some notes on *Torulopsis glabrata* (Anderson) nov. comb. Mycopathol. Mycol. Appl. 1, 98–103.

Lodder, J., and N.J.W. Kreger-van Rij. 1952. The Yeasts, A Taxonomic Study. North-Holland, Amsterdam.

Lodder, J., and N.J.W. Kreger-van Rij. 1978. Proposal (446) for the conservation of the generic name *Debaryomyces* Lodder et Kreger-van Rij against *Debaryomyces* Klöcker. Taxon 27, 306–307.

Lodder, J., and N.J.W. Kreger-van Rij. 1979. *Debaryomyces* or *Debaryozyma*? Int. J. Syst. Bacteriol. 29, 413.

Lodge, J.K., E. Jackson-Machelski, D.L. Toffaletti, J.R. Perfect and J.I. Gordon. 1994. Targeted gene replacement demonstrates that myristoyl-CoA: protein *N*-myristoyltransferase is essential for viability of *Cryptococcus neoformans*. Proc. Natl. Acad. Sci. 91, 12008–12012.

Lodolo, E.J., F.T. Rossouw and N.P. Ferreira. 1990. Mitochondrial DNA analyses of the Lipomycetaceae. Syst. Appl. Microbiol. 13, 1–7.

Loeffler, J., N. Henke, H. Hebart, D. Schmidt, L. Hagmeyer, U. Schumacher and H. Einsele. 2000. Quantification of fungal DNA by using fluorescence resonance energy transfer and the light cycler system. J. Clin. Microbiol. 38, 586–590.

Loftus, B.J., E. Fung, P. Roncaglia, D. Rowley, P. Amedeo, D. Bruno, J. Vamathevan, M. Miranda, L.J. Anderson, J.A. Fraser, J.E. Allen, I.E. Bosdet, M.R. Brent, R. Chiu, T.L. Doering, M.J. Donlin, C.A. D'Souza, D.S. Fox, V. Grinberg, J. Fu, M. Fukushima, V. Grinberg, J. Fu, M. Fukushima, B.J. Haas, J.C. Huang, G. Janbon, S.J.M. Jones, H.L. Koo, M.I. Krzywinski, K.J. Kwon-Chung, K.B. Lengeler, R. Maiti, M.A. Marra, R.E. Marra, C.A. Mathewson, T.J. Mitchell, M. Pertea, F.R. Riggs, S.L. Salzberg, J.E. Schein, A. Shvartsbeyn, H. Shin, M. Shumway, C.A. Specht, B.B. Suh, A. Tenney, T.R. Utterback, B.K. Wickes, J.R. Wortman, N.J. Wye, J.W. Kronstad, J.K. Lodge, J. Heitman, R.W. Davis, C.M. Fraser and R.W. Hyman. 2005. The genome and transcriptome of *Cryptococcus neoformans*, a basidiomycetous fungal pathogen of humans. Science 307, 1321–1324.

Lomascola, A., E. Dubreucq, V. Perrier and P. Galzy. 1994. Study of lipids in *Lipomyces* and *Waltomyces*. Can. J. Microbiol. 40, 724–729.

Lomascola, A., E. Dubreucq and P. Galzy. 1996. Study of the delta 1-2-desaturase system of *Lipomyces starkeyi*. Lipids 31, 253–259.

London, R., B.S. Orozco and E. Mylonakis. 2006. The pursuit of cryptococcal pathogenesis: heterologous hosts and the study of cryptococcal host–pathogen interactions. FEMS Yeast Res. 6, 567–573.

Lopandic, K., H. Prillinger, O. Molnár and G. Giménez-Jurado. 1996. Molecular characterization and genotypic identification of *Metschnikowia* species. Syst. Appl. Microbiol. 19, 393–402.

Lopandic, K., S. Zelger, L.K. Banszky, F. Eliskases-Lechner and H. Prillinger. 2001. Phenotypic and genotypic identification of yeasts from milk products. Forum Lebensmittel und Biotechnologie 1, 3. http://www.boku.ac.at/forumlbt/main_page.html

Lopandic, K., T. Sugita, W.J. Middelhoven, M. Herzberg, J.W. Fell, S. Zelger and H. Prillinger. 2004. *Trichosporon caseorum* sp. nov. and *Trichosporon lactis* sp. nov., two basidiomycetous yeasts isolated from cheeses. In: R. Agerer, M. Piepenbring and P. Blanz (Eds), Frontiers in Basidiomycota Mycology. IHW-Verlag and Verlagsbuchhandlung, Eching, pp. 99–116.

Lopandic, K., O. Molnár and H. Prillinger. 2005a. *Fellomyces mexicanus* sp. nov., a new member of the yeast genus *Fellomyces* isolated from lichen *Cryptothecia rubrocincta* collected in Mexico. Microbiol. Res. 160, 1–11.

Lopandic, K., O. Molnár and H. Prillinger. 2005b. Application of ITS sequence analysis, RAPD and AFLP fingerprinting in characterising the yeast genus *Fellomyces*. Microbiol. Res. 160, 13–26.

Lopandic, K., S. Zelger, L.K. Banszky, F. Eliskases-Lechner and H. Prillinger. 2006. Identification of yeasts associated with milk products using traditional and molecular techniques. Food Microbiol. 23, 341–350.

Lopandic, K., H. Gangl, E. Wallner, G. Tscheik, G. Leitner, A. Querol, N. Borth, M. Breitenbach, H. Prillinger and W. Tiefenbrunner. 2007. Genetically different wine yeasts isolated from Austrian vine-growing regions influence wine aroma differently and contain putative hybrids

between *Saccharomyces cerevisiae* and *Saccharomyces kudriavzevii*. FEMS Yeast Res. 7, 953–965.

Loper, J.E., D.Y. Kobayashi and I.T. Paulsen. 2007. The genomic sequence of *Pseudomonas fluorescens* PF-5: insights into biological control. Phytopathology 97, 233–238.

Lopes, J.O., S.H. Alves, C. Klock, L.T. Oliveira and N.R. Dal Forno. 1997. *Trichosporon inkin* peritonitis during continuous ambulatory peritoneal dialysis with bibliography review. Mycopathologia 139, 15–18.

López-Archilla, A., A. Gonzalez, M. Terron and R. Amils. 2004. Ecological study of the fungal populations of the acidic Tinto River in southwestern Spain. Can. J. Microbiol. 50, 923–934.

Lorenz, D.H. 1976. Contributions to the knowledge of the natural variability and the physiology of *Taphrina deformans*. Phytopathol. Z. 85, 117–344. In German.

Lorenz, P., and J. Eck. 2005. Metagenomics and industrial applications. Nat. Rev. Microbiol. 3, 510–516.

Lorenz, R., and H.P. Molitoris. 1997. Cultivation of fungi under simulated deep sea conditions. Mycol. Res. 101, 1355–1365.

Losev, E., C.A. Reinke, J. Jellen, D.E. Strongin, B.J. Bevis and B.S. Glick. 2006. Golgi maturation visualized in living yeast. Nature 441, 1002–1006.

Loureiro, V. 2000. Spoilage yeasts in food and beverages: characterization and ecology for improved diagnosis and control. Food Res. Int. 33, 247–256.

Loureiro, V., and M. Malfeito-Ferreira. 2003. Spoilage yeasts in the wine industry. Int. J. Food Microbiol. 86, 23–50.

Loureiro, V., and M. Malfeitto-Ferreira. 2006. *Dekkera*/*Brettanomyces* spp. In: C. de W. Blackburn (Ed.), Food Spoilage Microorganisms. Woodhead Publishing, Cambridge, pp. 354–400.

Louriero, V., and A. Querol. 1999. The prevalence and control of spoilage yeasts in foods and beverages. Trends Food Sci. Technol. 10, 356–365.

Lowes, K.F., C.A. Shearman, J. Payne, D. MacKenzie, D.B. Archer, R.J. Merry and M.J. Gasson. 2000. Prevention of yeast spoilage in feed and food by the yeast mycocin HMK. Appl. Environ. Microbiol. 66, 1066–1076.

Lowy, B. 1971. Tremellales. Flora Neotropica, Monograph No. 6. Hafner, New York, 153pp.

Lowy, B. 1979. A new genus and species of Tremellaceae from Mexico. Bol. Soc. Mex. Micol. 13, 223–227.

Lu, H.-Z., J.-H. Jia, Q.-M. Wang and F.-Y. Bai. 2004a. *Candida asparagi* sp. nov., *Candida diospyri* sp. nov. and *Candida qinlingensis* sp. nov., novel anamorphic, ascomycetous yeast species. Int. J. Syst. Evol. Microbiol. 54, 1409–1414.

Lu, H.-Z., Y. Cai, Z.-W. Wu, J.-H. Jia and F.-Y. Bai. 2004b. *Kazachstania aerobia* sp. nov., an ascomycetous yeast species from aerobically deteriorating corn silage. Int. J. Syst. Evol. Microbiol. 54, 2431–2435.

Lu, K.-C., D.G. Allen and W.B. Bollen. 1957. Association of yeasts with the Douglas-fir beetle. For. Sci. 3, 336–343.

Lu, X.-H., and M.-X. Li. 1989. A new species of yeast – *Pichia hangzhouana* Lu et Li. Acta Mycol. Sin. 8, 251–255.

Lu, X.-H., and M.-X. Li. 1991. Some new species and records of *Trichosporon* in China. Acta Mycol. Sinica. 10, 43–49.

Lucet, A. 1901. Contribution à l'étude étiologique et pathogénique de la langue noire pileuse. Arch. Parasitol. 4, 262–287.

Ludwig, F. 1886. Ueber Alkoholgärung und Schleimfluss lebender Bäume und deren Urheber. Ber. Dtsch. Bot. Ges. 4, 17–27.

Ludwig, F. 1891. Der Milch- und Rothfluss der Bäume und ihre Urheber. Vorläufige Mitt. Zentralbl. Bakteriol. Parasitenkd. 10, 10–13.

Ludwig, F. 1896. Sur les organismes des écoulements des arbres. Rev. Mycol. Toulouse 18, 45–57, 114–123.

Lugauskas, A., V. Raudonienė, R. Varnaité and V. Dirginčuité. 2006. Ecological and sanitary significance of micromycetes brought from abroad with various foodstuffs of floral origin. Ekologija 3, 28–41.

Lui, A.Y., G.S. Turett, D.L. Karter, P.C. Bellman and J.W. Kislak. 1998. Amphotericin B lipid complex therapy in an AIDS patient with *Rhodotorula rubra* fungemia. Clin. Infect. Dis. 27, 892–893.

Lukács, B., Linka and I. Nyilasa. 2006. *Phaffia rhodozyma* and *Xanthophyllomyces dendrorhous*: astaxanthin-producing yeasts of biotechnological importance. Acta Aliment. 35, 99–107.

Lund, A. 1954. Studies on the Ecology of Yeasts. Munsgaard, Copenhagen.

Lundgren, B., G.Y. Lipschik and J.A. Kovacs. 1991. Purification and characterization of a major human *Pneumocystis carinii* surface antigen. J. Clin. Invest 87, 163–170.

Luong, D.T., M. Takashima, P.V. Ty, N.L. Dung and T. Nakase. 2000. Four new species of *Kockovaella* isolated from plant leaves collected in Vietnam. J. Gen. Appl. Microbiol. 46, 297–310.

Luong, D.T., P. van Ty, N. Lan Dung, M. Takashima and T. Nakase. 2002. *Bullera ninhbinhensis* sp. nov., a new ballistoconidiogenous yeast isolated from Vietnam. J. Genet. Applic. Spec. Issue: Biotechnology 35–41. In Vietnamese.

Luong, D.T., M. Takasima, P. van Ty, N. Lan Dung and T. Nakase. 2005. *Bullera hoabinhensis* sp. nov., a new ballistoconidiogenous yeast isolated from a plant leaf in Vietnam. J. Gen. Appl. Microbiol. 6, 335–342.

Luongo, L., M. Galli, L. Corazza, E. Meekes, L. de Haas, C. Lombaers-van der Plas and J. Köhl. 2005. Potential of fungal antagonists for biocontrol of *Fusarium* spp. in wheat and maize through competition in crop debris. Biocontrol Sci. Technol. 15, 229–242.

Lurie, H.I., and H.J. Shadomy. 1971. Morphological variations of the hyphae-forming strain of *Cryptococcus neoformans* (Coward strain) in tissues of mice. Sabouraudia 9, 10–14.

Lushbaugh, W.B., E.D. Rowton and R.B. McGhee. 1976. Redescription of *Coccidiascus legeri* Chatton, 1913. (Nematosporaceae: Hemiascomycetidae), an intracellular, parasitic, yeast-like fungus from the intestinal epithelium of *Drosophila melanogaster*. J. Invertebr. Pathol. 28, 93–107.

Lutzoni, F., F. Kauff, C.J. Cox, D.J. McLaughlin, G. Celio, B. Dentinger, M. Padamsee, D. Hibbett, T.Y. James, E. Baloch, M. Grube, V. Reeb, V. Hofstetter, C. Schoch, A.E. Arnold, J. Miadlikowska, J. Spatafora, D. Johnson, S. Hambleton, M. Crockett, R. Shoemaker, G.-H. Sung, R. Lücking, T. Lumbsch, K. O'Donnell, M. Binder, P. Diederich, D. Ertz, C. Gueidan, K. Hansen, R.C. Harris, K. Hosaka, Y.-W. Lim, B. Matheny, H. Nishida, D. Pfister, J. Rogers, A. Rossman, I. Schmitt, H. Sipman, J. Stone, J. Sugiyama, R. Yahr and R. Vilgalys. 2004. Assembling the fungal tree of life: progress, classification, and evolution of subcellular traits. Am. J. Bot. 91, 1446–1480.

Lydolph, M.C., J. Jacobsen, P. Arctander, M.T.P. Gilbert, D.A. Gilichinsky, A.J. Hansen, E. Willerslev and L. Lange. 2005.

Beringian paleocology inferred from permafrost preserved fungal DNA. Appl. Environ. Microbiol. 71, 1012–1017.
Lynch, J.P. III., D.R. Schaberg, D.G. Kissner and C.A. Kauffman. 1981. *Cryptococcus laurentii* lung abscess. Am. Rev. Respir. Dis. 123, 135–138.
Lynch, M.D., and R.G. Thorn. 2006. Diversity of basidiomycetes in Michigan agricultural soils. Appl. Environ. Microbiol. 72, 7050–7056.
Lynd, L.R., P.J. Weimer, W.H. van Zyl and I.S. Pretorius. 2002. Microbial cellulose utilization: fundamentals and biotechnology. Microbiol. Mol. Biol. Rev. 66, 506–577.
Ma, L., and Z.B. Lin. 1992. Effect of *Tremella* polysaccharide on IL-2 production by mouse splenocytes. Yao Hsueh Pao 27, 1–4.
MacArthur, R.H. 1972. Geographical Ecology: Patterns in the Distribution of Species. Harper and Row, New York.
MacArthur, R.H., and E.O. Wilson. 1967. The Theory of Island Biogeography. Monographs in Population Biology. Princeton University Press, Princeton, NJ.
Macauley, B.J., and J.S. Waid. 1981. Fungal production on leaf surfaces. In: D.T. Wicklow and G.C. Carroll (Eds), The Fungal Community, Its Organization and Role in the Ecosystem. Marcel Dekker, New York, pp. 501–531.
Macauley-Patrick, S., M.L. Fazenda and L.M. Harvey. 2005. Heterologous protein production using the *Pichia pastoris* expression system. Yeast 22, 249–270.
MacDougall, L., and M. Fyfe. 2006. Emergence of *Cryptococcus gattii* in a novel environment provides clues to its incubation period. J. Clin. Microbiol. 44, 1851–1852.
MacDougall, L., S.E. Kidd, E. Galanis, S. Mak, M.J. Leslie, P.R. Cieslak, J.W. Kronstad, M.G. Morshed and K.H. Bartlett. 2007. Spread of *Cryptococcus gattii* in British Columbia, Canada, and detection in the Pacific Northwest, USA. Emerg. Infect. Dis. 13, 42–50.
Macfie, J.W.S. 1921. Notes on some fungal infections in West Africa. Ann. Trop. Med. Parasitol. 15, 271–282.
MacGillivray, A.R., and M.P. Shiaris. 1993. Biotransformation of polycyclic aromatic hydrocarbons by yeasts isolated from coastal sediments. Appl. Environ. Microbiol. 59, 1613–1618.
Maciel de Mancilha, I., and M.N. Karim. 2003. Evaluation of ion exchange resins for removal of inhibitory compounds from corn stover hydrolyzate for xylitol fermentation. Biotechnol. Prog. 19, 1837–1841.
Mackenzie, D.W.R., and B.J. Auret. 1963. *Rhodotorula nitens* sp. nov. isolated from the atmosphere. J. Gen. Microbiol. 31, 171–177.
Mackinnon, J.E. 1936. Carateres y grado de la virulencia experimental de las Torulopsidaceas de la sub-familia Micotoruleas (Monilias). Ann. Fac. Med. Montevideo 21, 320.
Mackinnon, J.E., and R.C. Artagaveytia-Allende. 1945. The so-called genus *Candida* Berkhout, 1923. J. Bacteriol. 49, 317–334.
Macy, J.M., and M.W. Miller. 1971. *Endomyces tetrasperma*, sp. n. J. Bacteriol. 105, 637–645.
Madariaga, M.G., A. Tenorio and L. Proia. 2003. *Trichosporon inkin* peritonitis treated with caspofungin. J. Clin. Microbiol. 41, 5827–5829.
Madelin, M.F., and A. Feest. 1982. *Dipodascus macrosporus* sp. nov. (Hemiascomycetes), associated with plasmodia of *Badhamia utricularis*. Trans. Br. Mycol. Soc. 79, 331–380.
Madzak, C., C. Gaillardin and J.M. Beckerich. 2004. Heterologous protein expression in the non-conventional yeast *Yarrowia lipolytica*. J. Biotechnol. 109, 63–81.
Magan, N., and D. Aldred. 2006. Managing microbial spoilage in cereal and baking products. In: C. de W. Blackburn (Ed.), Food Spoilage Microorganisms. Woodhead Publishing, Cambridge, pp. 195–212.
Mager, J., and M. Aschner. 1947. Biological studies on capsulated yeasts. J. Bacteriol. 53, 283–295.
Mager, W.H., and J. Winderickx. 2005. Yeast as a model for medical and medicinal research. Trends Pharmacol. Sci. 26, 265–273.
Maggon, K. 2007. Monoclonal antibody "gold rush". Curr. Med. Chem. 14, 1978–1987.
Magliani, W., S. Conti, M. Gerloni, D. Bertolotti and L. Polonelli. 1997. Yeast killer systems. Clin. Microbiol. Rev. 10, 369–400.
Magliani, W., S. Conti, A. Salati, S. Arseni, L. Ravanetti, R. Frazzi and L. Polonelli. 2003. Biotechnological approaches to the production of idiotypic vaccines and antiidiotypic antibiotics. Curr. Pharm. Biotechnol. 4, 91–97.
Magnelli, P., J.F. Cipollo and C. Abeijon. 2002. A refined method for the determination of *Saccharomyces cerevisiae* cell wall composition and beta-1,6-glucan fine structure. Anal. Biochem. 301, 136–150.
Magnelli, P.E., J.F. Cipollo and P.W. Robbins. 2005. A glucanase-driven fractionation allows redefinition of *Schizosaccharomyces pombe* cell wall composition and structure: assignment of diglucan. Anal. Biochem. 336, 202–212.
Magnus, P. 1890. Bemerkung uber die benennung zweier auf Alnus lebender Taphrina-arten. Hedwigia 29, 23.
Magnuson, J.A., A.D. King Jr. and T. Torok. 1990. Mycoflora of partially processed lettuce. Appl. Environ. Microbiol. 56, 3851–3854.
Mahdi, L.E., A. Statzell-Tallman, J.W. Fell, M.V. Brown and S.P. Donachie. 2008. *Sympodiomycopsis lanaiensis* sp. nov., a basidiomycetous yeast (Ustilaginomycotina: Microstromatales) from marine driftwood in Hawaii. FEMS Yeast Res. 8, 1357–1363.
Mahrous, M., T. Lott, S.A. Meyer, S.D. Savanat and D.G. Ahearn. 1990. Electrophoretic karyotyping of typical and atypical *Candida albicans*. J. Clin. Microbiol. 28, 876–881.
Maimer, E., and M. Busse. 1992. Growth properties and gas formation by yeasts isolated from processed fruits in media with various Brix values and sorbic acid contents. J. Food Prot. 55, 192–197.
Majoros, L., G. Kardos, A. Belak, A. Maraz, L. Asztalos, E. Csanky, Z. Barta and B. Szabo. 2003. Restriction enzyme analysis of ribosomal DNA shows that *Candida inconspicua* clinical isolates can be misidentified as *Candida norvegensis* with traditional diagnostic procedures. J. Clin. Microbiol. 41, 5250–5253.
Makimura, K., Y. Tamura, M. Kudo, K. Uchida, H. Saito and H. Yamaguchi. 2000. Species identification and strain typing of *Malassezia* species stock strains and clinical isolates based on the DNA sequences of nuclear ribosomal internal transcribed spacer 1 regions. J. Med. Microbiol. 49, 29–45.
Maksimova, I.A., and I.Yu. Chernov. 2004. Community structure of yeast fungi in forest biogeocenoses. Microbiology (Moscow) 73, 474–481. (translated from Mikrobiologiia 73, 558–566).

Malfeito-Ferreira, M., A.S. Aubyn and V. Loureiro. 1989. Long chain fatty acid composition as a tool for differentiating spoilage wine yeasts. Mycotaxon 36, 35–42.

Malgoire, J.Y., S. Bertout, F. Renaud, J.M. Bastide and M. Mallié. 2005. Typing of *Saccharomyces cerevisiae* clinical strains by using microsatellite sequence polymorphism. J. Clin. Microbiol. 43, 1133–1137.

Maligie, M.A., and C.P. Selitrennikoff. 2005. *Cryptococcus neoformans* resistance to echinocandins: (1,3)β-glucan synthase activity is sensitive to echinocandins. Antimicrob. Agents Chemother. 49, 2851–2856.

Malloch, D., and G.S. de Hoog. 1998. Endomycete-like genera of mycoparasitic fungi. In: C.P. Kurtzman and J.W. Fell (Eds), The Yeasts, A Taxonomic Study. Elsevier, Amsterdam, pp. 197–200.

Malloch, D., J. Kane and D.G. Lahaie. 1978. *Filobasidiella arachnophila* sp. nov. Can. J. Bot. 56, 1823–1826.

Mallow, D., and M. Blackwell. 1993. Dispersal biology of Ophiostomatoid fungi. In: M.J. Wingfield, K.A. Selfert and J.F. Webber (Eds), *Ceratocystis* and *Ophiostoma*: Taxonomy, Ecology and Pathogenicity. American Phytopathological Society Press, St. Paul, MN, pp. 195–206.

Malpertuy, A., B. Llorente, G. Blandin, F. Artiguenave, P. Wincker and B. Dujon. 2000. Genomic exploration of the hemiascomycetous yeasts: 10. *Kluyveromyces thermotolerans*. FEBS Lett. 487, 61–65.

Manachini, P.L. 1979. DNA sequence similarity, cell wall mannans, and physiological characteristics in some strains of *Candida utilis*, *Hansenula jadinii* and *Hansenula petersonii*. Antonie van Leeuwenhoek 45, 451–463.

Mancianti, F., S. Nardoni and R. Ceccherelli. 2001. Occurrence of yeasts in psittacines droppings from captive birds in Italy. Mycopathologia 153, 121–124.

Mangla, A.T., and W.D. Ness. 2000. Sterol C-methyl transferase from *Prototheca wickerhamii*, mechanism, sterol specificity and inhibition. Bioorg. Med. Chem. 8, 925–936.

Mann, D.A., and L.R. Beuchat. 2008. Combinations of antimycotics to inhibit the growth of molds capable of producing 1,3pentadiene. Food Microbiol. 25, 144–153.

Mannarelli, B.M., and C.P. Kurtzman. 1998. Rapid identification of *Candida albicans* and other human pathogenic yeasts by using short oligonucleotides in a PCR. J. Clin. Microbiol. 36, 1634–1641.

Manners, D.J., and M.T. Meyer. 1977. The molecular structures of some glucans from the cell walls of *Schizosaccharomyces pombe*. Carbohydr. Res. 57, 189–203.

Manners, D.J., I.R. Pennie and J.F. Ryley. 1967. The reserve polysaccharides of *Prototheca zopfii*. Proc. Biochem. Soc. 104, 32.

Manners, D.J., I.R. Pennie and J.F. Ryley. 1973. The molecular structures of a glucan and a galactan synthesised by *Prototheca zopfii*. Carbohydr. Res. 29, 63–77.

Manners, D.J., A.J. Masson and J.C. Patterson. 1974. The heterogeneity of glucan preparations from the walls of various yeasts. J. Gen. Microbiol. 80, 411–417.

Mansfield, M.A., and G.A. Kuldau. 2007. Microbiological and molecular determination of mycobiota in fresh and ensiled maize silage. Mycologia 99, 269–278.

Manson, J.S., M.A. Lachance and J.D. Thomson. 2007. *Candida gelsemii* sp. nov., a yeast of the Metschnikowiaceae clade isolated from nectar of the poisonous *Carolina jessamine*. Antonie van Leeuwenhoek 92, 37–42.

Mäntynen, V.H., M. Korhola, H. Gudmundsson, H. Turakainen, G.A. Alfredsson, H. Salovaara and K. Lindstrom. 1999. A polyphasic study on the taxonomic position of industrial sour dough yeasts. Syst. Appl. Microbiol. 22, 87–96.

Manzanares, P., D. Ramon and A. Querol. 1999. Screening of non-*Saccharomyces* wine yeasts for the production of beta-D-xylosidase activity. Int. J. Food Microbiol. 46, 105–112.

Manzanares, P., V. Rojas, S. Genoves and S. Valles. 2000. A preliminary search for anthocyanin-beta-D-glucosidase activity in non-*Saccharomyces* wine yeasts. Int. J. Food Sci. Technol. 35, 95–103.

Marcellino, N., E. Beuvier, R. Grappin, M. Guéguen and D.R. Benson. 2001. Diversity of *Geotrichum candidum* strains isolated from traditional cheesemaking fabrications in France. Appl. Environ. Microbiol. 67, 4752–4759.

Marchant, H.J. 1976. Plasmodesmata in algae and fungi. In: B. E.S. Gunning and A.W. Robards (Eds), Intercellular Communication in Plants: Studies on Plasmodesmata. Springer, Heidelberg, pp. 59–80.

Marchant, R., and J.G.H. Wessels. 1973. Septal structure in normal and modified strains of *Schizophyllum* commune carrying mutations affecting septal dissolution. Arch. Microbiol. 90, 35–45.

Marcilla, J., and E. Feduchy. 1943. Contribución al estudio de una levadura perteneciente al género *Saccharomycodes*, capaz de fermentar mostos de uva fuertemente sulfitados (mostos azufrados), sin previa desulfitación. Centros de Estudios Generales y de Ampelografía y Viticultura, Cuaderno No. 29.

Marcilla, J., E. Feduchy and J.M. Gomes. 1945. Contribucion al estudio de levaduras salvajes y cultivadas, de las microfloras españiola y portuguesa. Trab. Inst. Cajal. Invest. Biol. 3, 161–191.

Marcon, M.J., and D.A. Powell. 1992. Human infections due to *Malassezia* spp. Clin. Microbiol. Rev. 5, 101–119.

Marengo, G. 1926. Su di una paronichia dovuta ad una nuova specie di *Monilia*: la *Monilia onychophila* Pollacci e Nannizzi. Arch. Biol. 3, 25–36.

Maresová, L., and H. Sychrová. 2003. Physiological characterization of osmotolerant yeast *Pichia sorbitophila* and a comparison with a putative synonym *Pichia farinosa*. Folia Microbiol. 48, 211–217.

Margesin, R. 2007. Alpine microorganisms: Useful tools for low-temperature bioremediation. J. Microbiol. 45, 281–285.

Margesin, R., and J.W. Fell. 2008. *Mrakiella cryoconiti* gen. nov., sp. nov., a novel psychrophilic anamorphic basidiomycetous yeast from alpine and arctic habitats. Int. J. Syst. Evol. Microbiol. 58, 2977–2982.

Margesin, R., G. Zacke and F. Schinner. 2002. Characterization of heterotrophic microorganisms in alpine glacier cryoconite. Arct. Antarct. Alp. Res. 34, 88–93.

Margesin, R., V. Fauster and P.A. Fonteyne. 2005a. Characterization of cold-active pectate lyases from psychrophilic *Mrakia frigida*. Lett. Appl. Microbiol. 40, 453–459.

Margesin, R., P.A. Fonteyne and B. Redl. 2005b. Low-temperature biodegradation of high amounts of phenol by *Rhodococcus* spp. and basidiomycetous yeasts. Res. Microbiol. 156, 68–75.

Margesin, R., P.-A. Fonteyne, F. Schinner and J.P. Sampaio. 2007. *Rhodotorula psychrophila* sp. nov., *Rhodotorula*

psychrophenolica sp. nov. and *Rhodotorula glacialis* sp. nov., novel psychrophilic basidiomycetous yeast species isolated from alpine environments. Int. J. Syst. Evol. Microbiol. 57, 2179–2184.

Margush, T., and F.R. McMorris. 1981. Consensus n-trees. Bull. Math. Biol. 43, 239–244.

Mari, M., and A. Carati. 1998. Use of *Saccharomyces cerevisiae* with ethanol in the biological control of grey mould on pome fruits. In: P. Bertolini, P.C. Sijmons, M.E. Guerzoni and F. Serra (Eds), COST 914–COST 915 Joint Workshop — Non Conventional Methods for the Control of Postharvest Disease and Microbial Spoilage. Luxembourg: Publ. Eur. Community, pp. 85–89.

Mari, M., P. Bertolini and G.C. Pratella. 2003. Non-conventional methods for the control of post-harvest pear diseases. J. Appl. Microbiol. 94, 761–766.

Marín, D., D. Linde and M.F. Lobato. 2006. Purification and biochemical characterization of an a-glucosidase from *Xanthophyllomyces dendrorhous*. Yeast 23, 117–125.

Marinoni, G., and M.A. Lachance. 2004. Speciation in the largespored *Metschnikowia* clade and establishment of a new species, *Metschnikowia borealis* comb. nov. FEMS Yeast Res. 4, 587–596.

Mariononi, G., M. Manuel, R.F. Petersen, J. Hvidtfeldt, P. Sulo and J. Piśkur. 1999. Horizontal transfer of genetic material among *Saccharomyces* yeasts. J. Bacteriol. 181, 6486–6488.

Markham, P. 1994. Occlusions of septal pores in filamentous fungi. Mycol. Res. 98, 1089–1106.

Markham, P., and A.J. Collinge. 1987. Worinin bodies of filamentous fungi. FEMS Microbiol. Lett. 46, 1–11.

Marmur, J., and P. Doty. 1962. Determination of the base composition of DNA from its thermal denaturation temperature. J. Mol. Biol. 5, 109–118.

Marongiu, P., B.T. Linaldeddu and A. Francheschini. 2003. Sequence analysis of the 5.8S rRNA gene and internal transcribed spacers (ITS) of *Taphrina kruchii*. Proc. Joint Workshop on Molecular Diagnostics of Plant Pathogens. November 2003, Italy p. 27.

Marples, M.J., and D.A. Somerville. 1968. The oral and cutaneous distribution of *Candida albicans* and other yeasts in Raratonga, Cook Islands. Trans. R. Soc. Trop. Med. Hyg. 62, 256–262.

Marquina, D., C. Peres, F.V. Caldas, J.F. Marques, J.M. Peinado and I. Spencer-Martins. 1992. Characterization of the yeast population in olive brines. Lett. Appl. Microbiol. 14, 279–283.

Marquina, D., S. Toufani, P. Llorente, A. Santos and J.M. Peinado. 1997. Killer activity in yeast isolates from olive brines. Adv. Food Sci. 19, 1–2.

Martchenko, M., A. Levitin, H. Hogues, A. Nantel and M. Whiteway. 2007. Transcriptional rewiring of fungal galactose-metabolism circuitry. Curr. Biol. 17, 1007–1013.

Martin, D., F. Bedel de Buzareinques, P. Barry and S. Derridj. 1993. An epiphytic yeast (*Sporobolomyces roseus*) influencing in oviposition preference of the European corn borer (*Ostrinia nubilalis*) on maize. Acta Oecologica 14, 563–574.

Martin, D.S., C.P. Jones, K.F. Yao and L.E. Lee Jr. 1937. A practical classification of the Monilias. J. Bacteriol. 34, 99–129.

Martin, E.M. 1940. The morphology and cytology of *Taphrina deformans*. Am. J. Bot. 27, 743–751.

Martin, G.W. 1945. The classification of the Tremellales. Mycologia 37, 527–542.

Martin, G.W. 1952. Revision of the North Central Tremellales. Univ. Iowa Stud. Nat. Hist. 19, 1–122.

Martin, W., O. Deusch, N. Stawski, N. Grunheit and V. Goremykin. 2005. Chloroplast genome phylogenetics: why we need independent approaches to plant molecular evolution. Trends Plant Sci. 10, 203–209.

Martínez, A.T. 1979. Ultrastructure of *Moniliella, Trichosporonoides* and *Hyalodendron*. Stud. Mycol. 19, 50–57.

Martínez, A.T., G.S. de Hoog and M.Th. Smith. 1979. Physiological characteristics of *Moniliella, Trichosporonoides* and *Hyalodendron*. Stud. Mycol. 19, 58–68.

Martínez, A.T., A.E. González, L. Abarca and J. Cabañes. 1990. A new *Botryoascus* from the air of a poultry farm. Can. J. Bot. 68, 1738–1740.

Martinez-Espinoza, A.D., M.D. Garcia-Pedrajas and S.E. Gold. 2002. The Ustilaginales as plant pests and model systems. Fungal Genet. Biol. 35, 1–20.

Martini, A. 1973. Ibridazioni DNA/DNA tra specie di lieviti del genere *Kluyveromyces*. Ann. Fac. Agrar. Univ. Studi Perugia 28, 157–171.

Martini, A. 1993. Origin and domestication of the wine yeast *Saccharomyces cerevisiae*. J. Wine Res. 4, 165–176.

Martini, A. 2003. Biotechnology of natural and winery-associated strains of *Saccharomyces cerevisiae*. Int. Microbiol. 6, 207–209.

Martini, A., and F. Federici. 1976. A new approach to the study of the yeast flora associated with strawberry surfaces. G. Bot. Ital. 110, 297–301.

Martini, A., and H.J. Phaff. 1973. The optical determination of DNA – DNA homologies in yeasts. Ann. Microbiol. 23, 59–68.

Martini, A., and A. Vaughan-Martini. 1990. Grape must fermentation, past and present. In: J.F.T. Spencer and D. Spencer (Eds), Yeast Technology. Springer-Verlag, Berlin, pp. 105–123.

Martini, A., and A. Vaughan-Martini. 1992. Assignment of *Kluyveromyces cellobiovorus* nomen nudum *to* Candida intermedia *(Ciferri and Ashford) Langeron et Guerra*. Antonie van Leeuwenhoek 61, 57–60.

Martini, A., and A. Vaughan-Martini. 1998. Determination of ethanol production. In: C.P. Kurtzman and J.W. Fell (Eds), The Yeasts, A Taxonomic Study, 4th edn. Elsevier Science Publishers, Amsterdam. p. 107.

Martini, A., M. Ciani and G. Scorzetti. 1996. Direct enumeration and isolation of wine yeasts from grape surfaces. Am. J. Enol. Vitic. 47, 435–440.

Martino, R., M. Salavert, R. Parody, J.F. Tomas, R. de la Camara, L. Vazquez, I. Jarque, E. Prieto, J.L. Sastre, I. Gadea, J. Peman and J. Sierra. 2004. *Blastoschizomyces capitatus* infection in patients with leukemia: report of 26 cases. Clin. Infect. Dis. 38, 335–341.

Martorell, P., M.T. Fernandez-Espinar and A. Querol. 2005. Molecular monitoring of spoilage yeasts during the production of candied fruit nougats to determine food contamination sources. Int. J. Food Microbiol. 101, 293–302.

Martorell, P., M. Stratford, H. Steels, M.T. Fernandez-Espinar and A. Querol. 2007. Physiological characterization of spoilage strains of *Zygosaccharomyces bailii* and *Zygosaccharomyces rouxii* isolated from high sugar environments. Int. J. Food Microbiol. 114, 234–242.

Marty, F.M., D.H. Barouch, E.P. Coakley and L.R. Baden. 2003. Disseminated trichosporonosis caused by *Trichosporon loubieri*. J. Clin. Microbiol. 41, 5317–5320.

Marvanová, L. 1976. Two new *Blastobotrys* species. Trans. Br. Mycol. Soc. 66, 217–222.

Masih, E.I., and B. Paul. 2002. Secretion of β-1,3-glucanases by the yeast *Pichia membranifaciens* and its possible role in the biocontrol of *Botrytis cinerea* causing grey mold disease of the grapevine. Curr. Microbiol. 44, 391–395.

Masih, E.I., I. Alie and B. Paul. 2000. Can the grey mould disease of the grape-vine be controlled by yeast? FEMS Microbiol. Lett. 189, 233–237.

Masih, E.I., S. Slezack-Deschaumes, I. Marmaras, E.A. Barka, G. Vernet, C. Charpentier, A. Adholeya and B. Paul. 2001. Characterisation of the yeast *Pichia membranifaciens* and its possible use in the biological control of *Botrytis cinerea*, causing the grey mould disease of grapevine. FEMS Microbiol. Lett. 202, 227–232.

Masneuf-Pomarède, I., C. Le Jeune, P. Durrens, M. Lollier, M. Aigle and D. Dubourdieu. 2007. Molecular typing of wine yeast strains *Saccharomyces bayanus* var. *uvarum* using microsatellite markers. Syst. Appl. Microbiol. 30, 75–82.

Masoud, W., and L. Jespersen. 2006. Pectin degrading enzymes in yeasts involved in fermentation of *Coffea arabica* in East Africa. Int. J. Food Microbiol. 110, 291–296.

Masoud, W., and C.H. Kaltoft. 2006. The effects of yeasts involved in the fermentation of *Coffea arabica* in East Africa on growth and ochratoxin A (OTA) production by *Aspergillus ochraceus*. Int. J. Food Microbiol. 106, 229–234.

Masoud, W., L.B. Cesar, L. Jespersen and M. Jakobsen. 2004. Yeasts involved in fermentation of *Coffea arabica* in East Africa, determined by genotyping and by direct denaturing gradient gel electropheresis (DGGE). Yeast 21, 549–556.

Masoud, W., L. Poll and M. Jakobsen. 2005. Influence of volatile compounds produced by yeasts predominant during processing of *Coffea arabica* in East Africa on growth and ochratoxin A (OTA) production by *Aspergillus ochraceus*. Yeast 22, 1133–1142.

Massey, S.E., G. Moura, P. Beltrao, R. Almeida, J.R. Garey, M.F. Tuite and M.A. Santos. 2003. Comparative evolutionary genomics unveils the molecular mechanism of reassignment of the CTG codon in *Candida* spp. Genome Res. 13, 544–557.

Masuda, Y., K. Kato, Y. Takayama, K. Kida and M. Nakanishi. 1975. Ethanol assimilating yeast. US Patent 3868305.

Matheny, P.B., J.M. Curtis, V. Hofstetter, M.C. Aime, J.M. Moncalvo, Z.W. Ge, J.C. Slot, J.F. Ammirati, T.J. Baroni, N.L. Bougher, K.W. Hughes, D.J. Lodge, R.W. Kerrigan, M.T. Seidl, D.K. Aanen, M. DeNitis, G.M. Daniele, D.E. Desjardin, B.R. Kropp, L.L. Norvell, A. Parker, E.C. Vellinga, R. Vilgalys and D.S. Hibbett. 2006. Major clades of *Agaricales*: a multilocus phylogenetic overview. Mycologia 98, 982–985.

Mathews, H.L., S. Conti, L. Witek-Janusek and L. Polonelli. 1998. Effect of *Pichia anomala* killer toxin on *Candida albicans*. Med. Mycol. 36, 199–204.

Matile, Ph., H. Moor and C.F. Robinow. 1969. Yeast cytology. In: A.H. Rose and J.S. Harrison (Eds), The Yeasts, Vol. 1. Biology of Yeasts. Academic Press, New York, pp. 218–302.

Matorell, P., A. Querol and M.T. Fernandez-Espinar. 2005. Rapid identification and enumeration of *Saccharomyces cerevisiae* cells in wine by real-time PCR. Appl. Environ. Microbiol. 71, 6823–6830.

Matos, T., G. Haase, A.H. Gerrits van den Ende and G.S. de Hoog. 2003. Molecular diversity of oligotrophic and neurotropic members of the black yeast genus *Exophiala*, with accent on *E. dermatitidis*. Antonie van Leeuwenhoek 83, 293–303.

Matsue, K., H. Uryu, M. Koseki, N. Asada and M. Takeuchi. 2006. Breakthrough trichosporonosis in patients with hematologic malignancies receiving micafungin. Clin. Infect. Dis. 42, 753–757.

Matsumoto, T., S. Takahashi, M. Kaieda, M. Ueda, A. Tanaka, H. Fukuda and A. Kondo. 2001. Yeast whole-cell biocatalyst constructed by intracellular overproduction of *Rhizopus oryzae* lipase is applicable to biodiesel fuel production. Appl. Microbiol. Biotechnol. 57, 515–520.

Matsunaga, Y., Y. Usui and Y. Yoshizawa. 2003. TA-19, a novel protein antigen of *Trichosporon asahii*, in summer-type hypersensitivity pneumonitis. Am. J. Respir. Crit. Care Med. 167, 991–998.

Matte, O., C. Chabalier, R. Ratomahenina, J.P. Bossy and P. Galzy. 1990. Isolation and characterization of a RNA-virus like particle from *Candida curvata*. Biol. Cell 68, 159–162.

Matteson-Heidenreich, M.C., M.R. Corral-Garcia, E.A. Momol and T.J. Burr. 1997. Russet of apple fruit caused by *Aureobasidium pullulans* and *Rhodotorula glutinis*. Plant Dis. 81, 339–342.

Mattlet, G. 1926. Mycoses dans l'Urundi. Ann. Soc. Belge Méd. Trop. 6, 1–41.

Mattson, R., P.D. Haemig and B. Olsen. 1999. Feral pigeons as carriers of *Cryptococcus laurentii*, *Cryptococcus uniguttulatus* and *Debaryomyces hansenii*. Med. Mycol. 37, 367–369.

Mau, B., and M.A. Newton. 1997. Phylogenetic inference for binary data on dendrograms using Markov chain Monte Carlo. J. Comput. Graph. Stat. 6, 122–131.

Maugeri, F., and S. Hernalsteens. 2007. Screening of yeast strains for transfructoglycosylating activity. J. Mol. Catal. B. Enzymat. 49, 43–49.

Maury, J., M.A. Asadollahi and K. Møller. 2005. Microbial isoprenoid production: an example of green chemistry through metabolic engineering. Adv. Biochem. Eng. Biotechnol. 100, 19–151.

Mayer, R.M. 1971. The enzymatic synthesis of the phosphomannan of *Hansenula capsulata*. Biochim. Biophys. Acta 252, 39–47.

Mayeux, P., L. Dupepe, K. Dunn, J. Balsamo and J. Domer. 1995. Massive fungal contamination in animal care facilities traced to bedding supply. Appl. Environ. Microbiol. 61, 2297–2301.

Mayr, P., B. Petschacher and B. Nidetzky. 2003. Xylose reductase from the basidiomycete fungus *Cryptococcus flavus*: purification, steady-state kinetic characterization, and detailed analysis of the substrate binding pocket using structure–activity relationships. J. Biochem. (Tokyo) 133, 553–562.

Mayser, P., S. Fromme, C. Leitzman and K. Gründer. 1995. The yeast spectrum of the "tea fungus Kombucha". Mycoses 38, 289–295.

Mayser, P., M. Huppertz, C. Papavassilis and K. Grunder. 1996. Fungi of the *Trichosporon* genus. Identification, epidemiology and significance of dermatologic disease. Hautarzt 47, 913–920.

Mayser, P., P. Haze, C. Papavassilis, M. Pickel, K. Gründer and E. Guého. 1997. Differentiation of *Malassezia* species:

selectivity of Cremophor EL, castor oil and ricinoleic acid for *M. furfur*. Br. J. Dermatol. 137, 208–213.
Mazars, E., C. Odberg-Ferragut, E. Dei-Cas, M.N. Fourmaux, E.M. Aliouat, M. Brun-Pascaud, G. Mougeot and D. Camus. 1995. Polymorphism of the thymidylate synthase gene of *Pneumocystis carinii* from different host species. J. Eukaryot. Microbiol. 42, 26–32.
Mazé, P. 1910. Technique fromagère, théorie et pratique. Ann. Inst. Pasteur 24, 395–562.
Mazza, S., and B. Palamedi. 1932. Caso mortal de blastomicosis cutaneo mucosa. Reunion de la Sociedad Argentina de Patologia Regional del Norte. Bol. Inst. Clin. Quir. 7, 424–467.
Mazza, S., and M. de los Rios. 1931. Sobre un caso de Moniliasis vaginal. Bol. Inst. Clin. Quir. 6, 215–225.
Mazza, S., F.L. Niño and A. Egües. 1930. Perionixis blastomyctuca por *Monilia* (n. sp.). Bol. Inst. Clin. Quirur. 5, 284–288.
Mazza, S., F.L. Niño, H. Quintana and V. Bernasconi. 1931. Blastomicosis grave generalizada por *Monilia* (n. sp.). Bol. Inst. Clin. Quirurg. Univ. Buenos Aires 6, 180–214.
McArthur, C.R., and G.D. Clark-Walker. 1983. Mitochondrial DNA size diversity in the *Dekkera*/*Brettanomyces* yeasts. Curr. Genet. 7, 29–35.
McCabe, R.W., and A. Taylor. 2002. Synthesis of novel polyurethane polyesters using the enzyme *Candida antarctica* lipase B. Chem. Commun. (Cambridge) 7, 934–935.
McClary, D.O., W.L. Nulty and G.R. Miller. 1959. Effect of potassium versus sodium in the sporulation of *Saccharomyces*. J. Bacteriol. 78, 362–368.
McCormack, P.J., H.G. Wildman and P. Jeffries. 1994. Production of antibacterial compounds by phylloplane-inhabiting yeasts and yeastlike fungi. Appl. Environ. Microbiol. 60, 927–931.
McCullough, M.J., K.V. Clemons and D.A. Stevens. 1999. Molecular and phenotypic characterization of genotypic *Candida albicans* subgroups and comparison with *Candida dubliniensis* and *Candida stellatoidea*. J. Clin. Microbiol. 37, 417–421.
McCully, E.K., and C.F. Robinow. 1971. Mitosis in the fission yeast *Schizosaccharomyces pombe*: a comparative study with light and electron microscopy. J. Cell Sci. 9, 475–507.
McCully, E.K., and C.F. Robinow. 1972a. Mitosis in heterobasidiomycetous yeasts. I. *Leucosporidium scottii* (*Candida scottii*). J. Cell Sci. 10, 857–881.
McCully, E.K., and C.F. Robinow. 1972b. Mitosis in heterobasidiomycetous yeasts. II. *Rhodosporidium* sp. (*Rhodotorula glutinis*) and *Aessosporon salmonicolor* (*Sporobolomyces salmonicolor*). J. Cell Sci. 11, 1–31.
McCurdy, L.H., and J.D. Morrow. 2003. Infections due to non-neoformans cryptococcal species. Comp. Ther. 29, 95–101.
McCusker, J.H., K.V. Clemons, D.A. Stevens and R.W. Davis. 1996. Genetic characterization of pathogenic *Saccharomyces cerevisiae* isolates. Genetics 136, 1261–1269.
Mendonça-Hagler, A.N., and L.C. Mendonça-Hagler. 1991. A Diazonium blue B test for yeasts grown on yeast carbon base–urea agar. Rev. Microbiol. Sao Paulo 22, 71–74.
McGinnis, M.R., A.A. Padhye and L. Ajello. 1974. Storage of stock cultures of filamentous fungi, yeasts, and some aerobic actinomycetes in sterile distilled water. Appl. Microbiol. 28, 218–222.
McGovern, P.E. 2003. Ancient wine: The Scientific Search for the Origins of Viniculture. Princeton University Press, Princeton, New Jersey.
McGovern, P.E., U. Hartung, V.R. Badler, D.L. Glusker and L.J. Exner. 1997. The beginnings of winemaking and viniculture in the ancient Near East and Egypt. 39, 3–21.
McGovern, P.E., J. Zhang, J. Tang, Z. Zhang, G.R. Hall, R.A. Moreau, A. Nuñez, E.D. Dutyrm, M.P. Richards, C.-S. Wang, G. Cheng, Z. Zhao and C. Wang. 2004. Fermented beverages of pre-proto-historic China. Proc. Natl. Acad. Sci. USA 101, 17593–17598.
McGovern, R.J., and T.E. Seijo. 1999. Petal blight of *Callistephus chinensis* by *Itersonilia perplexans*. Plant Dis. 83, 397.
McGrath, J.W., and J.P. Quinn. 2000. Intracellular accumulation of polyphosphate by the yeast *Candida humicola* G-1 in response to acid pH. Appl. Environ. Microbiol. 66, 4068–4073.
McGuire, R.C. 1994. Application of *Candida guilliermondii* in commercial citrus coatings for biocontrol of *Penicillium digitatum* on grapefruits. Biol. Control 4, 1–7.
McKenzie, R.A., M.D. Connole, M.R. McGinnis and R. Lepelaar. 1984. Subcutaneous phaeohyphomycosis caused by *Moniliella suaveolens* in two cats. Vet. Pathol. 21, 582–586.
McLaughlin, D.J., E.M. Frieders and H. Lü. 1995. A microscopist's view of heterbasidiomycete phylogeny. Stud. Mycol. 38, 91–109.
McLaughlin, D.J., E.M. Frieders, M.E. Berres, J.C. Doublés and S.M. Wick. 1996. Immunofluorescence analysis of the microtubule cytoskeleton in the yeast phase of the basidiomycetes *Kriegeria eriophori* and *Septobasidiom cerastianum*. Mycologie 88, 339–349.
McLaughlin, D.J., R.W. Hanson Jr., E.M. Frieders, E.C. Swann and L.J. Szabo. 2004. Mitosis in the yeast phase of the basidiomycetes *Bensingtonia yuccicola* and *Stilbum vulgare* and its phylogenetic implications. Am. J. Bot. 91, 808–815.
McLaughlin, R.J., M.E. Wisniewski, C.L. Wilson and E. Chalutz. 1990. Effect of inoculum concentration and salt solutions on biological control of postharvest diseases of apple with *Candida* sp. Phytopathology 80, 456–461.
McManus, B.A., D.C. Coleman, G. Moran, E. Pinjon, D. Diogo, M.E. Bougnoux, S. Borecká-Melkusova, H. Bujdákova, P. Murphy, C. d'Enfert and D.J. Sullivan. 2008. Multilocus sequence typing reveals that the population structure of *Candida dubliniensis* is significantly less divergent than that of *Candida albicans*. J. Clin. Microbiol. 46, 652–664.
McNabb, R.F.R. 1965. Some Auriculariaceous fungi from the British Isles. Trans. Br. Mycol. Soc. 48, 187–192.
McNabb, R.F.R., and P.H.B. Talbot. 1973. Holobasidiomycetidae: Exobasidiales, Brachybasidiales, Dacrymycetales. In: G.C. Ainsworth, F.K. Sparrow and A.S. Sussman (Eds), The Fungi, Vol. IV B. Academic Press, New York, pp. 317–325.
McNaughton, S.J. 1981. Niche definition and generalizations. In: D.T. Wicklow and G.C. Carroll (Eds), The Fungal Community, Its Organization and Role in the Ecosystem. Marcel Dekker, New York, pp. 79–88.
McNaughton, S.J., and L.L. Wolf. 1970. Dominance and the niche in ecological systems. Science 167, 131–139.
McNeill, J., F.R. Barrie, H.M. Burdet, V. Demoulin, D.L. Hawksworth, K. Marhold, D.H. Nicolson, J. Prado, P.C. Silva, J.E. Skog, J.H. Wiersema and N.J. Turland (Eds).

2006. International Code of Botanical Nomenclature (Vienna Code). A.R.G. Gantner Verlag KG, Ruggell, Liechenstein. http://ibot.sav.sk/icbn/main.htm

McRitchie, J.J., J.W. Kimbrough and A.W. Engelhard. 1973. *Itersonilia* petal blight of chrysanthemum in Florida. Plant Dis. Rep. 57, 181–182.

Meesters, P.A.E.P., and G. Eggink. 1996. Isolation and characterization of a delta-9 fatty acid desaturase gene from the oleaginous yeast *Cryptococcus curvatus* CBS 570. Yeast 12, 723–730.

Meganathan, R. 2001. Ubiquinone biosynthesis in microorganisms. FEMS Microbiol. Lett. 203, 131–139.

Meijer, W.H., I.J. van der Klei, M. Veenhuis and J.A. Kiel. 2007. ATG Genes involved in nonselective autophagy are conserved from yeast to man, but the selective Cvt and pexophagy pathways also require organism-specific genes. Autophagy 3, 106–116.

Meis, J.F.G.M., M. Ruhnke, B.E. de Pauw, F.C. Odds, W. Siegert and P.E. Verweij. 1999. *Candida dubliniensis* candidemia in patients with chemotherapy-induced neutropenia and bone marrow transplantation. Emerg. Infect. Dis. 5, 150–153.

Mélard, L. 1910. Note sur un organisme isolé d'une bière de fermentation haute. Le Petit Journal du Brasseur 18, 1049–1051.

Melin, P., S. Hakansson, T.H. Eberhard and J. Schnürer. 2006. Survival of the biocontrol yeast *Pichia anomala* after long-term storage in liquid formulations at different temperatures, assessed byflow cytometry. J. Appl. Microbiol. 100, 264–271.

Melin, P., S. Håkansson and J. Schnürer. 2007. Optimisation and comparison of liquid and dry formulations of the biocontrol yeast *Pichia anomala* J121. Appl. Microbiol Biotechnol. 73, 1008–1016.

Melliger, R. 1931. Contribution a l'étude des ferments figurés et des fermentations de la datte. Thèse (No. 893) Genève, 146.

Melmer, G. 2005. Production of Recombinant Proteins. Wiley-VCH Verlag, Weinheim, pp. 361–383.

Membre, J.M., M. Kubaczka and C. Chene. 1999. Combined effects of pH, and sugar on growth rate of *Zygosaccharomyces rouxii*, a bakery product spoilage yeast. Appl. Environ. Microbiol. 65, 4921–4925.

Mendel, E.B., S. Haberman and D.K. Hall. 1960. Isolation of *Candida* from clinical specimens. Comparative study of Pagano-Levin and Nickerson's culture media. Obstet. Gynecol. 16, 180–184.

Mendes-Ferreira, A., A. Mendes-Faia and C. Leao. 2002. Survey of hydrogen sulphide production by wine yeasts. J. Food Prot. 65, 1033–1037.

Mendonça-Hagler, A.N., and L.C. Mendonça-Hagler. 1991. A diazonium blue B test for yeasts grown on yeast carbon base–urea agar. Rev. Microbiol. Sao Paulo 22, 71–74.

Mendonça-Hagler, L.C., and H.J. Phaff. 1975. Deoxyribonucleic acid base composition and deoxyribonucleic acid/deoxyribonucleic acid hybrid formation in psychrophobic and related yeasts. Int. J. Syst. Bacteriol. 25, 222–229.

Mendonça-Hagler, L.C., A.N. Hagler, H.J. Phaff and J. Tredick. 1985. DNA relatedness among aquatic yeasts of the genus *Metschnikowia* and proposal of the species *Metschnikowia australis* comb. nov. Can. J. Microbiol. 31, 905–909.

Mendonça-Previato, L., D. Burke and C.E. Ballou. 1982. Sexual agglutination factors from the yeast *Pichia amethionina*. J. Cell Biochem. 19, 171–178.

Mendoza, L., R. Vilela, P.S. Rosa and A.F. Fernandes Belone. 2005. *Lacazia loboi* and *Rhinosporidium seeberi*: a genomic perspective. Rev. Iberoam. Micol. 22, 213–216.

Menkis, A., R. Vasiliauskas, A.F. Taylor, J. Stenlid and R. Finlay. 2005. Fungal communities in mycorrhizal roots of conifer seedlings in forest nurseries under different cultivation systems, assessed by morphotyping, direct sequencing and mycelial isolation. Mycorrhiza 16, 33–41.

Merali, S., and A.B. Clarkson Jr. 1996. Polyamine content of *Pneumocystis carinii* and response to the ornithine decarboxylase inhibitor DL-alpha-difluoromethylornithine. Antimicrob. Agents Chemother. 40, 973–978.

Mercado, L., A. Dalcero, R. Masuelli and M. Combina. 2007. Diversity of *Saccharomyces* strains on grapes and winery surfaces, analysis of their contribution to fermentative flora of Malbec wine from Mendoza Argentina during two consecutive years. Food Microbiol. 24, 403–412.

Merico, A., P. Sulo, J. Piškur and C. Compagno. 2007. Fermentative lifestyle in yeasts belonging to the *Saccharomyces* complex. FEBS J. 274, 976–989.

Merkur, A.B., and W.G. Hodge. 2002. *Rhodotorula rubra* endophthalmitis in an HIV positive patient. Br. J. Ophthalmol. 86, 1444–1445.

Meroth, C.B., W.P. Hammes and C. Hertel. 2003. Identification and population dynamics of yeasts in sourdough fermentation processes by PCR-denaturing gradient gel electrophoresis. Appl. Environ. Microbiol. 69, 7453–7461.

Merz, W.G., and R.J. Hay (Eds). 2005. Medical Mycology, 10th edn. Hodder Arnold, London.

Merz, W.G., U. Khazan, M.A. Jabra-Rizk, L.C. Wu, G.J. Osterhout and P.F. Lehman. 1992. Strain delineation and epidemiology of *Candida* (*Clavispora*) *lusitaniae*. J. Clin. Microbiol. 30, 449–454.

Messenguy, F., B. Andre and E. Dubois. 2006. Diversity of nitrogen metabolism among yeast species: regulatory and evolutionary aspects. In: C.A. Rosa and G. Peter (Eds), Biodiversity and Ecophysiology of Yeasts. Springer-Verlag, Berlin, pp. 123–154.

Messner, R., H. Prillinger, F. Altmann, K. Lopandic, K. Wimmes, O. Molnár and F. Weigang. 1994. Molecular characterization and application of random amplified polymorphic DNA analysis of *Mrakia* and *Sterigmatomyces*. Int. J. Syst. Bacteriol. 44, 694–703.

Messner, R., H. Prillinger, M. Ibl and G. Himmler. 1995. Sequences of ribosomal genes and internal transcribed spacers move three plant parasitic fungi, *Eremothecium ashbyi*, *Ashbya gossypii*, and *Nematospora coryli*, towards *Saccharomyces cerevisiae*. J. Gen. Appl. Microbiol. 41, 31–42.

Mestre, M.C., C.A. Rosa and S.B. Fontenla. (2010) *Lindnera rhizosphaerae* sp. nov., a novel yeast species isolated from rhizospheric soil in a Patagonian native forest (Argentina). Int. J. Syst. Evol. Microbiol. doi:ijs.0.022863-0.

Metcalf, C.L., and W.P. Flint. 1939. Destructive and Useful Insects. McGrawHill Book Company, New York, 981pp.

Metchnikoff, E. 1908. The Prolongation of Life. Putnam and Sons, New York.

Metin, B., F. Findley and J. Heitman. 2010. The mating type locus (*MAT*) and sexual reproduction of *Cryptococcus*

heveanensis: insights into the evolution of sex and sex-determining chromosomal regions in fungi. PLOS Genetics 6, e1000961.

Metropolis, N., A.W. Rosenbluth, M.N. Rosenbluth, A.H. Teller and E. Teller. 1953. Equation of state calculations by fast computing machines. J. Chem. Phys. 21, 1087–1092.

Metschnikoff, E. 1884. Uber eine Sprosspilzkrankheit der Daphnien. Beitrag zur Lehre bei dem Kampf der Phagocyten gegen Krankheitserreger. Arch. Pathol. Anat. Physiol. R. Virchow 96, 177–195.

Metzler, B., F. Oberwinkler and H. Petzold. 1989. *Rhynchogastrema* gen. nov. and Rhynchogastremaceae fam. nov. (Tremellales). Syst. Appl. Microbiol. 12, 280–287.

Meyer, S.A. 1979. DNA relatedness between physiologically similar strains and species of yeasts of medical and industrial importance. In: S. Garrattini, S. Paglialunga and N.S. Scrimshaw (Eds), Investigation of Single Cell Protein. Pergamon Press, New York, pp. 13–19.

Meyer, S.A., and D.G. Ahearn. 1983. Validation of the names of some *Candida* species. Mycotaxon 17, 297–298.

Meyer, S.A., and H.J. Phaff. 1969. Deoxyribonucleic acid base composition in yeasts. J. Bacteriol. 97, 52–56.

Meyer, S.A., and H.J. Phaff. 1972. DNA base composition and DNA-DNA homology studies as tools in yeast systematics. In: A. Kocková-Kratochvílová and E. Minarik (Eds), Yeasts. Models in Science and Technics. Proc. Spec. Symp. on Yeasts, Smolenice. Slovak Academy of Sciences, Bratislava, pp. 375–387.

Meyer, S.A., and F.R. Simione. 1978. Heterogeneity within the species *Candida sake* and *Candida diddensii*. Abstr. Annu. Meet. Am. Soc. Microbiol. 81.

Meyer, S.A., and D. Yarrow. 1998. Validation of the names of three *Candida* species. Mycotaxon 66, 99–101.

Meyer, S.A., K. Anderson, R.E. Brown, M.T. Smith, D. Yarrow, G. Mitchell and D.G. Ahearn. 1975. Physiological and DNA characterization of *Candida maltosa*, a hydrocarbon-utilizing yeast. Arch. Microbiol. 104, 225–231.

Meyer, S.A., R.E. Brown and M.Th. Smith. 1977. Species status of *Hanseniaspora guilliermondii* Pijper. Int. J. Syst. Bacteriol. 27, 162–164.

Meyer, S.A., M.T. Smith and F.P. Simione. 1978. Systematics of *Hanseniaspora* Zikes and *Kloeckera* Janke. Antonie van Leeuwenhoek 44, 79–96.

Meyer, S.A., D.G. Ahearn and D. Yarrow. 1984. *Candida* Berkhout. In: N.J.W. Kreger-van Rij (Ed.), The Yeasts, A Taxonomic Study, 3rd edn. Elsevier, Amsterdam, pp. 585–844.

Meyer, S.A., R.W. Payne and D. Yarrow. 1998. *Candida* Berkhout. In: C.P. Kurtzman and J.W. Fell (Eds), The Yeasts, A Taxonomic Study, 4th edn. Elsevier, Amsterdam, pp. 454–573.

Meyer, W., K. Marszewska, M. Amirmostofian, R.P. Igreja, C. Hardtke, K. Methling, M.A. Viviani, A. Chindamporn, S. Sukroongreung, M.A. John, D.H. Ellis and T.C. Sorrell. 1999. Molecular typing of global isolates of *Cryptococcus neoformans* var. *neoformans* by polymerase chain reaction fingerprinting and randomly amplified polymorphic DNA – a pilot study to standardize techniques on which to base a detailed epidemiological survey. Electrophoresis 20, 1790–1799.

Meyer, W., A. Castaneda, S. Jackson, M. Huynh and E. Castañeda. 2003. Molecular typing of IberoAmerican *Cryptococcus neoformans* isolates. Emerg. Infect. Dis. 9, 189–195.

Meyer, W., T. Boekhout, E. Castaneda, H. Karaoglu, P. Ngamskulrungroj, S. Kidd, P. Escandon, F. Hagen, K. Marszewska, A. Velegraki et al. 2005. Molecular characterization of the *Cryptoroccus neoform* species complex. In: S. Levits (Ed.), Proc. 6th Int. Conf. *Cryptococcus* and Cryptococcosis. Boston, MA, pp. 41–42.

Meyer, W., D.M. Aanensen, T. Boekhout, M. Cogliati, M.R. Diaz, M. Carmela Esposto, M. Fisher, F. Gilgado, F. Hagen, S. Kaocharoen, A.P. Litvintseva, T.G. Mitchell, S.P. Simwami, L. Trilles, M.A. Viviani and K.J. Kwon-Chung. 2009. Consensus multi-locus sequence typing scheme for *Cryptococcus neoformans* and *Cryptococcus gattii*. Med. Mycol. 47, 561–570.

Meyer, W., F. Gilgado, P. Ngamskulrungroj, L. Trilles, F. Hagen, E. Castañeda and T. Boekhout. 2010. Molecular typing of the *Cryptococcus neoformans*/C. *gattii* complex. In: J. Heitman, T. Kozel, J. Kwon-Chung, J. Perfect and A. Casadevall (Eds), *Cryptococcus*: From Human Pathogen to Model Yeast. ASM Press, Washington, DC. (in press).

MFK Research 2007. The Impact of Wine, Grapes, and Grape Products on the American Economy. The Wine Business Center, St. Helena.

Micales, J.A., M.R. Bonde and G.L. Peterson. 1986. The use of isozyme analysis in fungal taxonomy and genetics. Mycotaxon 27, 405–449.

Micales, J.A., and M.R. Bonde. 1995. Isozymes: methods and applications. In: R.P. Singh and U.S. Singh (Eds), Molecular Methods in Plant Pathology. CRC Press, Boca Raton, FL, pp. 115–130.

Michalcakova, S., P. Sulo and E. Slavikova. 1993. Killer yeasts of *Kluyveromyces* and *Hansenula* genera with potential application in fermentation and therapy. Acta Biotechnol. 13, 341–350.

Mickelsen, P.A., M.C. Viano-Paulson, D.A. Stevens and P. Diaz. 1988. Clinical and microbiological features of infection with *Malassezia pachydermatis* in high-risk infants. J. Infect. Dis. 157, 1163–1168.

Middelhoven, W.J. 1993. Catabolism of benzene compounds by ascomycetous and basidiomycetous yeasts and yeast-like fungi. Antonie van Leeuwenhoek 63, 125–144.

Middelhoven, W.J. 1997. Identity and biodegradative abilities of yeasts isolated from plants growing in an arid climate. Antonie van Leeuwenhoek 72, 81–89.

Middelhoven, W.J. 2001. Identification of yeasts present in sour fermented foods and fodders. In: J.F.T. Spencer and A.L. Ragout de Spencer (Eds), Food Microbiology Protocols. Humana Press, Totowa, NJ, pp. 209–224.

Middelhoven, W.J. 2003. The yeast flora of the coast redwood, *Sequoia sempervirens*. Folia Microbiol. 48, 361–362.

Middelhoven, W.J. 2004a. The yeast flora of some decaying mushrooms on trunks of living trees. Folia Microbiol. 49, 569–573.

Middelhoven, W.J. 2004b. *Trichosporon wieringae* sp. nov., an anamorphic basidiomycetous yeast from soil, and assimilation of some phenolic compounds, polysaccharides and other non-conventional carbon sources by saprophytic *Trichosporon* species. Antonie van Leeuwenhoek 86, 329–337.

Middelhoven, W.J. 2005. *Cryptococcus allantoinivorans* sp. nov., an anamorphic basidiomycetous yeast (Tremellales)

physiologically resembling other species of the *Cryptococcus laurentii* complex that degrade polysaccharides and C-2 compounds. Antonie van Leeuwenhoek 87, 101–108.

Middelhoven, W.J. 2006. Polysaccharides and phenolic compounds as substrates for yeasts isolated from rotten wood and description of *Cryptococcus fagi* sp. nov. Antonie van Leeuwenhoek 90, 57–67.

Middelhoven, W.J., and M.M. Franzen. 1986. The yeast flora of ensiled whole-crop maize. J. Sci. Food Agric. 37, 855–861.

Middelhoven, W.J., and C.P. Kurtzman. 2003. Relation between phylogeny and physiology in some ascomycetous yeasts. Antonie van Leeuwenhoek 83, 69–74.

Middelhoven, W.J., and C.P. Kurtzman. 2007. Four novel yeasts from decaying organic matter: *Blastobotrys robertii* sp. nov., *Candida cretensis* sp. nov., *C. scorzettiae* sp. nov. and *C. vadensis* sp. nov. Antonie van Leeuwenhoek 92, 233–244.

Middelhoven, W.J., and M.D. Sollewijn Gelpke. 1995. Partial conversion of cinnamic acid into styrene by growing cultures and cell-free extracts of the yeast *Cryptococcus elinovii*. Antonie van Leeuwenhoek 67, 217–219.

Middelhoven, W.J., and F. Spaaij. 1997. *Rhodotorula cresolica* sp. nov., a cresol-assimilating yeast species isolated from soil. Int. J. Syst. Bacteriol. 47, 324–327.

Middelhoven, W.J., T .E. Hoogkamer, M.C. Niet and N.J.W. Krieger van Rij. 1984. *Trichosporon adeninovorans* sp. nov., a yeast species utilizing adenine, xanthine, uric acid, putrescine, and primary *n*-alkylamines as sole source of carbon. Antonie van Leeuwenhoek 50, 369–378.

Middelhoven, W.J., M.C. Hoogkamer-Te Niet, W.T. de Laat, C. Weijers and C.J. Bulder. 1986. Oxidation of amines by yeasts grown on 1-aminoalkanes or putrescine as the sole source of carbon, nitrogen and energy. Antonie van Leeuwenhoek 52, 525–535.

Middelhoven, W.J., I.M. de Jong and M. de Winter. 1990. Yeasts and fungi occurring in ensiled whole-crop maize and other ensiled vegetable crops. Antonie van Leeuwenhoek 57, 3, 153–158.

Middelhoven, W.J., I.M. de Jong and M. de Winter. 1991. *Arxula adeninivorans*, a yeast assimilating many nitrogenous and aromatic compounds. Antonie van Leeuwenhoek 59, 129–137.

Middelhoven, W.J., M. Koorevaar and G.W. Schuur. 1992. Degradation of benzene compounds by yeasts in acidic soils. Plant Soil 145, 37–43.

Middelhoven, W.J., G. Scorzetti and J.W. Fell. 1999. *Trichosporon guehoae* sp. nov., an anamorphic basidiomycetous yeast. Can. J. Microbiol. 45, 686–690.

Middelhoven, W.J., G. Scorzetti and J.W. Fell. 2001. *Trichosporon porosum* comb. nov., an anamorphic basidiomycetous yeast inhabiting soil, related to the *loubieri/laibachii* group of species that assimilate hemicelluloses and phenolic compounds. FEMS Yeast Res. 1, 15–22.

Middelhoven, W., C.P. Kurtzman and A. Vaughan-Martini. 2000a. *Saccharomyces bulderi* sp. nov., a yeast that ferments gluconolactone. Antonie van Leeuwenhoek 77, 223–228.

Middelhoven, W.J., G. Scorzetti and J.W. Fell. 2000b. *Trichosporon veenhuisii* sp. nov., an alkane-assimilating anamorphic basidiomycetous yeast. Int. J. Syst. Evol. Microbiol. 50, 381–387.

Middelhoven, W.J., E. Guého and G.S. de Hoog. 2000c. Phylogenetic position and physiology of *Cerinosterus cyanescens*. Antonie van Leeuwenhoek 77, 313–320.

Middelhoven, W.J., Á. Fonseca, S.C. Carreiro, F.C. Pagnocca and O.C. Bueno. 2003. *Cryptococcus haglerorum*, sp. nov.: an anamorphic basidiomycetous yeast isolated from nests of the leaf-cutting ant *Atta sexdens*. Antonie van Leeuwenhoek 83, 167–174.

Middelhoven, W.J., G. Scorzetti and J.W. Fell. 2004. Systematics of the anamorphic basidomycetous yeast genus *Trichosporon* Behrend with the description of five novel species: *Trichosporon vadense*, *T. smithiae, T. dehoogii, T. scarabaeorum*, and *T. gamsii*. Int. J. Syst. Evol. Biol. 54, 975–986.

Midgley, G. 1989. The diversity of *Pityrosporum* (*Malassezia*) yeasts *in vivo* and *in vitro*. Mycopathologia 106, 143–153.

Midgley, G. 1993. Morphological variation in *Malassezia* and its significance in pityriasis versicolor. In: H. van de Bossche, F.C. Odds and D. Kerridge (Eds), Dimorphic Fungi in Biology and Medicine. Plenum Press, New York, pp. 267–277.

Midgley, G. 2000. The lipohilic yeasts: state of the art and prospects. Med. Mycol. 38 (Suppl. 1), 9–16.

Midgley, G., E. Guého and J. Guillot. 1998. Diseases caused by *Malassezia* species. In: L. Ajello and R.J. Ray (Eds), Topley and Wilson's Microbiology and Microbial Infections, Vol. 4, Chapter 12, Medical Mycology. Hodder Arnold, London, pp. 201–211.

Midreuil, F., J. Guillot, E. Guého, F. Renaud, M. Mallié and J.M. Bastide. 1999. Genetic diversity in the yeast species *Malassezia pachydermatis* analysed by multilocus enzyme electrophoresis. Int. J. Syst. Bacteriol. 49, 1287–1294.

Migula, W. 1900. System der Bakterien, Vol. 2. Fischer, Jena.

Migula, W. 1912. Kryptogamen-Flora von Deutschland, Deutsch-Osterreich und der Schweiz, Band III. Verlag F. von Zezschwitz, Gera, pp. 324–418.

Mikata, K., and I. Banno. 1985. Scanning electron microscopy of ascospores of *Pichia membranaefaciens* Hansen. Inst. Ferment. Osaka Res. Commun. 12, 70–77.

Mikata, K., and I. Banno. 1987. Surface structure of ascospores of the genus *Schizosaccharomyces*. Inst. Ferment. Osaka Res. Commun. 13, 45–51.

Mikata, K., and I. Banno. 1989. Preservation of yeast cultures by L-drying: viability after 5 years of storage at 5°C. Inst. Ferment. Osaka Res. Commun. 14, 80–103.

Mikata, K., and K. Ueda-Nishimura. 2000. Reclassification of *Pichia membranifaciens* sensu Kurtzman. Antonie van Leeuwenhoek 77, 159–171.

Mikata, K., and Y. Yamada. 1995. *Ogataea kodamae*, a new combination for a methanol-assimilating yeast species, *Pichia kodamae* van der Walt et Yarrow. Inst. Ferment. Osaka Res. Commun. 17, 99–101.

Mikata, K., K. Ueda-Nishimura, S. Goto, C.P. Kurtzman, M. Suzuki, D. Yarrow and T. Nakase. 1999. Reidentification of yeast strains deposited as *Candida agrestis*, with a description of *Candida kofuensis* sp. nov. Microbiol. Cult. Collect. 15, 49–57.

Mikata, K., K. Ueda-Nishimura and T. Hisatomi. 2001. Three new species of *Saccharomyces* sensu lato van der Walt from Yaku Island in Japan: *Saccharomyces naganishii* sp. nov., *Saccharomyces humaticus* sp. nov. and *Saccharomyces*

yakushimaensis sp. nov. Int. J. Syst. Evol. Microbiol. 51, 2189–2198.
Miková, H., M. Rosenberg, L. Kritofíková and P. Sulo. 1999. Production of L-malate from fumarate by the yeast *Dipodascus magnusii*. Acta Biotechnol. 19, 357–363.
Milla, P., F. Viola, B.S. Oliaro, F. Rocco, L. Cattel, B.M. Joubert, R.J. LeClair, S.P. Matsuda and G. Balliano. 2002. Subcellular localization of oxidosqualene cyclases from *Arabidopsis thaliana, Trypanosoma cruzi*, and *Pneumocystis carinii* expressed in yeast. Lipids 37, 1171–1176.
Miller, G.R., and S. Baharaeen. 1979. DNA base composition and photo-reactivation capabilities of six *Hansenula* species. Antonie van Leeuwenhoek 45, 365–368.
Miller, J.M., and F.P. Keen. 1960. Biology and control of the western pine beetle. U.S. Dept. Agric. Misc. Publ. 800, 381.
Miller, M., and A.D. Johnson. 2006. Mating and parasexual genetics in *Candida albicans*. In: J. Heitman, S.G. Filler, J.E. Edwards, Jr. and A.P. Mitchell (Eds), Molecular Principles of Fungal Pathogenesis. ASM Press, Washington, DC, pp. 71–88.
Miller, M.W., and E.M. Mrak. 1953. Yeasts associated with dried-fruit beetles in figs. Appl. Microbiol. 1, 174–178.
Miller, M.W., and H.J. Phaff. 1958. A comparative study of the apiculate yeasts. Mycopathol. Mycol. Appl. 10, 113–141.
Miller, M.W., and H.J. Phaff. 1962. Successive microbial populations in Calimyrna figs. Appl. Microbiol. 10, 394–400.
Miller, M.W., and H.J. Phaff. 1984. *Nadsonia* Sydow. In: N.J.W. Kreger-van Rij (Ed.), The Yeasts, A Taxonomic Study, 3rd edn. Elsevier, Amsterdam, pp. 279–284.
Miller, M.W., and H.J. Phaff. 1998a. *Metschnikowia* Kamienski. In: C.P. Kurtzman and J.W. Fell (Eds), The Yeasts, A Taxonomic Study, 4th edn. Elsevier, Amsterdam, pp. 256–267.
Miller, M.W., and H.J. Phaff. 1998b. *Saccharomycodes* E.C. Hansen. In: C.P. Kurtzman and J.W. Fell (Eds), The Yeasts, A Taxonomic Study, 4th edn. Elsevier Science, Amsterdam, pp. 372–373.
Miller, M.W., and N. van Uden. 1970. *Metschnikowia* Kamienski. In: J. Lodder (Ed.), The Yeasts, A Taxonomic Study, 2nd edn. North Holland, Amsterdam, pp. 408–429.
Miller, M.W., E.R. Barker and J.I. Pitt. 1967. Ascospore numbers in *Metschnikowia*. J. Bacteriol. 94, 258–259.
Miller, M.W., H.J. Phaff, M. Miranda, W.B. Heed and W.T. Starmer. 1976a. *Torulopsis sonorensis*, a new species of the genus *Torulopsis*. Int. J. Syst. Bacteriol. 26, 88–91.
Miller, M.W., M. Yoneyama and M. Soneda. 1976b. *Phaffia*, a new yeast genus in the Deuteromycotina (Blastomycetes). Int. J. Syst. Bacteriol. 26, 286–291.
Miller, M., J.L.F. Kock, G.H.J. Pretorius and D.J. Coetzee. 1989. The value of orthogonal-field-alteration gel electrophoresis and other criteria in the taxonomy of the genus *Pichia* Hansen emend. Kurtzman. System. Appl. Microbiol. 12, 191–202.
Miller, W.G., A.A. Padhye, W. van Bonn, E. Jensen, M.E. Brandt and S.H. Ridgway. 2002. Cryptococcosis in a bottlenose dolphin (*Tursiops truncates*) caused by *Cryptococcus neoformans* var. *gattii*. J. Clin. Microbiol. 40, 721–724.
Mills, D.A., E.A. Johannsen and L. Cocolin. 2002. Yeast diversity and persistence in *Botrytis*-affected wine fermentations. Appl. Environ. Microbiol. 68, 4884–4893.
Millson, S.H., and I.H. Evans. 2007. Multiple dextranases from the yeast *Lipomyces starkeyi*. Antonie van Leeuwenhoek 92, 399–404.
Mimee, B., C. Labbé, R. Pelletier and R.R. Bélanger. 2005. Antifungal activity of flocculosin, a novel glycolipid isolated from *Pseudozyma flocculosa*. Antimicrob. Agents Chemother. 49, 1597–1599.
Min, K.H., and K.J. Kwon-Chung. 1986. The biochemical basis for the distinction between the two *Cryptococcus neoformans* varieties with CGB medium. Zbl. Bakt. Hyg. A 261, 471–480.
Minami, K., M. Yamamura, S. Shimizu, K. Ogawa and N. Sekine. 1978. A new methanol-assimilating, high productive, thermophilic yeast. J. Ferment. Technol. 56, 1–7.
Minegishi, H., T. Miura, Y. Yoshida, R. Usami and F. Abe. 2006. Phylogenetic analysis of pectin-degrading yeasts from deep-sea environments. J. Jpn. Soc. Extremophile. 5, 21–26.
Minervini, F., M.T. Montagna, G. Spilotros, L. Monaci, M.P. Santacroce and A. Visconti. 2001. Survey on mycoflora of cow and buffalo dairy products from southern Italy. Int. J. Food Microbiol. 69, 141–146.
Minh, B.Q., L.S. Vinh, A. von Haeseler and H.A. Schmidt. 2005. pIQPNNI: parallel reconstruction of large maximum likelihood phylogenies. Bioinformatics 21, 3794–3796.
Minin, V., Z. Abdo, P. Joyce and J. Sullivan. 2003. Performance-based selection of likelihood models for phylogeny estimation. Syst. Biol. 52, 674–683.
Minter, D.M. 2009. *Cyberlindnera*, a replacement name for *Lindnera* Kurtzman et al., nom. illegit. Mycotaxon 110, 473–476.
Miranda, I., R. Silva and M.A.S. Santos. 2006. Evolution of the genetic code in yeasts. Yeast 23, 203–213.
Miranda, L.N., I.M. van der Heijden, S.F. Costa, A.P.I. Sousa, R. A. Sienra, S. Gobara, C.R. Santos, R.D. Lobo, V.P. Pessoa Jr. and A.S. Levin. 2009. *Candida* colonisation as a source for candidaemia. J. Hosp. Infect. 72, 9–16.
Miranda, M., D.L. Holzschu, H.J. Phaff and W.T. Starmer. 1982. *Pichia mexicana*, a new heterothallic yeast from cereoid cacti in the North American Sonoran Desert. Int. J. Syst. Bacteriol. 32, 101–107.
Mirhendi, H., K. Makimura, K.K. Zomorodian, T. Yamada, T. Sugita and H. Yamaguchi. 2005. A simple PCR-RFLP method for identification and differentiation of 11 *Malassezia* species. J. Microbiol. Methods 61, 281–284.
Mirzaee, M.R., M.R. Safarnedjad and M. Mohammadi. 2007. A new report of preharvest ear rot of corn caused by *Geotrichum candidum* from Iran. Agric. Appl. Biol. Sci. 72, 925–933.
Misra, V.C., and H.S. Randhawa. 1976. *Sporobolomyces salmonicolor* var. *fischeri*, a new yeast. Arch. Microbiol. 108, 141–143.
Mitchell, D.H., T.C. Sorrell, A.M. Allworth, C.H. Heath, A.R. McGregor, K. Papahaoum, M.J. Richards and T. Gottlieb. 1995. Cryptococcal disease of the CNS in immunocompetent hosts: influence of cryptococcal variety on clinical manifestations and outcome. Clin. Infect. Dis. 20, 611–616.
Mitchell, T.G., and J.R. Perfect. 1995. Cryptococcosis in the era of AIDS – 100 years after the discovery of *Cryptococcus neoformans*. Clin. Microbiol. Rev. 8, 515–548.
Mitchell, T.G., T.J. White and J.W. Taylor. 1992. Comparison of 5.8S ribosomal DNA sequences among the basidiomycetous yeast genera *Cystofilobasidium*, *Filobasidium* and *Filobasidiella*. J. Med. Vet. Mycol. 30, 207–218.

Mitrakul, C.M., T. Henick-Kling and C.M. Egli. 1999. Discrimination of *Brettanomyces*/*Dekkera* yeast isolates from wine by using various DNA fingerprinting. Food Microbiol. 16, 314.

Mittag, H. 1994. Fine structural investigation of *Malassezia furfur*. II. The envelope of the yeast cells. Mycoses 38, 13–21.

Miura, T., F. Abe, A. Inoue, R. Usami and K. Horikoshi. 2001. Purification and characterization of novel extracellular endopolygalacturonases from a deep-sea yeast, *Cryptococcus* sp. N6, isolated from the Japan Trench. Biotechnol. Lett. 23, 1735–1739.

Miura, T., F. Abe, A. Inoue, R. Usami and K. Horikoshi. 2002. Superoxide dismutase is involved in high tolerance to copper in the deep-sea yeast, *Cryptococcus* sp. N6. Biotechnol. Lett. 24, 1069–1074.

Miura, Y., K. Kondo, T. Saito, H. Shimada, P.D. Fraser and N. Misawa. 1998. Production of the carotenoids lycopene, beta-carotene, and astaxanthin in the food yeast *Candida utilis*. Appl. Environ. Microbiol. 64, 1226–1229.

Mix, A.J. 1935. The life history of *Taphrina deformans*. Phytopathology 25, 41–66.

Mix, A.J. 1936a. The genus *Taphrina*. I: an annotated bibliography. Univ. Kansas Sci. Bull. 24, 113–149.

Mix, A.J. 1936b. The genus *Taphrina*. II: a list of valid species. Univ. Kansas Sci. Bull. 24, 151–176.

Mix, A.J. 1947a. Some new species of *Taphrina*. Trans. Kansas Acad. Sci. 50, 77–83.

Mix, A.J. 1947b. *Taphrina osmundae* Nishida and *Taphrina higginsii* sp. nov. Mycologia 39, 71–76.

Mix, A.J. 1949. A monograph of the genus *Taphrina*. Univ. Kansas Sci. Bull. [Reprinted: 1969, Bibliotheca Mycologica, Vol. 18. Cramer, Vaduz] 33, 1–167.

Mix, A.J. 1953. Differentiation of species of *Taphrina* in culture. Utilization of nitrogen compounds. Mycologia 45, 649–670.

Mix, A.J. 1954. Additions and emendations to a monograph of the genus *Taphrina*. Trans. Kansas Acad. Sci. 57, 55–65.

Miyake, S., A. Hamaoka and Y. Yoshizawa. 2001. Clinical usefulness of antigen-captured ELISA method using mouse anti-*Trichosporon asahii* monoclonal antibody D-8 for diagnosis of summer-type hypersensitivity pneumonitis. Nihon Kokyuki Gakkai Zasshi. 39, 7–11.

Miyata, M., T. Kanbe and K. Tanaka. 1985. Morphological alterations of the fission yeast *Schizosaccharomyces pombe* in the presence of aculeacin A: spherical wall formation. J. Gen. Microbiol. 131, 611–621.

MFK Research. 2007. The Impact of Wine, Grapes and Grape Products on the American Economy. The Wine Business Center, St. Helena.

Mocan, H., A.V. Murphy, T.J. Beattie and T.A. McAllister. 1989. Fungal peritonitis in children on continuous ambulatory peritoneal dialysis. Scott. Med. J. 34, 494–496.

Mocroft, A., S. Vella, T.L. Benfield, A. Chiesi, V. Miller, P. Gargalianos, A. d'Arminio Monforte, I. Yust, J.N. Bruun, A.N. Philips and J.D. Lungren. 1998. Changing patterns of mortality across Europe in patients infected with HIV-1. Lancet 352, 1725–1730.

Mogi, M. 1938a. Studies on the yeasts found in "Miso". J. Agric. Chem. Soc. Jpn. 14, 951–988. In Japanese.

Mogi, M. 1938b. Studies on the yeasts found in "Miso" IV. J. Agric. Chem. Soc. Jpn. 14, 1297–1324. In Japanese.

Mogi, M. 1939. Yeasts from a soybean paste "Miso". Part III. Taxonomy, affinity and characteristic properties of the yeasts isolated from a soybean paste "Miso". J. Agric. Chem. Soc. Jpn. 15, 1221–1232. In Japanese.

Mogi, M. 1942. Studies on the yeasts found in "Miso". J. Agric. Chem. Soc. Jpn. 18, 733–741. In Japanese.

Mohl, W., M.M. Lerch, M. Klotz, H. Freidank and M. Zeitz. 1998. Infection of an intravenous port system with *Metschnikowia pulcherrima* Pitt et Miller. Mycoses 41, 425–426.

Mokwena, T.A., E. Jansen van Rensburg and J. Myburgh. 2000. The isolation and classification of *Candida mokoenaii* sp. nov.: a new yeast isolate from South African soil. Antonie van Leeuwenhoek 77, 43–47.

Mol, P.C., and J.G.H. Wessels. 1987. Linkages between glucosaminoglycan and glucan determine alkali-insolubility of the glucan in walls of S. *cerevisiae*. FEMS Microbiol. Lett. 41, 95–99.

Molina, F.I., P. Shen and S.-C. Jong. 1993. Validation of the species concept in the genus *Dekkera* by restriction analysis of genes coding for rRNA. Int. J. Syst. Bacteriol. 43, 32–35.

Mollapour, M., and P.W. Piper. 2001a. The ZbYME2 gene from the food spoilage yeast *Zygosaccharomyces bailii* confers not only YME2 function in *Saccharomyces cerevisiae*, but also the capacity for catabolism of sorbate and benzoate, two major weak organic acid preservatives. Mol. Microbiol. 42, 919–930.

Mollapour, M., and P.W. Piper. 2001b. Targeted gene deletion in *Zygosaccharomyces bailii*. Yeast 18, 173–186.

Möller, A. 1895. Protobasidiomyceten. In: A.F.W. Schimper (Ed.), Botanische Mitteilungen aus den Tropen, Vol. 8. Gustav Fischer, Jena, pp. 1–179.

Molnár, O., and H. Prillinger. 2005. Analysis of yeast isolates related to *Metschnikowia pulcherrima* using the partial sequences of the large subunit rDNA and the actin gene; description of *Metschnikowia andauensis* sp. nov. Syst. Appl. Microbiol. 28, 717–726.

Molnár, O., and H. Prillinger. 2006. *Cryptococcus zeae*, a new yeast species associated with *Zea mays*. Microbiol. Res. 161, 347–354.

Molnár, O., H. Prillinger, K. Lopandic, F. Weigang and E. Staudacher. 1996. Analysis of coenzyme Q systems, monosaccharide patterns of purified cell walls, and RAPD-PCR patterns in the genus *Kluyveromyces*. Antonie van Leeuwenhoek 70, 67–78.

Molnar, O., G. Schatzmayr, E. Fuchs and H. Prillinger. 2004. *Trichosporon mycotoxinivorans* sp. nov., a new yeast species useful in biological detoxification of various mycotoxins. Syst. Appl. Microbiol. 27, 661–671.

Momany, M. 2002. Polarity in filamentous fungi: establishment, maintenance and new axes. Curr. Opin. Microbiol. 5, 580–585.

Montague, J.R., and K.Y. Kaneshiro. 1982. Flower-breeding species of Hawaiian drosophilids in an early stage of sympatry. Pac. Insects 24, 209–213.

Montcalm, L.J., and K. Wolfe. 2006. Genome evolution in hemiascomycete yeasts. In: A.J.P. Brown (Ed.), The Mycota XIII. Springer-Verlag, Berlin, pp. 19–34.

Montes, M.J., C. Belloch, M. Galiana, M.D. Garcia, C. Andres, S. Ferrer, J.M. Torres-Rodriguez and J. Guinea. 1999. Polyphasic taxonomy of a novel yeast isolated from

antarctic environment; description of *Cryptococcus victoriae* sp. nov. Syst. Appl. Microbiol. 22, 97–105.
Montijn, R.C., P. van Wolven, S. de Hoog and F.M. Klis. 1997. β-Glucosylated proteins in the cell wall of the black yeast *Exophiala* (*Wangiella*) *dermatitidis*. Microbiology 143, 1673–1680.
Montour, L., R. Tey and J. Xu. 2003. Isolation of *Candida dubliniensis* in an aboriginal community in Ontario, Can. J. Clin. Microbiol. 41, 3423–3426.
Montrocher, R. 1967. Quelques nouvelles espèces et variétés du genre *Candida* (levures asporogènes). Rev. Mycol. 32, 69–92.
Montrocher, R. 1980. Significance of immunoprecipitation in yeast taxonomy: antigenic analyses of some species within the genus *Candida*. Cell. Mol. Biol. 26, 293–302.
Montrocher, R., and M.L. Claisse. 1984. Biochemical studies in the yeast genus *Candida*. Cell. Mol. Biol. 30, 291–301.
Moon, N.J., E.G. Hammond and B.A. Glatz. 1978. Conversion of cheese whey and whey permeate to oil and single cell protein. J. Dairy Sci. 61, 1537–1547.
Moore, J.E., J. Xu, B.C. Millar and S. Elshibly. 2002. Edible dates (*Phoenix dactylifera*), a potential source of *Cladosporium cladosporioides* and *Sporobolomyces roseus*: implications for public health. Mycopathologia 154, 25–28.
Moore, K.J., M.G. Johnson and J.R. Morris. 1988. Indigenous yeast microflora on Arkansas White Riesling (*Vitis vinifera*) grapes and in model must systems. J. Food Sci. 53, 1725–1728.
Moore, M. 1934. A new *Geotrichum* from bronchial and pulmonary infection, *Geotrichum versiforme* Moore n. sp. Ann. Mo. Bot. Gard. 21, 349–366.
Moore, M. 1935. Head infection caused by a new *Hemispora*, *H. coremiformis*. Ann. Mo. Bot. Gard. 22, 317–332.
Moore, M.M., and M.S. Strom. 2003. Infection and mortality by the yeast *Metschnikowia bicuspidata* var. *bicuspidata* in chinook salmon fed live adult brine shrimp (*Artemia franciscana*). Aquaculture 220, 43–57.
Moore, R.T. 1965. The ultrastructure of fungal cells. In: G.C. Ainsworth and A.S. Sussman (Eds), The Fungi, An Advanced Treatise, Vol. 1. Academic Press, New York, pp. 95–118.
Moore, R.T. 1972. Ustomycota, a new division of higher fungi. Antonie van Leeuwenhoek 38, 567–584.
Moore, R.T. 1978. Taxonomic significance of septal ultrastructure with particular reference to the jelly fungi. Mycologia 70, 1007–1024.
Moore, R.T. 1979. Septal ultrastructure in *Sirobasidium magnum* and its taxonomic implications. Antonie van Leeuwenhoek 45, 113–118.
Moore, R.T. 1980. Taxonomic proposals for the classification of marine yeasts and other yeast-like fungi including the smuts. Bot. Mar. 23, 361–373.
Moore, R.T. 1985. The challenge of the dolipore/parenthesome septum. In: D. Moore, L.A. Casselton, D.A. Wood and J.A. Frankland (Eds), Developmental Biology of Higher Fungi. Cambridge University Press, Cambridge, pp. 175–212.
Moore, R.T. 1987a. Additions to the genus *Vanrija*. Bibl. Mycol. 108, 167–173.
Moore, R.T. 1987b. Micromorphology of yeasts and yeast-like fungi and its taxonomic implications. In: G.S. de Hoog, M.Th. Smith and A.C.M. Weijman (Eds), The Expanding Realm of Yeast-like Fungi. Elsevier, Amsterdam, pp. 203–226. (Stud. Mycol. 30, 203–226).
Moore, R.T. 1988b. Taxonomic implications of septal ultrastructure in the Aphyllophorales. In: F. Wolkinger (Ed.), Internationales Aphyllophorales-Symposium Eisenstadt, 1982. Austrian Academy of Sciences, Graz, pp. 55–63.
Moore, R.T. 1990. The genus *Lalaria* gen. nov.: *Taphrinales anamorphosum*. Mycotaxon 38, 315–330.
Moore, R.T. 1996a. The dolipore/parenthesome spectrum in modern taxonomy. In: B. Sney, S. Jabali-Hare, S. Neate and G. Dijst (Eds), *Rhizoctonia* Species: Taxonomy, Molecular Biology, Ecology, Pathology and Disease Control. Kluwer, Dordrecht, pp. 1–23.
Moore, R.T. 1998a. *Lalaria* R.T. Moore. In: C.P. Kurtzman and J. W. Fell (Eds), The Yeasts, A Taxonomic Study, 4th edn. Elsevier, Amsterdam, pp. 582–591.
Moore, R.T. 1998b. Cytology and ultrastructure of yeasts and yeastlike fungi. In: C.P. Kurtzman and J.W. Fell (Eds), The Yeasts, A Taxonomic Study. Elsevier, Amsterdam, pp. 33–44.
Moore, R.T., and N.J.W. Kreger-van Rij. 1972. Ultrastructure of *Filobasidium* Olive. Can. J. Microbiol. 18, 1949–1951.
Moore, R.T., and J.H. McAlear. 1962. Fine structures of mycota. Observations on septa of ascomycetes and basidiomycetes. Am. J. Bot. 49, 86–94.
Morais, P.B., A.N. Hagler, C.A. Rosa and L.C. Mendonça-Hagler. 1992. Yeast associated with *Drosophila* in tropical forests of Rio de Janeiro, Brazil. Can. J. Microbiol. 38, 1150–1155.
Morais, P.B., C.A. Rosa, A.N. Hagler and L.C. Mendonça-Hagler. 1994. Yeast communities of the cactus *Pilosocereus arrabidae* as resources for larval and adult stages of *Drosophila serido*. Antonie van Leeuwenhoek 66, 313–317.
Morais, P.B., C.A. Rosa, A.N. Hagler and L.C. Mendonca-Hagler. 1995a. Yeast communities as descriptors of habitat use by the *Drosophila fasciola* subgroup (replete group) in Atlantic rain forests. Oecologia 104, 45–51.
Morais, P.B., M.B. Martins, L.B. Klaczko, L.C. Mendonça-Hagler and A.N. Hagler. 1995b. Yeast succession in the Amazon fruit *Parahancornia amapa* as resource partitioning among *Drosophila* species. Appl. Environ. Microbiol. 61, 4251–4257.
Morais, P.B., C.A. Rosa, S.A. Meyer, L.C. Mendonça-Hagler and A.N. Hagler. 1995c. *Candida amapae*, a new amino acid-requiring yeast from Amazonian fruit, *Parahancornia amapa*. J. Ind. Microbiol. 14, 531–535.
Morais, P.B., C.A. Rosa, J. Abranches, L.C. Mendonça-Hagler and A.N. Hagler. 1996. Yeasts vectored by *Drosophila quadrum* (Calloptera group) in tropical rain forests. Rev. Microbiol. 27, 87–91.
Morais, P.B., C.A. Rosa, V.R. Linardi, C. Pataro and A. Maia. 1997. Characterization and succession of yeast populations associated with spontaneous fermentations during the production of Brazilian sugar-cane aguardente. World J. Microbiol. Biotechnol. 13, 241–243.
Morais, P.B., L.C.R.S. Teixeira, J.M. Bowles, M.A. Lachance and C.A. Rosa. 2004. *Ogataea falcaomoraisii* sp. nov., a sporogenous methylotrophic yeast from tree exudates. FEMS Yeast Res. 5, 81–85.
Morais, P.B., M.-A. Lachance and C.A. Rosa. 2005. *Saturnispora hagleri* sp. nov., a yeast species isolated from *Drosophila* flies in Atlantic rainforest in Brazil. Int. J. Syst. Evol. Microbiol. 55, 1725–1727.
Morales, I.J., P.K. Vohra, V. Puri, T.J. Kottom, A.H. Limper and C.F. Thomas Jr. 2003. Characterization of a lanosterol 14

alphademethylase from *Pneumocystis carinii*. Am. J. Respir. Cell Mol. Biol. 29, 232–238.

Moran, G.P., D.J. Sullivan and D.C. Coleman. 2002. Emergence of non-*Candida albicans Candida* species as pathogens. In: R.A. Calderone (Ed.), *Candida* and Candidiasis. ASM Press, Washington, DC, pp. 37–53.

Moreau, A., S. Durand and R. Morosoli. 1992. Secretion of a *Cryptococcus albidus* xylanase in *Saccharomyces cerevisiae*. Gene 116, 109–113.

Moreira, N., F. Mendes, T. Hogg and I. Vasconcelos. 2005. Alcohols, esters and heavy sulphur compounds production by pure and mixed cultures of apiculate wine yeasts. Int. J. Food Microbiol. 103, 285–294.

Moreira, S.R., R.F. Schwan, E.P. Carvalho and A.E. Wheals. 2001. Isolation and identification of yeasts and filamentous fungi from yoghurts in Brazil. Braz. J. Microbiol. 32, 1–11.

Moreno-Arribas, M.V., and M.C. Polo. 2005. Winemaking biochemistry and microbiology: current knowledge and future trends. Crit. Rev. Food Sci. Nutr. 45, 265–286.

Morenz, J. 1963. *Geotrichum candidum* Link. Taxonomie, Diagnose und medizinische Bedeutung. Mykol. Schr. Reihe 1, 1–79.

Morenz, J. 1964. Taxonomische Untersuchungen zur Gattung *Geotrichum* Link. Mykol. Schr. Reihe 2, 33–64.

Moreteau, B., Y. Carton, M.C. Pignal and J.R. David. 1992. Intraspecific variation of *Drosophila buzzatii* larval breeding success on *Opuntia*: a yeast–plant–insect relationship. Entomol. Exp. Appl. 64, 87–95.

Moretti, A., K. Fukushima, K. Takizawa, M. Suzuki, V. Vidotto, F.T. Cannizzo, L. Boncio and E. Bollo. 2007. First report of oral colonization by *Debaryomyces nepalensis* in a dog. Mycopathologia 164, 189–192.

Morgenstern, B. 1999. DIALIGN 2: improvement of the segment-to-segment-approach to multiple sequence alignment. Bioinformatics 15, 211–218.

Mori, H., and H. Onishi. 1967. Diploid hybridization in a heterothallic haploid yeast, *Saccharomyces rouxii*. Appl. Microbiol. 15, 928–934.

Morikawa, Y., S. Takasawa, I. Masunaga and K. Takayama. 1985. Ethanol production from D-xylose and cellobiose by *Kluyveromyces cellobiovorus*. Biotechnol. Bioeng. 27, 509–513.

Morimoto, T., H. Oishi, Y. Watanabe and Y. Tamai. 1998. Phospholipid deacylating activities included in yeast. Biosci. Biotechnol. Biochem. 62, 1633–1636.

Morishita, N., Y. Sei and T. Sugita. 2006. Molecular analysis of *Malassezia* microflora from patients with pityriasis versicolor. Mycopathologia 161, 61–65.

Morita, T., M. Konishi, T. Fukuoka, T. Imura and D. Kitamoto. 2007. Physiological differences in the formation of the glycolipid biosurfactants, mannosylerythritol lipids, between *Pseudozyma antarctica* and *Pseudozyma aphidis*. Appl. Microbiol. Biotechnol. 74, 307–315.

Moriya, K., R. Usami and K. Horikoshi. 1995. Marine killer yeasts isolated from deep sea and their properties. J. Mar. Biotechnol. 2, 135–138.

Moriyon, I., and C. Ramírez. 1974. New species of yeasts isolated from an acid washed brown soil. Proc. 4th Int. Symp. Yeasts Vienna, Part I, 233–234.

Morosoli, R., C. Roy and M. Yaguchi. 1986. Isolation and partial primary sequence of a xylanase from the yeast *Cryptococcus albidus*. Biochim. Biophys. Acta 870, 473–478.

Morris, A., J.D. Lundgren, H. Masur, P.D. Walzer, D.L. Hanson, T. Frederick, L. Huang, C.B. Beard and J.E. Kaplan. 2004a. Current epidemiology of *Pneumocystis* pneumonia. Emerg. Infect. Dis. 10, 1713–1720.

Morris, A., F.C. Sciurba, I.P. Lebedeva, A. Githaiga, W.M. Elliott, J.C. Hogg, L. Huang and K.A. Norris. 2004b. Association of chronic obstructive pulmonary disease severity and *Pneumocystis* colonization. Am. J. Respir. Crit Care Med. 170, 408–413.

Morris, A., F.C. Sciurba and K.A. Norris. 2008a. *Pneumocystis*: a novel pathogen in chronic obstructive pulmonary disease? COPD 5, 43–51.

Morris, A., K. Wei, K. Afshar and L. Huang. 2008b. Epidemiology and clinical significance of *Pneumocystis* colonization. J. Infect. Dis. 197, 10–17.

Morris, D.O., K. O'Shea, F.S. Shofer and S. Rankin. 2005. *Malassezia pachydermatis* carriage in dog owners. Emerg. Infect. Dis. 11, 83–88.

Morris, J.T., M. Beckius and C.K. McAllister. 1991. *Sporobolomyces* infection in an AIDS patient. J. Infect. Dis. 164, 623–624.

Morris, S.C. 1985. Tomato postharvest diseases and their control. Commercial Horticulture 5, 18–21.

Morrison, D.A., and J.T. Ellis. 1997. Efffects of nucleotide sequence alignment on phylogeny estimation: a case study of 18S rDNAs of Apicomplexa. Mol. Biol. Evol. 14, 428–441.

Morrissey, W.F., B. Davenport, A. Querol and A.D. Dobson. 2004. The role of indigenous yeasts in traditional Irish cider fermentations. J. Appl. Microbiol. 97, 647–655.

Morrow, J.D. 1994. Prosthetic cranioplasty infection due to *Sporobolomyces*. J. Tenn. Med. Assoc. 87, 466–467.

Morrow, C., and J. Fraser. 2009. Sexual reproduction in the pathogenic basidiomycetes. FEMS Yeast Res. 9, 2, 161–177.

Mörsen, A., and H.-J. Rehm. 1987. Degradation of phenol by a mixed culture of *Pseudomonas putida* and *Cryptococcus elinovii* adsorbed on activated carbon. Appl. Microbiol. Biotechnol. 26, 283–288.

Mörsen, A., and H.-J. Rehm. 1990. Degradation of phenol by a defined mixed culture immobilized by adsorption on activated carbon and sintered glass. Appl. Microbiol. Biotechnol. 33, 206–212.

Mortimer, R., and M. Polsinelli. 1999. On the origins of wine yeast. Res. Microbiol. 150, 199–204.

Moseley, J.B., and B.L. Goode. 2006. The yeast actin cytoskeleton: from cellular function to biochemical mechanism. Microbiol. Mol. Biol. Rev. 70, 605–645.

Moses, A., and G. Vianna. 1913. Sobre nova micose humana, causada por cogumelo ainda nâo descrito: *Proteomyces infestans*. Mem. Inst. Oswaldo Cruz 5, 192–210.

Moss, M.O., and M.T. Long. 2002. Fate of patulin in the presence of the yeast *Saccharomyces cerevisiae*. Food Addit. Contam. 19, 387–399.

Motarjemi, Y. 2002. Impact of small scale fermentation technology on food safety in developing countries. Int. J. Food Microbiol. 75, 213–229.

Motta, R. 1926. Nuova specie di *Cryptococcus* isolata dalla gola (*Cryptococcus uvae* Pollacci & Nannizzi). Att. R. Accad. Fisiocrit. Siena, IX 17, 633–638.

Moylett, E.H., J. Chinen and W.T. Shearer. 2003. *Trichosporon pullulans* infection in 2 patients with chronic granulomatous disease: an emerging pathogen and review of the literature. J. Allergy Clin. Immunol. 111, 1370–1374.

Moylett, E.H., J. Chinen, B. Wickes and W.T. Shearer. 2004. Reply. J. Allergy Clin. Immunol. 114, 206.

Mrak, E.M., and L.S. McClung. 1940. Yeasts occurring on grapes and in grape products in California. J. Bacteriol. 40, 395–407.

Mrak, E.M., and H.J. Phaff. 1948. Yeasts. Annu. Rev. Microbiol. 2, 1–46.

Mrak, E.M., H.J. Phaff and H.C. Douglas. 1942a. A sporulation stock medium for yeasts and other fungi. Science 96, 432.

Mrak, E.M., H.J. Phaff and R.H. Vaughn. 1942b. Yeasts occurring on dates. J. Bacteriol. 43, 689–700.

Mrak, E.M., H.J. Phaff, R.H. Vaughn and H.V. Hansen. 1942c. Yeasts occurring in souring figs. J. Bacteriol. 44, 441–450.

Mtui, G., and Y. Nakamura. 2005. Bioconversion of lignocellulosic waste from selected dumping sites in Dar es Salaam, Tanzania. Biodegradation 16, 493–499.

Mu, C., H. Gao, Y. Li, Z. Li, W. Tan and X. Zhang. 1979. A new species of yeast *Pichia* Hansen. Acta Microbiol. Sin. 19, 259–264.

Mueller, U.G., and N. Gerardo. 2002. Fungus-farming insects: multiple origins and diverse evolutionary histories. Proc. Natl. Acad. Sci. USA 99, 15247–15249.

Mukerji, K.G. 1968. *Eremothecium ashbyi*. CMI Descr. Pathog. Fungi Bact. Set 19, 181.

Müller, D. 1954. Die Abschleuderung der Sporen von *Sporobolomyces*-Spiegelhefe gefilmt. Friesia 5, 65–74.

Muller, H.B., and J.L.F. Kock. 1986. *Waltiozyma* gen. nov. (Saccharomycetaceae), a new genus of the Endomycetales. S. Afr. J. Sci. 82, 491–492.

Müller, W.H., A.C. van Aelst, T.P. van der Krift and T. Boekhout. 1995. Novel approaches to visualize the septal pore cap. Stud. Mycol. 38, 111–117.

Müller, W.H., R.C. Montijn, B.M. Humbel, A.C. van Aelst, E.J.M. Boon, T.P. van der Krift and T. Boekhout. 1998a. Structural differences between two types of basidiomycete septal pore caps. Microbiology 144, 17–21.

Müller, W.H., J.A. Stalpers, A.C. van Aelst, T.P. van der Krift and T. Boekhout. 1998b. Field emission gun-scanning electron microscopy of septal pore caps of selected species in the *Rhizoctonia* s.l. complex. Mycologia 90, 170–179.

Müller, W.H., B.M. Humbel, A.C. van Aelst, T.P. van der Krift, and T. Boekhout. 1999. The perforate septal pore cap of Basidiomycetes. In: A.J.E. van Bel and W.J.P. van Kesteren (Eds), Plasmodesmata: Structure, Function, Role in Cell Communication. Springer, Berlin, pp. 119–127.

Müller, W.H., A.J. Koster, B.M. Humbel, U. Ziese, A.J. Verkleij, A.C. van Aelst, T.P. van der Krift, R.C. Montijn and T. Boekhout. 2000a. Automated electron tomography of the septal pore cap in *Rhizoctonia solani*. J. Struct. Biol. 131, 10.

Müller, W.H., J.A. Stalpers, A.C. van Aelst, M.D.M. de Jong, T.P. van der Krift and T. Boekhout. 2000b. The taxonomic position of *Asterodon*, *Asterostroma* and *Coltricia* inferred from the septal pore cap ultrastructure. Mycol. Res. 104, 1485–1491.

Müller, W.H., A.C. van Aelst, B.M. Humbel, T.P. van der Krift and T. Boekhout. 2000c. Field-emission scanning electron microscopy of the internal cellular organization of fungi. Scanning 22, 295–303.

Müller, W.H., Y.E. Thomassen, C.M.J. Sagt and B. Humbel. 2002. Immuno-electron microscopy in yeast cell research. Recent Res. Dev. Mol. Microbiol. 1, 119–145.

Mulligan, C.N., R.N. Yong and B.F. Gibbs. 2001. Surfactant-enhanced remediation of contaminated soil: a review. Eng. Geol. 60, 371–380.

Mulvany, J.G. 1969. Membrane filter techniques in microbiology. In: J.R. Norris and D.W. Ribbons (Eds), Methods in Microbiology, Vol. 1. Academic Press, New York, pp. 205–253.

Mundkur, B. 1963. Electron microscopical studies of frozen-dried yeast. IV. *Schizosaccharomyces*, *Nadsonia* and *Saccharomycodes*. Z. Naturforsch. 18b, 1073–1082.

Muñoz, P., E. Bouza, M. Cuenca-Estrella, J.M. Eiros, M.J. Perez, M. Sanchez-Somolinos, C. Rincon, J. Hortal and T. Pelaez. 2005. *Saccharomyces cerevisiae* fungemia: an emerging infectious disease. Clin. Infect. Dis. 40, 1625–1634.

Murai, T., Y. Nakamura, R. Kano, S. Watanabe and A. Hasegawa. 2002. Differentiation of *Malassezia furfur* and *Malassezia sympodialis* by glycine utilization. Mycoses 45, 180–183.

Murakami-Nitta, T., K. Kirimura and K. Kino. 2003. Oxidative degradation of dimethyl sulfoxide by *Cryptococcus humicolus* WU-2, a newly isolated yeast. J. Biosci. Bioeng. 95, 109–111.

Murphy, A., and K. Kavanagh. 1999. Emergence of *Saccharomyces cerevisiae* as a human pathogen. Implications for biotechnology. Enzyme Microb. Technol. 25, 551–557.

Murphy, R.H., J.W. Sites and C.H. Hanfler. 1990. Proteins: isozyme electrophoresis. In: D.M. Hillis and C. Moritz (Eds), Molecular Systematics. Sinauer Associates, Sunderland, MA, pp. 45–126.

Murphy, R.W., J.W. Sites Jr., D.G. Buth and C.H. Haufler. 1996. Proteins: isozyme electrophoresis. In: D.M. Hillis, C. Moritz and B.K. Mable (Eds), Molecular Systematics, 2nd edn. Sinauer Associates, Sunderland, MA, pp. 51–120.

Murray, C.K., M.L. Beckius, J.A. Green and D.R. Hospenthal. 2005. Use of chromogenic medium in the isolation of yeasts from clinical specimens. J. Med. Microbiol. 54, 981–985.

Mushtaq, M., Faiza-Iftikhar and Sharfun-Nahar. 2007a. Detection of yeast mycoflora from butter. Pak. J. Bot. 39, 887–896.

Mushtaq, M., Ayesha-Jamal and Sharfun-Nahar. 2007b. Biodiversity of yeast mycoflora in nectar of *Hibiscus rosa-sinensis* and *Ixora coccinea* flowers. Pak. J. Bot. 39, 1367–1376.

Mussa, A.Y., H.S. Randhawa and Z.U. Khan. 2000. Decaying wood as a natural habitat of melanin-forming (Mel+) variant of *Cryptococcus laurentii*. Curr. Sci. 79, 1471–1474.

Mustacchi, R., S. Hohmann and J. Nielsen. 2006. Yeast systems biology to unravel the network of life. Yeast 23, 227–238.

Mutka, S.C., S.M. Bondi, J.R. Carney, N.A. DaSilva and J.T. Kealey. 2006. Metabolic pathway engineering for complex polyketide biosynthesis in *Saccharomyces cerevisiae*. FEMS Yeast Res. 6, 40–47.

Mutlu, O.F., S. Seckin, S.K. Ravelhofer, R.A. Hildebrand and F. Grimm. 1997. Proventriculitis in fowl caused by megabacteria. Tierärztl. Prax. 25, 460–462.

Muyzer, G., and K. Smalla. 1998. Application of denaturing gradient gel electrophoresis (DGGE) and temperature

gradient gel electrophoresis (TGGE) in microbial ecology. Antonie van Leeuwenhoek 73, 127–141.

Nadson, G.A., and A.G. Konokotina. 1911. *Guilliermondia*, un nouveau genre de la famille des Saccharomycètes à copulation hétérogamique. Bull. Jard. Imp. St. Pétersbourg 11, 117–143.

Nadson, G.A., and N.A. Krasil'nikov. 1928. Un nouveau genre d'Endomyétacées: *Guilliermondella*, nov. gen. Compt. Rend. 187, 307–309.

Nadson, G.A., and N.A. Krasil'nikov. 1932. Stroenie, razvitie i rasoobrazovanie u Ridomitsetov (Endomycetaceae) [Structure, development and formation of stable races in the Endomycetaceae]. Dokl. Akad. Nauk SSSR 13, 313–322.

Nagahama, T. 2006. Yeast biodiversity in freshwater, marine and deep-sea environments. In: G. Peter and C.A. Rosa (Eds), Biodiversity and Ecophysiology of Yeasts. Springer, Berlin, pp. 241–262.

Nagahama, T., M. Hamamoto, T. Nakase and K. Horikoshi. 1999. *Kluyveromyces* non*fermentans* sp. nov., a new yeast species isolated from the deep sea. Int. J. Syst. Evol. Microbiol. 49, 1899–1905.

Nagahama, T., M. Hamamoto, T. Nakase, H. Takami and K. Horikoshi. 2001a. Distribution and identification of red yeasts in deep-sea environments around the northwest Pacific Ocean. Antonie van Leeuwenhoek 80, 101–110.

Nagahama, T., M. Hamamoto, T. Nakase and K. Horikoshi. 2001b. *Rhodotorula lamellibrachii* sp. nov., a new yeast species from a tubeworm collected at the deep-sea floor in Sagami Bay and its phylogenetic analysis. Antonie van Leeuwenhoek 80, 317–323.

Nagahama, T., M. Hamamoto, T. Nakase, Y. Takaki and K. Horikoshi. 2003a. *Cryptococcus surugaensis* sp. nov., a novel yeast species from sediment collected on the deep-sea floor of Suruga Bay. Int. J. Syst. Evol. Microbiol. 53, 2095–2098.

Nagahama, T., M. Hamamoto, T. Nakase and K. Horikoshi. 2003b. *Rhodotorula benthica* sp. nov. and *Rhodotorula calyptogenae* sp. nov., novel yeast species from animals collected from the deep-sea floor, and *Rhodotorula lysiniphila* sp. nov., which is related phylogenetically. Int. J. Syst. Evol. Microbiol. 53, 897–903.

Nagahama, T., M. Hamamoto and K. Horikoshi. 2006a. *Rhodotorula pacifica* sp. nov., novel yeast species from sediment collected on the deep-sea floor of the north-west Pacific Ocean. Int. J. Syst. Evol. Microbiol. 56, 295–299.

Nagahama, T., M. Hamamoto, T. Nakase, S. Shimamura and K. Horikoshi. 2006b. Phylogenetic relationship within the *Erythrobasidium* clade: molecular phylogenies, secondary structure, and intron positions inferred from partial sequences of ribosomal RNA and elongation factor-1alpha genes. J. Gen. Appl. Microbiol. 52, 37–45.

Nagahama, T., M.A. Abdel-Wahab, Y. Nogi, M. Miyazaki, K. Uematsu, M. Hamamoto and K. Horikoshi. 2008. *Dipodascus tetrasporeus* sp. nov., an ascosporogenous yeast isolated from deepsea sediments in the Japan Trench. Int. J. Syst. Evol. Microbiol. 58, 1040–1046.

Naganishi, H. 1917. Three new species of yeasts. Bot. Mag. Tokyo 31, 107–115. In Japanese.

Naganishi, H. 1924. Mycological study of Manchurian kwass. Rep. Cent. Lab. S. Manchurian Railway Co. 10, 425–452. In Japanese.

Naganishi, H. 1928. The study of five new species of yeast. J. Zymol. 6, 1–12. In Japanese.

Naganishi, H. 1933. On the heterogamic conjugation in *Pichia alcoholophila* var. *naganishi* Lodder. J. Ferment. Technol. 11, 88–92. In Japanese.

Naganishi, H. 1941a. On the yeasts isolated from sediment of spoiled sake. J. Ferment. Technol. 19, 14–42. In Japanese.

Naganishi, H. 1941b. Studies on the microorganisms in fermenting vinegar mash from rice. Rep. Sci. Assoc. Jpn 15, 419–422. In Japanese.

Nagao, H., and K. Katumoto. 1998. Leaf blister of *Quercus phillyraeoides* caused by *Taphrina caerulescens*. Mycoscience 39, 173–178.

Nagatsuka, Y., H. Kawasaki, S. Limtong, K. Mikata and T. Seki. 2002. *Citeromyces siamensis* sp. nov., a novel halotolerant yeast isolated in Thailand. Int. J. Syst. Evol. Microbiol. 52, 2315–2319.

Nagatsuka, Y., S. Saito and J. Sugiyama. 2008. *Ogataea neopini* sp. nov. and *O. corticis* sp. nov., with the emendation of the ascomycete yeast genus *Ogataea*, and transfer of *Pichia zsoltii, P. dorogensis*, and *P. trehaloabstinens* to it. J. Gen. Appl. Microbiol. 54, 353–365.

Nagatsuka, Y., T. Kiyuna, R. Kigawa, C. Sano, S. Miura and J. Sugiyama. 2009. *Candida tumulicola* sp. nov. and *Candida takamatsuzukensis* sp. nov., novel yeast species assignable to the *Candida membranifaciens* clade, isolated from the stone chamber of the Takamatsu-zuka tumulus. Int. J. Syst. Evol. Microbiol. 59, 186–194.

Nakabayashi, A., Y. Sei and J. Guillot. 2000. Identification of *Malassezia* species isolated from patients with seborrhoeic dermatitis, atopic dermatitis, pityriasis versicolor and normal subjects. Med. Mycol. 38, 337–341.

Nakagawa, T., K. Yamada, T. Miyaji and N. Tomizuka. 2002. Cold-active pectinolytic activity of psychrophilic–basidiomycetous yeast *Cystofilobasidium capitatum* strain PPY–1. J. Biosci. Bioeng. 94, 175–177.

Nakagawa, T., T. Nagaoka, S. Taniguchi, T. Miyaji and N. Tomizuka. 2004. Isolation and characterization of psychrophilic yeasts producing cold-adapted pectinolytic enzymes. Lett. Appl. Microbiol. 38, 383–387.

Nakagawa, T., K. Yamada, S. Fujimura, T. Ito, T. Miyaji and N. Tomizuka. 2005. Pectin utilization by the methylotrophic yeast *Pichia methanolica*. Microbiology 151, 2047–2052.

Nakagawa, T., R. Ikehata, M. Uchino, T. Miyaji, K. Takano and N. Tomizuka. 2006. Cold active beta-galactosidase activity of isolated psychrophilic–basidiomycetous yeast *Guehomyces pullulans*. Microbiol. Res. 16, 75–79.

Nakamura, Y., H. Fukuhara and K. Sano. 2000. Secreted phytase activities of yeasts. Biosci. Biotechnol. Biochem. 64, 841–844.

Nakase, T. 1971a. New species of yeasts found in Japan. J. Gen. Appl. Microbiol. 17, 409–419.

Nakase, T. 1971b. Four new yeasts found in Japan. J. Gen. Appl. Microbiol. 17, 469–478.

Nakase, T. 1971c. New species of yeasts resembling *Candida krusei* (Cast.) Berkhout. J. Gen. Appl. Microbiol. 17, 383–398.

Nakase, T. 1972a. A comparative study on *Pichia dispora* and *Pichia saitoi*. J. Gen. Appl. Microbiol. 18, 377–382.

Nakase, T. 1972b. Significance of DNA base composition in the classification of yeasts and yeast-like fungi. In: G. Terui (Ed.), Fermentation Technology Today, Proc. IV Int.

Ferment. Symp. Soc. Ferment. Technol., Osaka, Japan, pp. 785–791.
Nakase, T. 1975. Three new asporogenous yeasts found in industrial waste water. Antonie van Leeuwenhoek 41, 201–210.
Nakase, T. 1987. Isolation and maintenance of ballistospore-forming yeasts. In: G.S. de Hoog, M.Th. Smith and A.C.M. Weijman (Eds), The Expanding Realm of Yeast-like Fungi. Elsevier, Amsterdam, pp. 375–387. (Stud. Mycol. 30, 375–387).
Nakase, T. 1989. Classification of ballistosporous yeasts. Yeast 5, S511–S516.
Nakase, T. 2000. Expanding world of ballistosporous yeasts: distribution in the phyllosphere, systematics and phylogeny. J. Gen. Appl. Microbiol. 46, 189–216.
Nakase, T., and T. Boekhout. 1988. Emendation of the genus *Bensingtonia* Ingold. J. Gen. Appl. Microbiol. 34, 433–437.
Nakase, T., and M. Itoh. 1988. Two new combinations of ballistospore-forming yeasts: *Sporobolomyces tsugae* comb. nov. and *Sporobolomyces salicinus* comb. nov. J. Gen. Appl. Microbiol. 34, 499–502.
Nakase, T., and K. Komagata. 1966. New yeasts, *Endomycopsis muscicola* and *Pichia zaruensis*. J. Gen. Appl. Microbiol. 12, 347–352.
Nakase, T., and K. Komagata. 1968. Taxonomic significance of base composition of yeast DNA. J. Gen. Appl. Microbiol. 14, 345–357.
Nakase, T., and K. Komagata. 1969. DNA base composition of the genus *Hansenula*. J. Gen. Appl. Microbiol. 15, 85–95.
Nakase, T., and K. Komagata. 1970a. Significance of DNA base composition in the classification of the yeast genera *Hanseniaspora* and *Kloeckera*. J. Gen. Appl. Microbiol. 16, 241–250.
Nakase, T., and K. Komagata. 1970b. Significance of DNA base composition in the classification of the yeast genus *Pichia*. J. Gen. Appl. Microbiol. 16, 511–521.
Nakase, T., and K. Komagata. 1971a. Significance of DNA base composition in the classification of the yeast genus *Debaryomyces*. J. Gen. Appl. Microbiol. 17, 43–50.
Nakase, T., and K. Komagata. 1971b. Further investigation on the DNA base composition of the genus *Hansenula*. J. Gen. Appl. Microbiol. 17, 77–84.
Nakase, T., and K. Komagata. 1971c. Significance of DNA base composition in the classification of the yeast genera *Cryptococcus* and *Rhodotorula*. J. Gen. Appl. Microbiol. 17, 121–130.
Nakase, T., and K. Komagata. 1971d. Significance of DNA base composition in the classification of the yeast genus *Torulopsis*. J. Gen. Appl. Microbiol. 17, 161–166.
Nakase, T., and K. Komagata. 1971e. Significance of DNA base composition in the classification of the yeast genus *Saccharomyces*. J. Gen. Appl. Microbiol. 17, 227–238.
Nakase, T., and K. Komagata. 1971f. Significance of DNA base composition in the classification of the yeast genus *Candida*. J. Gen. Appl. Microbiol. 17, 259–279.
Nakase, T., and K. Komagata. 1971g. DNA base composition of some species of yeasts and yeast-like fungi. J. Gen. Appl. Microbiol. 17, 363–369.
Nakase, T., and M. Suzuki. 1985a. Taxonomic studies on *Debaryomyces hansenii* (Zopf) Lodder et Kreger-van Rij and related species. I. Chemotaxonomic investigations. J. Gen. Appl. Microbiol. 31, 49–69.
Nakase, T., and M. Suzuki. 1985b. Taxonomic studies on *Debaryomyces hansenii* (Zopf) Lodder et Kreger-van Rij and related species. II. Practical discrimination and nomenclature. J. Gen. Appl. Microbiol. 31, 71–86.
Nakase, T., and M. Suzuki. 1985c. Ballistospore-forming yeasts found on the surface of the Japanese rice plant, *Oryza sativa* L. J. Gen. Appl. Microbiol. 31, 457–474.
Nakase, T., and M. Suzuki. 1985d. *Candida tsuchiyae,* nov. sp., isolated from moss collected in Japan. J. Gen. Appl. Microbiol. 31, 507–512.
Nakase, T., and M. Suzuki. 1986a. *Bullera derxii* sp. nov. and *Bullera pseudoalba* sp. nov. isolated from dead leaves of *Oryza sativa* and *Miscanthus sinensis*. J. Gen. Appl. Microbiol. 32, 125–135.
Nakase, T., and M. Suzuki. 1986b. *Bullera intermedia* sp. nov. and *Sporobolomyces* oryzi*cola* sp. nov. isolated from dead leaves of *Oryza sativa*. J. Gen. Appl. Microbiol. 32, 149–155.
Nakase, T., and M. Suzuki. 1986c. *Bullera megalospora*, a new species of yeast forming large ballistospores isolated from dead leaves of *Oryza sativa*, *Miscanthus sinensis* and *Sasa* sp. in Japan. J. Gen. Appl. Microbiol. 32, 225–240.
Nakase, T., and M. Suzuki. 1986d. The ubiquinone system in strains of species in the ballistospore-forming yeast genera *Sporidiobolus, Sporobolomyces* and *Bullera*. J. Gen. Appl. Microbiol. 32, 251–258.
Nakase, T., and M. Suzuki. 1987a. *Sporobolomyces naganoensis*, a new species of ballistosporous yeast equipped with ubiquinone-9, isolated from a dead leaf of *Sasa* sp. in Japan. Trans. Mycol. Soc. Jpn 28, 1–8.
Nakase, T., and M. Suzuki. 1987b. *Sporobolomyces griseoflavus* and *Sporobolomyces* sasi*cola*, two new species of ballistosporous yeasts isolated from dead leaves of *Sasa* sp. in Japan. J. Gen. Appl. Microbiol. 33, 167–175.
Nakase, T., and M. Suzuki. 1987c. Studies on ballistospore-forming yeasts from the dead leaves of *Miscanthus sinensis* with descriptions of the new species *Sporobolomyces miscanthii*, *Sporobolomyces subroseus* and *Sporobolomyces weijmanii*. J. Gen. Appl. Microbiol. 33, 177–196.
Nakase, T., and M. Suzuki. 1987d. *Bullera variabilis*, a new species of yeast with uniquely-shaped ballistospores isolated from various plant materials. J. Gen. Appl. Microbiol. 33, 343–354.
Nakase, T., and M. Suzuki. 1987e. *Sporobolomyces inositophilus*, a new species of ballistosporous yeast isolated from a dead leaf of *Sasa* sp. in Japan. Antonie van Leeuwenhoek 53, 245–251.
Nakase, T., and M. Suzuki. 1988. *Sporobolomyces yuccicola*, a new species of ballistosporous yeast equipped with ubiquinone-9. Antonie van Leeuwenhoek 54, 47–55.
Nakase, T., and M. Suzuki. 1997. *Candida gotoi*, new species of anamorphic yeast isolated from insect frass in bark of Japanese maple. Microbiol. Cult. Coll. 13, 109–112.
Nakase, T., and A. Takematsu. 1992. *Udeniomyces*, a new ballistosporous anamorphic yeast genus in the Cryptococcaceae proposed for three *Bullera* species which produce large bilaterally symmetrical ballistospores. FEMS Microbiol. Lett. 100, 497–502.
Nakase, T., Y. Fukazawa and T. Tsuchiya. 1972. A comparative study of two forms of *Candida tropicalis* (Cast.) Berkhout. J. Gen. Appl. Microbiol. 18, 349–363.

Nakase, T., K. Komagata and Y. Fukazawa. 1976. *Candida pseudointermedia* sp. nov., isolated from "Kamaboko", a traditional fish-paste product in Japan. J. Gen. Appl. Microbiol. 22, 177–182.

Nakase, T., K. Komagata and S. Konishi. 1977. Yeasts found in the extraction process of water-soluble substances of defatted soybean flakes. Trans. Mycol. Soc. Jpn 18, 186–196. In Japanese.

Nakase, T., K. Komagata and Y. Fukazawa. 1978. *Candida pararugosa*, a new species of asporogenous yeast. J. Gen. Appl. Microbiol. 24, 17–25.

Nakase, T., K. Komagata and Y. Fukazawa. 1979. A comparative taxonomic study on two forms of *Candida parapsilosis* (Ashford) Langeron et Talice. J. Gen. Appl. Microbiol. 25, 375–386.

Nakase, T., M. Itoh and M. Suzuki. 1987a. *Sporobolomyces falcatus* sp. nov., isolated from a dead leaf of *Miscanthus sinensis* in Japan. Trans. Mycol. Soc. Jpn 28, 295–301.

Nakase, T., M. Suzuki and M. Itoh. 1987b. *Sporobolomyces yamatoanus*, a new species of ballistosporous yeast equipped with ubiquinone-9 isolated from dead leaves of various plants in Japan. J. Gen. Appl. Microbiol. 33, 445–454.

Nakase, T., M. Itoh, M. Suzuki, K. Komagata and T. Kodama. 1988a. *Candida palmioleophila* sp. nov., a yeast capable of assimilating crude palm oil, formerly identified as *Torulopsis candida*. J. Gen. Appl. Microbiol. 34, 493–498.

Nakase, T., M. Itoh, A. Takematsu and K. Komagata. 1988b. *Candida tanzawaensis*, a new species of yeast isolated from moss collected in Japan. Trans. Mycol. Soc. Jpn 29, 331–338.

Nakase, T., M. Itoh and J. Sugiyama. 1989a. *Bensingtonia ingoldii* sp. nov., a ballistospore-forming yeast isolated from *Knightia excelsa* collected in New Zealand. J. Gen. Appl. Microbiol. 35, 53–58.

Nakase, T., G. Okada, J. Sugiyama, M. Itoh and M. Suzuki. 1989b. *Ballistosporomyces*, a new ballistospore-forming anamorphic yeast genus. J. Gen. Appl. Microbiol. 35, 289–309.

Nakase, T., M. Itoh, A. Takematsu and R.J. Bandoni. 1990a. *Bullera miyagiana*, a new species of ballistospore-forming yeast isolated from *Abies firma* collected in Japan. J. Gen. Appl. Microbiol. 36, 33–39.

Nakase, T., M. Itoh, M. Suzuki and R.J. Bandoni. 1990b. *Sporobolomyces lactophilus* sp. nov., a ballistosporous yeast isolated from *Abies firma* collected in Japan. Trans. Mycol. Soc. Jpn 36, 159–167.

Nakase, T., A. Takematsu, M. Itoh and T. Boekhout. 1990c. Conspecificity of *Bullera derxii*, *Bullera sinensis* and *Bullera alba* var. *lactis*. J. Gen. Appl. Microbiol. 36, 209–213.

Nakase, T., M. Itoh, A. Takematsu, K. Mikata, I. Banno and Y. Yamada. 1991. *Kockovaella*, a new ballistospore-forming anamorphic yeast genus. J. Gen. Appl. Microbiol. 37, 175–197.

Nakase, T., A. Takematsu and Y. Yamada. 1993. Molecular approaches to the taxonomy of ballistosporous yeasts based on the analysis of the partial nucleotide sequences of 18S ribosomal ribonucleic acids. J. Gen. Appl. Microbiol. 39, 107–134.

Nakase, T., M. Suzuki, S.-O. Suh and M. Takashima. 1994a. Reclassification of *Candida magnoliae*, a chemotaxonomic investigation. Abstr. Int. Union Microbiol. Soc. IUMS Congr. 1994, 327.

Nakase, T., M. Suzuki, M. Takashima, Y. Miyakawa, K. Kagaya, Y. Fukazawa and K. Komagata. 1994b. *Candida sojae*, a new species of yeast isolated from an extraction process of water-soluble substances of defatted soybean flakes. J. Gen. Appl. Microbiol. 40, 161–169.

Nakase, T., M. Suzuki, M. Takashima, M. Hamamoto, T. Hatano and S. Fukui. 1994c. A taxonomic study on cellulolytic yeast and yeast-like microorganisms isolated in Japan. I. Ascomycetous yeast genera *Candida* and *Williopsis* and a yeast-like genus *Prototheca*. J. Gen. Appl. Microbiol. 40, 519–531.

Nakase, T., M. Suzuki, M. Takashima, D. Rosadi, A.M. Hermosillo and K. Komagata. 1994d. *Candida akabanensis*, a new species of yeast isolated from insect frass in bark of a grape-vine. Microbiol. Cult. Coll. 10, 35–43.

Nakase, T., M. Takashima and M. Hamamoto. 1994e. *Sporobolomyces linderae*, a new ballistosporous anamorphic yeast found on a dead leaf of *Lindera obtusiloba* collected at Mt. Fuji. J. Gen. Appl. Microbiol. 40, 95–101.

Nakase, T., S.-O. Suh and M. Hamamoto. 1995. Molecular systrematics of ballistoconidium-forming yeasts. Stud. Mycol. 38, 163–173.

Nakase, T., M. Suzuki, M. Hamamoto, M. Takashima, T. Hatano and S. Fukui. 1996. A taxonomic study on cellulolytic yeasts and yeast-like microorganisms isolated in Japan. II. The genus *Cryptococcus*. J. Gen. Appl. Microbiol. 42, 7–15.

Nakase, T., M. Suzuki, H.J. Phaff and C.P. Kurtzman. 1998. *Debaryomyces* Lodder & Kreger–van Rij. Nom. Cons. In: C.P. Kurtzman and J.W. Fell (Eds), The Yeasts, A Taxonomic Study. Elsevier, Amsterdam, pp. 157–173.

Nakase, T., M. Suzuki, T. Sugita, S.-O. Suh and K. Komagata. 1999. Three new species of anamorphic yeasts phenotypically and phylogenetically related to *Candida mesenterica*. The description of *Candida fungicola* sp. nov., *Candida sagamina* sp. nov., and *Candida fukazawae* sp. nov. isolated from fruit bodies of mushrooms. Mycoscience 40, 465–476.

Nakase, T., S. Tsuzuki and M. Takashima. 2002. *Bullera taiwanensis* sp. nov. and *Bullera formosensis* sp. nov., two new ballistoconidium-forming yeast species isolated from plant leaves in Taiwan. J. Gen. Appl. Microbiol. 48, 345–355.

Nakase, T., S. Tsuzuki, F.-L. Lee, T. Sugita, S. Jindamorakot, H. Jan-ngam, W. Potacharoen, M. Tanticharoen, T. Kudo and M. Takashima. 2003. *Sporobolomyces magnisporus* sp. nov., a new yeast species in the *Erythrobasidium* cluster isolated from plants in Taiwan. J. Gen. Appl. Microbiol. 49, 337–344.

Nakase, T., H. Jan-ngam, S. Tsuzuki, F.-L. Lee, S. Jindamorakot, W. Potacharoen, M. Tanticharoen and M. Takashima. 2004a. Two new ballistoconidium-forming yeast species, *Bullera melastomae* and *Bullera formosana*, found in Taiwan. Syst. Appl. Microbiol. 27, 558–564.

Nakase, T., S. Tsuzuki, F.-L. Lee, S. Jindarakot, H. Jan-ngam, W. Potacharoen, M. Tanticharoen, K. Toshiaki and M. Takashima. 2004b. *Bullera begoniae* sp. nov. and *Bullera setariae* sp. nov., two new species of ballistoconidium-forming yeasts in the *Bullera variabilis* (*Bulleribasidium*) cluster isolated from plants in Taiwan. Mycoscience 45, 287–294.

Nakase, T., F.-L. Lee, S. Am-in, S. Jindamorakot, W. Potacharoen, M. Tanticharoen and M. Takashima. 2005a. *Sporobolomyces fushanensis* sp. nov., a new species of ballistoconidium-forming yeast in the *Microbotryum* lineage isolated from a plant in Taiwan. J. Gen. Appl. Microbiol. 51, 41–45.

Nakase, T., S. Tsuzuki, F.-L. Lee, S. Jindamorakot, H. Jan-ngam, S. Am-in, W. Potacharoen, M. Tanticharoen and M. Takashima. 2005b. *Sporobolomyces diospyroris* sp. nov., *Sporobolomyces lophatheri* sp. nov. and *Sporobolomyces pyrrosiae* sp. nov., three new species of ballistoconidium-forming yeasts in the *Agaricostilbum* lineage isolated from plants in Taiwan. J. Gen. Appl. Microbiol. 51, 277–286.

Nakase, T., S. Jindamorakot, S. Am-in, H. Kawasaki, W. Potacharoen and M. Tanticharoen. 2005c. *Pichia nongkratonensis* sp. nov., a new species of ascomycetous yeast isolated from insect frass collected in Thailand. Mycoscience 46, 192–195.

Nakase, T., S. Jindamorakot, S. Am-In, W. Potacharoen and M. Tanticharoen. 2006a. Yeast biodiversity in tropical forests of Asia. In: G. Peter and C.A. Rosa (Eds), Biodiversity and Ecophysiology of Yeasts. Springer, Berlin, pp. 441–460.

Nakase, T., S. Jindamorakot, T. Sugita, S. Am-in, H. Kawasaki, W. Potacharoen and M. Tanticharoen. 2006b. *Trichosporon siamense* sp. nov. isolated from insect frass in Thailand. Myoscience 47, 106–109.

Nakase, T., S. Jindamorakot, K. Mikata, S. Ninomiya, H. Kawasaki, S. Limtong, W. Potacharoen and M. Tanticharoen. 2007a. *Pichia koratensis* sp. nov., a new ascomycetous yeast related to *Pichia acaciae* isolated from insect frass in Thailand. J. Gen. Appl. Microbiol. 53, 345–351.

Nakase, T., S. Jindamorakot, S. Limtong, S. Am-In, H. Kawasaki, Y. Imanishi, W. Potacharoen and M. Tanticharoen. 2007b. *Candida kazuoi* sp. nov. and *Candida hasegawae* sp. nov., two new species of ascomycetous anamorphic yeasts isolated from insect frass in Thailand. J. Gen. Appl. Microbiol. 53, 239–245.

Nakase, T., S. Ninomiya, Y. Imanishi, A. Nakagiri, H. Kawasaki and S. Limtong. 2008a. *Ogataea paradorogensis* sp. nov., a novel methylotrophic ascomycetous yeast species isolated from galleries of ambrosia beetles in Japan, with a close relation to *Pichia dorogensis*. J. Gen. Appl. Microbiol. 54, 377–383.

Nakase, T., S. Jindamorakot, S. Ninomiya, Y. Imanishi, H. Kawasaki and W. Potacharoen. 2008b. *Candida kanchanaburiensis* sp. nov., a new ascomycetous yeast species related to *Pichia nakazawae* isolated in Thailand. J. Gen. Appl. Microbiol. 54, 259–265.

Nakase, T., S. Jindamorakot, S. Am-In, H. Ninomiya, Kawasaki and S. Limtong. 2009a. *Candida nonsorbophila* sp. nov., a new ascomycetous yeast species isolated in Thailand. FEMS Yeast Res. 9, 663–667.

Nakase, T., S. Jindamorakot, S. Ninomiya, Y. Imanishi and H. Kawasaki. 2009b. *Candida wancherniae* sp. nov. and *Candida morakotiae* sp. nov., two novel ascomycetous anamorphic yeast species found in Thailand. J. Gen. Appl. Microbiol. 55, 93–100.

Nakayama, T., G. Machinney and H.J. Phaff. 1954. Carotenoids in asporogenous yeasts. Antonie van Leeuwenhoek 20, 217–228.

Nakayashiki, T., C.P. Kurtzman, H.K. Edskes and R.B. Wickner. 2005. Yeast prions URE3 and PSI+ are diseases. Proc. Natl. Acad. Sci. USA 102, 10575–10580.

Nakazawa, R. 1909. Zwei Saccharomyceten aus Sakéhefe. Zentralbl. Bakteriol. Parasitenkd., Abt. II, 22, 529–540.

Nakazawa, R. 1914. The fission yeasts of cane-sugar molasses. Taiwan Sotokufu Kenkyujo Hokaku 111, 113–138. In Japanese.

Nakazawa, R. 1919. Research on various kinds of yeasts in Taiwan (Formosa). Rep. Taiwan Government Lab. 7. In Japanese.

Nakazawa, R. 1933. Melasse vergärende Hefe (Sammlungs Nr. 396 Forschungsinstitut der Regierung Formosa) *Saccharomyces formosensis* nov. sp. J. Agric. Chem. Soc. 102, 285–291.

Nakazawa, R., and M. Simo. 1936. Two new yeasts. *Saccharomyces robustus* nov. sp. and *Saccharomyces praecisus* nov. sp. J. Agric. Chem. Soc. Jpn 12, 356–366. In Japanese.

Nannizzi, A. 1934. Repertorio sistematico dei miceti dell'uomo e degli animali. In: G. Pollacci (Ed.), Trattato di Micopathologia umana, Vol. IV. Poligrafia Meimi, Siena.

Narasimharao, K., A. Lee and K. Wilson. 2007. Catalysts in production of biodiesel: a review. J. Biobased Mater. Bioenergy 1, 19–30.

Narayan, S., K. Batta, P. Colloby and C.Y. Tan. 2000. Cutaneous *Cryptococcus* infection due to C. *albidus* associated with Sezary syndrome. Br. J. Dermatol. 143, 632–634.

Nardi, J.B., C.M. Bee, L.A. Miller, N.H. Nguyen, S.-O. Suh and M. Blackwell. 2006. Communities of microbes that inhabit the changing hindgut landscape of a subsocial beetle. Arthropod Struct. Dev. 35, 57–68.

Nash, R., S. Weng, B. Hitz, R. Balakrishnan, K.R. Christie, M.C. Costanzo, S.S. Dwight, S.R. Engel, D.G. Fisk, J.E. Hirschman, E.L. Hong, M.S. Livstone, R. Oughtred, J. Park, M. Skrzypek, C.L. Theesfeld, G. Binkley, Q. Dong, C. Lane, S. Miyasato, A. Sethuraman, M. Schroeder, K. Dolinski, D. Botstein and J. M. Cherry. 2007. Expanded protein information at SGD: new pages and proteome browser. Nucleic Acids Res. 35, D468–D471.

Nasir, H., and H. Noda. 2003. Yeast-like symbiotes as a sterol source in anobiid beetles (Coleoptera, Anobiidae): possible metabolic pathways from fungal sterols to 7-dehydrocholesterol. Arch. Insect Biochem. Physiol. 52, 175–182.

Nassenstein, A., J. Hemberger, H. Schwartz and M.R. Kula. 1992. Studies on the enzymatic reduction of N-Boc-4S-amino-3-oxo-5-phenylpentanoic acid methyl ester. J. Biotechnol. 26, 183–201.

Nasuno, S. 1971. Polyacrylamide gel disc electrophoresis of alkaline proteinases from *Aspergillus* species. Agric. Biol. Chem. 35, 1147–1150.

Naumov, G.I. 1986a. Genosystematics of yeasts of the genus *Zygofabospora* Kudriavzev emend. G. Naumov. Mol. Genet. Microbiol. Virol. (USSR) 5, 10–13.

Naumov, G.I. 1986b. Genetic differentiation and ecology of the yeast *Saccharomyces*. Proc. Acad. Sci. USSR Bot. Soc. DKBSBT 289/290, 213–216.

Naumov, G.I. 1987a. Developments in the genosystematics of the yeast genera *Williopsis* Zender and *Zygowilliopsis* Kudriavzev. Mol. Genet. Mikrobiol. Virusol. 2, 3–7. In Russian.

Naumov, G.I. 1987b. Nomenclature of a yeast genus, *Zygofabospora* Kudriavzev emend. G. Naumov. Mycol. Phytopathol. (USSR) 21, 134–139.

Naumov, G.I. 1987c. Genetic basis for clarification and identification of the ascomycetous yeasts. In: G.S. de Hoog, M.Th. Smith and A.C.M. Weijman (Eds), The Expanding Realm of Yeast-like Fungi. Elsevier, Amsterdam, pp. 469–475.

Naumov, G.I. 2000. *Saccharomyces bayanus* var. *uvarum* comb. nov. a new variety established by genetic analysis. Mikrobiologiia 69, 410–414.

Naumov, G.I. 2005a. Domestication of dairy yeast *Kluyveromyces lactis*: transfer of the β-galactosidase (LAC4) and lactose permease (LAC12) gene cluster? Dokl. Biol. Sci. 401, 120–122.

Naumov, G.I. 2005b. Why does the yeast *Kluyveromyces wickerhamii* assimilate but not ferment lactose? Dokl. Biol. Sci. 403, 310–312.

Naumov G.I., and E.S. Naumova. 2000. Taxonomic and evolutionary genetics of the yeast *Zygofabospora* (*Kluyveromyces*) *lactis*. In: 10th Int. Symp. on Yeasts, Aug. 27–Sept. 1, 2000, Papendal, Arnhem, The Netherlands, pp. 185–186.

Naumov, G.I., and T.A. Nikonenko. 1988. East Asia is the probable original habitat of the cultured yeast *Saccharomyces cerevisiae*. Akad. Nauk SSSR Ser. Biol. Nauk 20(3), 97–101.

Naumov, G.I., M.M. Vustin and T.I. Naumova. 1981. *Zygowilliopsis californica*, *Williopsis saturnus*, W. *beijerinckii* comb. nov., W. *mrakii* comb. nov. Dokl. Akad. Nauk SSSR 259, 718–722. In Russian.

Naumov, G.I., M.M. Vustin, I.P. Bab'eva and I.S. Reshetova. 1985a. Additions to the genotaxonomy of *Williopsis* and *Zygowilliopsis* yeast genera. Mikrobiologiia 54, 239–244. In Russian.

Naumov, G.I., M.M. Vustin and I.P. Bab'eva. 1985b. Geneticheskaya identifikatsiya dvukh vidow drozhzhepodobnykh gribov v rode *Arthroascus* von Arx [Genetic identification of two species of the genus *Arthroascus* von Arx]. Dokl. Akad. Nauk SSSR 281, 1463–1465. In Russian.

Naumov, G.I., E.S. Naumova, A.N. Hagler, L.C. Mendonça-Hagler and E.J. Louis. 1995. A new genetically isolated population of the *Saccharomyces sensu stricto* complex from Brazil. Antonie van Leeuwenhoek 67, 4, 351–355.

Naumov, G.I., E.S. Naumova and P.D. Sniegowski. 1997. Differentiation of European and Far East Asian populations of *Saccharomyces paradoxus* by allozyme analysis. Int. J. Syst. Bacteriol. 47, 341–344.

Naumov, G.I., E.S. Naumova and P.D. Sniegowski. 1998. *Saccharomyces paradoxus* and *Saccharomyces cerevisiae* are associated with exudates of North American oaks. Can. J. Microbiol. 44, 1045–1050.

Naumov, G.I., S.A. James, E.S. Naumova, E.J. Louis and I.N. Roberts. 2000. Three new species in the *Saccharomyces sensu stricto* complex: *Saccharomyces cariocanus*, *Saccharomyces kudriavzevii* and *Saccharomyces mikatae*. Int. J. Syst. Evol. Microbiol. 50, 1931–1942.

Naumov, G.I., H.V. Nguyen, E.S. Naumova, A. Michel, M. Aigle and C. Gaillardin. 2001. Identification of *Saccharomyces bayanus* var. *uvarum*, a cider-fermenting yeast. Int. J. Food Microbiol. 65, 163–171.

Naumov, G.I., and E.S. Naumova. 2002a. Five new combinations in the yeast genus *Zygofabospora* Kudriavzev emend. G. Naumov (pro parte *Kluyveromyces*) based on genetic data. FEMS Yeast Res. 2, 39–46.

Naumov, G.I., E.S. Naumova, Z. Antunovics and M. Sipiczki. 2002b. *Saccharomyces bayanus* var. *uvarum* in Tokaj wine-making of Slovakia and Hungary. Appl. Microbiol. Biotechnol. 59, 727–730.

Naumov, G.I., D.O. Gaxdiev and E.S. Naumovia. 2003a. Identification of the yeast species *Saccharomyces bayanus* in Far East Asia. Mikrobiologiia. 72, 834–839. In Russian.

Naumov, G.I., E.S. Naumova, M.Th. Smith and G. Sybren de Hoog. 2003b. Ribosomal DNA sequencing and reinstatement of the genus *Arthroascus* von Arx. J. Gen. Appl. Microbiol. 49, 267–270.

Naumov, G.I., E.S. Naumova, M.Th. Smith and G.S. de Hoog. 2006. Molecular-genetic diversity of the ascomycetous yeast genus *Arthroascus: Arthroascus babjevae* sp. nov., *Arthroascus fermentans* var. *arxii* var. nov. and geographical populations of *Arthroascus schoenii*. Int. J. Syst. Evol. Microbiol. 56, 1997–2007.

Naumova, E.S., N.G. Tokareva, I.P. Bab'eva and G.I. Naumov. 2001. Molecular genetic analysis of the yeast *Komagataea (Williopsis) pratensis* populations from Caucasian and Tien Shan regions. Mikrobiologiia. 70, 241–247. In Russian.

Naumova, E.S., I.V. Kurshunova, L. Jespersen and G.I. Naumova. 2003a. Molecular genetic identification of *Saccharomyces sensu strictu* strains from African Sorghum beer. FEMS Yeast Res. 3, 177–184.

Naumova, E.S., S.A. Bulat, N.V. Mironenko and G.I. Naumov. 2003b. Differentiation of six sibling species in the *Saccharomyces sensu stricto* complex by multilocus enzyme electrophoresis and UP-PCR analysis. Antonie van Leeuwenhoek 83, 155–166.

Naumova, E.S., N.N. Sukhotina and G.I. Naumov. 2004a. Molecular genetic differentiation of the dairy yeast *Kluyveromyces lactis* and its closest wild relatives. FEMS Yeast Res. 5, 263–269.

Naumova, E.S., G.I. Naumov, J. Nosek and L. Tomáška. 2004b. Differentiation of the yeasts *Williopsis*, *Zygowilliopsis* and *Komagataea* by karyotypic and PCR analyses. Syst. Appl. Microbiol. 27, 192–197.

Naumova, E.S., E.V. Serpova and G.I. Naumov. 2005. Speciation in the yeast *Lachancea thermotolerans*: molecular genetic evidence. Doklady Biol. Sci. 405, 469–471.

Naumova, E.S., E.V. Serpova and G.I. Naumov. 2007. Molecular systematics of *Lachancea* yeasts. Biochemistry (Moscow) 72, 1356–1362.

Ncango, D.M., C.H. Pohl, O.M. Sebolai, P.J. Botes, C.J. Strauss, M. Joseph, P.W.J. van Wijk, S. Nigam and J.L.F. Kock. 2006. Oxylipin-coated hat-shaped ascospores of *Ascoidea corymbosa*. Can. J. Microbiol. 52, 1046–1050.

Nealson, K.H., and E.D. Garber. 1967. An eletrophoretic survey of esterase, phosphatases, and leucine amino-peptidases in mycelial extracts of species of *Aspergillus*. Mycologia 59, 330–336.

Nechitsch, A. 1904. Sur les ferments de deux levains de l'Inde, le *Mucor praini* et le *Dematium chodati*. Inst. Bot. Univ. Genève 5, 1.

Nedelcu, A.M. 2001. Complex patterns of plastid 16S rRNA gene evolution in nonphotosynthetic green algae. J. Mol. Evol. 53, 670–679.

Neel, J., J. Tariqo and C. Grindem. 2006. Gall-bladder aspirate from a dog. Vet. Clin. Pathol. 35, 467–470.

Negroni, P., and R. Blaisten. 1941. Estudio morfologico y fisiologico de una nueva especie de *Prototheca*: *Prototheca ciferrii* n. sp., aislada de epidermis de papa. Mycopathologia 3, 94–104.

Negroni, P., and I. Fischer. 1940. Flora micologica (Eumycetes) de las material fecales. Rev. Argent. Dermat. 24, 135–154.
Negroni, P., and I. Fischer. 1941. Contribución al conocimiento de la flora micológica (microfitos) del delta de Paraná. Rev. Inst. Bacteriol. Dep. Higiene 10, 334–342.
Neilson, J.B., M.H. Ivey and G.S. Bulmer. 1978. *Cryptococcus neoformans*: pseudohyphal forms surviving culture with *Acanthamoeba polyphaga*. Infect. Immun. 20, 262–266.
Nel, E.E., and J.P. van der Walt. 1968. *Torulopsis humilis*, sp. n. Mycopathol. Mycol. Appl. 36, 94–96.
Nell, A., S.A. James, C.J. Bond, B. Hunt and M.E. Herrtage. 2002. Identification and distribution of a novel *Malassezia* species yeast on normal equine skin. Vet. Rec. 150, 395–398.
Neuhoff, W. 1924. Zytologie und systematische Stellung der Auriculariaceen und Tremellaceen. Bot. Arch. 8, 250–297.
Neuhoff, W. 1936. Die Gallertpilze Schwedens (Tremellaceae, Dacrymycetaceae, Tulasnellaceae, Auriculariaceae). Ark. Bot. A 1, 1–57.
Neujahr, H.Y. 1990. Yeasts in biodegradation and biodeterioration processes. In: H. Verachtert and R. Mot (Eds), Yeast Biotechnology and Biocatalysis, Vol. 5. Marcel Dekker, New York, pp. 321–348.
Neuvéglise, C., E. Bon, A. Lépingle, P. Wincker, F. Artiguenave, C. Gaillardin and S. Casarégola. 2000. Genomic exploration of the Hemiascomycetous yeasts: 9. *Saccharomyces kluyveri*. FEBS Lett. 487, 56–60.
Neuvéglise, C., H. Feldmann, E. Bon, C. Gaillardin and S. Casaregola. 2002. Genomic evolution of the long terminal repeat retrotransposons in hemiascomycetous yeasts. Genome Res. 12, 930–943.
Neveu, B., C. Labbe and R.R. Bélanger. 2007. GFP technology for the study of biocontrol agents in tritrophic interactions: a case study with *Pseudozyma flocculosa*. J. Microbiol. Methods 68, 275–281.
Neveu-Lemaire, M. 1912. Recherche des Saccharomycètes et des Blastomycètes dans l'organisme de leur hôte. In: Parasitologie des Animaux Domestiques. J. Lamarre & Cie., Paris, p. 60.
Neveu-Lemaire, M. 1921. Précis de Parasitologie Humaine, 5th edn. Lamarre, Paris.
Nevzglyadova, O.V., A.V. Artyomov, A.A. Gaivoronskii and T.R. Soidla. 2002. Concealed nuclei in *Saccharomyces* strains. FEMS Yeast Res. 2, 471–479.
Newell, S.Y., and J.W. Fell. 1970. The perfect form of a marine-occurring yeast of the genus *Rhodotorula*. Mycologia 62, 272–281.
Newell, S.Y., and I.L. Hunter. 1970. *Rhodosporidium diobovatum* sp. n., the perfect form of an asporogenous yeast (*Rhodotorula* sp.). J. Bacteriol. 104, 503–508.
Ng, H. 1972. Factors affecting organic acid production by sourdough (San Francisco) bacteria. Appl. Microbiol. 23, 1153–1159.
Ngamskulrungroj, P., F. Gilgado, J. Faganello, A.P. Litvintseva, A.L. Leal, K.M. Tsui, T.G. Mitchell, M. Henning Vainstain and W. Meyer. 2009. Genetic diversity of the *Cryptococcus* species complex suggests that *Cryptococcus gattii* deserves to have varieties. PLoS ONE 4, e58–e62.
Nguyen, H.-V., and C. Gaillardin. 2005. Evolutionary relationships between the former species *Saccharomyces uvarum* and the hybrids *Saccharomyces bayanus* and *Saccharomyces pastorianus*; reinstatement of *Saccharomyces uvarum* (Beijerinck) as a distinct species. FEMS Yeast Res. 5, 471–483.
Nguyen, H.-V., A. Lepingle and C.A. Gaillardin. 2000. Molecular typing demonstrates homogeneity of *Saccharomyces uvarum* strains and reveals the existence of hybrids between *S. uvarum* and *S. cerevisiae*, including the *S. bayanus* type strain CBS 380. Syst. Appl. Microbiol. 23, 71–85.
Nguyen, N.H., S.O. Suh, C.K. Erbil and M. Blackwell. 2006a. *Metschnikowia noctiluminum* sp. nov., *Metschnikowia corniflorae* sp. nov., and *Candida chrysomelidarum* sp. nov., isolated from green lacewings and beetles. Mycol. Res. 110, 346–356.
Nguyen, N.H., S.-O. Suh, C.J. Marshall and M. Blackwell. 2006b. Morphological and ecological similarities: wood-boring beetles associated with novel xylose-fermenting yeasts, *Spathaspora passalidarum* gen. sp. nov. and *Candida jeffriesii* sp. nov. Mycol. Res. 110, 1232–1241.
Nguyen, N.H., S.O. Suh and M. Blackwell. 2007. Five novel *Candida* species in insect-associated yeast clades isolated from Neuroptera and other insects. Mycologia 99, 842–858.
Nguyen, H.-V., C. Gaillardin and C. Neuveglise. 2009. Differentiation of *Debaryomyces hansenii* and *Candida famata* by rRNA gene intergenic spacer fingerprinting and reassessment of phylogenetic relationships among *D. hansenii*, C. *famata*, *D. fabryi, C. flareri (=D. subglobosus)* and *D. prosopidis*: description of *D. vietnamensis* sp. nov. closely related to *D. nepalensis*. FEMS Yeast Res. 9, 641–662.
Nguyen, T.H., G.H. Fleet and P.L. Rogers. 1998. Composition of the cell walls of several yeast species. Appl. Microbiol. Biotechnol. 50, 206–212.
Nguyen-the, C., and F. Carlin. 2000. Fresh and processed vegetables. In: B.M. Lund, T.C. Baird-Parker and G.W. Gould (Eds), The Microbiological Safety and Quality of Food. Aspen Publishers, Gaithersberg, MD, pp. 620–684.
Nguyen, N.H., S.O. Suh and M. Blackwell. 2007. Five novel *Candida* species in insect-associated yeast clades isolated from Neuroptera and other insects. Mycologia 99, 842–858.
Ni, H.J., Q.H. Bao, T.S. Sun, X. Chen and H.P. Zhang. 2007. Identification and biodiversity of yeasts isolated from Koumiss in Xinjiang of China. Wei Sheng Wu Xue Bao 47, 578–582. In Chinese.
Nicholas, R.O., D.W. Williams and P.A. Hunter. 1994. Investigation of the value of β-glucan-specific fluorochromes for predicting the β-glucan content of the cell walls of zoopathogenic fungi. Mycol. Res. 98, 694–698.
Nickerson, W.J. 1943. *Zygosaccharomyces acidifaciens*: a new acetifying yeast. Mycologia 35, 66–78.
Nickerson, W.J. 1944a. Studies on film-forming yeasts. Acid production by *Zygopichia* and *Zygohansenula*. Mycologia 36, 224–233.
Nickerson, W.J. 1944b. Studies in the genus *Zygosaccharomyces* I. Transfer of pellicle–forming yeasts to *Zygopichia*. Farlowia 1, 469–481.
Niehaus, C.J.G. 1932. Untersuchungen über Apiculatushefen. Zentralbl. Bakteriol Parasitenkd., Abt. II, 86, 97–150.
Nielsen, D.S., O.D. Teniola, L. Ban-Koffi, M. Owusu, T.S. Andersson and W.H. Holzapfel. 2007. The microbiology of Ghanaian cocoa fermentations analysed using culture-dependent and culture-independent methods. Int. J. Food Microbiol. 114, 168–186.
Nielsen, D.S., M. Jakobsen and L. Jespersen. 2010a. *Candida halmiae* sp. nov., *Geotrichum ghanense* sp. nov. and

Candida awuaii sp. nov., novel yeast species isolated from Ghanian cocoa fermentations. Int. J. Syst. Evol. Microbiol. 60, 1460–1465.

Nielsen, D.S., M. Jakobsen and L. Jespersen. 2010b. *Candida halmiae* sp. nov., *Geotrichum ghanense* sp. nov. and *Candida awuaii* sp. nov., isolated from Ghanaian cocoa fermentations. Int. J. Syst. Evol. Microbiol. 60, 1460–1465.

Nielsen, J., and M.C. Jewett. 2007. Impact of systems biology on metabolic engineering of *Saccharomyces cerevisiae*. FEMS Yeast Res. 8, 122–131.

Nielsen, K., G.M. Cox, A.P. Litvintseva, E. Mylonakis, S.D. Malliaris, D.K. Benjamin Jr., S.S. Giles, T.G. Mitchell, A. Casadevall, J.R. Perfect and J. Heitman. 2005. *Cryptococcus neoformans* alpha strains preferentially disseminate to the central nervous system during coinfection. Infect. Immun. 73, 4922–4933.

Nielsen, K., A.L. de Obaldia and J. Heitman. 2007. *Cryptococcus neoformans* mates on pigeon guano: implications for the realized ecological niche and globalization. Eukaryot. Cell 6, 949–959.

Nieuwdorp, P.J., P. Bos and W.C. Slooff. 1974. Classification of *Lipomyces*. Antonie van Leeuwenhoek 40, 241–254.

Nigam, J.N., A. Margaritis and M.A. Lachance. 1985. Aerobic fermentation of D-xylose to ethanol by *Clavispora* sp. Appl. Environ. Microbiol. 50, 763–766.

Nigro, F., M.M. Finetti Sialer and D. Gallitelli. 1999. Transformation of *Metschnikowia pulcherrima* 320, biocontrol agent of storage rots, with the green fluorescent protein gene. J. Plant Pathol. 81, 205–208.

Nikolaev, A.V., I.A. Ivanova and V.N. Shibaev. 1993. The stepwise synthesis of oligo(glycosyl phosphates) via glycosyl hydrogen-phosphonates. The chemical synthesis of oligomeric fragments from *Hansenula capsulata* Y1842 exophosphomannan and from *Escherichia coli* K51 capsular antigen. Carbohydr. Res. 242, 91–107.

Nilsson-Tillgren, T., T.C. Gjermansen, S. Holmberg and J.G.L. Petersen. 1986. Analysis of chromosome V and the ILV 1 gene from *Saccharomyces carlsbergensis*. Carlsberg Res. Commun. 51, 309–326.

Niño, F.L. 1930. Onixis y perionixis de origen blastomicosico (estudio clinico y micologico). Bol. Inst. Clin. Quirurg. 5, 270–281.

Niño, F.L. 1934. Blastomycosis humana generalizada por *Cryptococcus* (n. sp.) Buenos Aires (cited by Lodder and Kreger-van Rij 1952).

Niño, F.L. 1938. Contribución al estudio de las blastomicosis en la República Argentina. Bol. Inst. Clin. Quirurg. Univ. Buenos Aires 14, 591–1042.

Niño, F.L., and A. Puglisi. 1927. Moniliasis bucal. Su estudio clinico y micologico. Sem. Med. 34, 222–229.

Nishida, H., and J. Sugiyama. 1994. Archiascomycetes: detection of a major new lineage within the Ascomycota. Mycoscience 35, 361–366.

Nishida, H., and J. Sugiyama. 1993. Phylogenetic relationships among *Taphrina, Saitoella*, and other higher fungi. Mol. Biol. Evol. 10, 431–436.

Nishida, H., P.A. Blanz and J. Sugiyama. 1993. The higher fungus *Protomyces inouyei* has two group I introns in the 18S rRNA gene. J. Mol. Evol. 37, 25–28.

Nishida, H., K. Ando, Y. Ando, A. Hirata and J. Sugiyama. 1995. *Mixia osmundae*: transfer from the Ascomycota to the Basidiomycota based on evidence from molecules and morphology. Can. J. Bot. 73, S660–S666.

Nishida, T. 1911. A contribution to the monograph of the parasitic Exoascaceae of Japan. In: Y. Takahashi (Ed.) Collection of Botanical Papers Presented to Prof. Dr. Kingo Miyabe on the Twenty-fifth Anniversary of his Academic Service by his Friends and Pupils [the title is abbreviated as "Miyabe-Festschrift"]. Rokumeikwan, Tokyo, pp. 157–212.

Nishida, T. 1957. Food plants, distribution, and variation in abundance of *Conotelus mexicanus* Murray, a recently discovered immigrant insect in Hawaii (Coleoptera: Nitidulidae). Proc. Haw. Ent. Soc. 16, 307–312.

Nishikawa, M.M., M.S. Lazera, G.G. Barbosa, L. Trilles, B.R. Balassiano, R.C.L. Macedo, C.C.F. Bezerra, M.A. Perez, P. Cardarelli and B. Wanke. 2003. Serotyping of 467 *Cryptococcus neoformans* isolates from clinical and environmental sources in Brazil: analysis of host and regional patterns. J. Clin. Microbiol. 4, 73–77.

Nishimura, T. 1910. Naikokuzei-ishu, Japan, No. 45, 47. In Japanese.

Nishimura, K., Y. Asada, S. Tanaka and S. Watanabe. 1991. Ultrastructure of budding process of *Malassezia pachydermatis*. J. Med. Vet. Mycol. 29, 387–393.

Nishimura, K., M. Yamamoto, T. Nakagomi, Y. Takiguchi, T. Naganuma and Y. Uzuka. 2002. Biodegradation of triazine herbicides on polyvinylalcohol gel plates by the soil yeast *Lipomyces starkeyi*. Appl. Microbiol. Biotechnol. 58, 848–852.

Nishimura, Y., K. Nakagawa-Yoshida, M. Suga, T. Shinoda, E. Guého and M. Ando. 1997. Assignment and serotyping of *Trichosporon* species: the causative agents of summer-type hypersensitivity pneumonitis. J. Med. Vet. Mycol. 35, 45–52.

Nishiwaki, Y. 1910. Isolation of a red, spore-forming yeast. J. Ind. Chem. Jpn 13, 1071–1075. In Japanese.

Nishiwaki, Y. 1929. Über eine neue Nachreif Hefe in dem dunklen Bodensediment des japanischen Saké und über eine neue Hefegattung *Zygosaccharomycodes*. Zentralbl. Bakteriol. Parasitenkd., Abt. II, 78, 403–410.

Nisiotou, A.A., and G.R. Gibson. 2005. Isolation of culturable yeasts from market wines and evaluation of the 5.8S-ITS DNA sequence analysis for identification purposes. Lett. Appl. Microbiol. 41, 454–463.

Nisiotou, A.A., and G.J.E. Nychas. 2007. Yeast populations residing on healthy or *Botrytis*-infected grapes from a vineyard in Attica, Greece. Appl. Environ. Microbiol. 73, 2765–2768.

Nisiotou, A.A., E.Z. Panagou and G.J.E. Nychas. 2010. *Candida olivae* sp. nov., a novel yeast species from "Greek-style" black olive fermentation. Int. J. Syst. Evol. Microbiol. 60, 1219–1223.

Nislow, C., and G. Giaever. 2007. Chemical genomic tools for understanding gene function and drug action. Methods Microbiol. 36, 387–414.

Nitiyon, S., C. Boonmak, S. Am-In, S. Jindamorakot, H. Kawasaki, W. Yongmanitchai and S. Limtong. 2010. *Candida saraburiensis* sp. nov. and *Candida prachuapensis* sp. nov., two xylose-utilizing yeast species isolated in Thailand. Int. J. Syst. Evol. Microbiol. doi: 10.1099/ijs.0.023317-0

Niwata, Y., M. Takashima, J. Tornai-Lehoczki, T. Deák and T. Nakase. 2002. *Udeniomyces pannonicus* sp. nov., a ballistoconidium-forming yeast isolated from leaves of plants in Hungary. Int. J. Syst. Evol. Microbiol. 52, 1887–1892.

Nixon, K.C. 1999. The parsimony ratchet, a new method for rapid parsimony analysis. Cladistics 15, 407–414.

Noda, H., and N. Kawahara. 1995. Electrophoretic karyotype of intracellular yeast-like symbiotes in rice planthoppers and anobiid beetles. J. Invertebr. Pathol. 65, 118–124.

Noda, H., and K. Kodama. 1996. Phylogenetic position of yeastlike endosymbionts of anobiid beetles. Appl. Environ. Microbiol. 62, 162–167.

Noda, H., N. Nakashima and M. Koizumi. 1995. Phylogenetic position of yeast-like symbiotes of rice planthoppers based on partial 18S rDNA sequences. Insect Biochem. Mol. Biol. 25, 639–646.

Normand, V., G. Dardelle, P.E. Bouquerand, L. Nicolas and D.J. Johnston. 2005. Flavor encapsulation in yeasts: limonene used as a model system for characterization of the release mechanism. J. Agric. Food Chem. 53, 7532–7543.

Norris, D.M. 1966. The complex of fungi essential to the growth and development of *Xyleborus sharpi* in wood. Holz und Organismen. Int. Symp. Berlin-Dahlem 1965, 1, 523–529.

Norrman, J. 1969. Production of volatile organic compounds by the yeast fungus *Dipodascus aggregatus*. Arch. Microbiol. 68, 133–149.

Norrman, J. 1971a. A gas chromatographic investigation of the influence of different carbon sources on the production of volatile compounds by *Dipodascus aggregatus*. Arch. Microbiol. 75, 145–162.

Norrman, J. 1971b. The influence of different nitrogen sources on the production of volatile compounds by *Dipodascus aggregatus*. Arch. Microbiol. 80, 338–350.

Norry, F.M., and J.C. Vilardi. 1996. Size-related sexual selection and yeast diet in *Drosophila buzzatii* (Diptera: Drosophilidae). J. Insect Behav. 9, 329–338.

Northrup, J.H. 1917. The role of yeast in the nutrition of an insect (*Drosophila*). J. Biol. Chem. 30, 181–187.

Nosanchuk, J.D., and A. Casadevall. 2003. The contribution of melanin to microbial pathogenesis. Cell. Microbiol. 5, 203–223.

Notario, V., T.G. Villa, T. Benitez and J.R. Villanueva. 1976a. Beta-glucanases in the yeast *Cryptococcus albidus* var. *aerius*. Production and separation of beta-glucanases in asynchronous cultures. Can. J. Microbiol. 22, 261–268.

Notario, V., T.G. Villa and J.R. Villanueva. 1976b. Beta-xylosidases in the yeast *Cryptococcus albidus* var. *aerius*. Can. J. Microbiol. 22, 312–315.

Notario, V., T.G. Villa and J.R. Villanueva. 1979. Cell wall-associated 1,4-beta-D-xylanase in *Cryptococcus albidus* var. *aerius*: *in situ* characterization of the activity. J. Gen. Microbiol. 114, 415–422.

Nout, M.J.R. 2003. Traditional fermented products from Africa, Latin America and Asia. In: T. Boekhout and V. Robert (Eds), Yeasts in Food: Beneficial and Detrimental Aspects. Behrs Verlag, Hamburg, pp. 451–473.

Nout, M.J.R. 2009. Rich nutrition from the poorest – cereal fermentations in Africa and Asia. Food Microbiol. 26, 685–692.

Nout, M.J.R., and R.J. Bartelt. 1998. Attraction of a flying nitidulid (*Carpophilus humeralis*) to volatiles produced by yeasts grown on sweet corn and a corn-based medium. J. Chem. Ecol. 24, 1217–1239.

Nout, M.J.R., C.E. Platis and D.T. Wicklow. 1997. Biodiversity of yeasts from Illinois maize. Can. J. Microbiol. 43, 362–367.

Novák, E.K. 1964. *Candida soosii* nov. sp., a new yeast related to *Candida requinyii* Szép et Novák 1963. Acta Microbiol. Acad. Sci. Hung. 11, 51–54.

Novák, E.K., and I. Vitéz. 1964. Mycological investigations on clinical materials. II. Description of new yeasts. Zentralbl. Bakteriol. Parasitenkd., Abt. I, Orig. 193, 127–133.

Novák, E.K., and C. Vörös-Felkai. 1962. *Rhodotorula slooffii* n. sp. Acta Microbiol. Acad. Sci. Hung. 9, 261–263.

Novák, E.K., and J. Zsolt. 1961. A new system proposed for yeasts. Acta Bot. Acad. Sci. Hung. 7, 93–145.

Novo, M., G. Beltran, N. Rozes, J.M. Guillamon, S. Sokol, V. Leberre, J. Francois and A. Mas. 2007. Early transcriptional response of wine yeast after rehydration: osmotic shock and metabolic activation. FEMS Yeast Res. 7, 304–316.

Nowakowska-Waszczuk, A., and M. Pietka. 1983. Taxonomic study of four yeast strains assimilating methanol. Acta Microbiol. Pol. 32, 73–85.

Nunes, C., J. Usall, N. Teixido, M. Miro and I. Vinas. 2001. Nutritional enhancement of biocontrol activity of *Candida sake* (CPA-1) against *Penicillium expansum* on apples and pears. Eur. J. Plant Pathol. 107, 543–551.

Nunes, C., J. Usall, N. Teixido, R. Torres and I. Vinas. 2002a. Control of *Penicillium expansum* and *Botrytis cinerea* on apples and pears with the combination of *Candida sake* and *Pantoea agglomerans*. J. Food Prot. 65, 178–184.

Nunes, C., J. Usall, N. Teixido and I. Vinas. 2002b. Improvement of *Candida sake* biocontrol activity against post-harvest decay by addition of ammonium molybdate. J. Appl. Microbiol. 92, 927–935.

Nunez, F., M.M. Rodriquez, J.J. Cordoba, M.E. Bermundez and M.A. Asensio. 1996. Yeast population during ripening of dry-cured Iberian ham. Int. J. Food Microbiol. 29, 271–280.

Nunn, C.J. 2004. The morphology and molecular physiology of *Zygosaccharomyces* spoilage yeasts. PhD Thesis, Cardiff University.

Nunn, M.A., S.M. Schäefer, M.A. Petrou and J.R. Brown. 2007. Environmental source of *Candida dubliniensis*. Emerg. Infect. Dis. 13, 747–750.

Nurudeen, T.A., and D.G. Ahearn. 1979. Regulation of melanin production by *Cryptococcus neoformans*. J. Clin. Microbiol. 10, 724–729.

Nyanga, L.K., M.J. Nout, T.H. Gadaga, B. Theelen, T. Boekhout and M.H. Zwietering. 2007. Yeasts and lactic acid bacteria microbiota from masau (*Ziziphus mauritiana*) fruits and their fermented fruit pulp in Zimbabwe. Int. J. Food Microbiol. 120, 159–166.

Nyland, G. 1948. Preliminary observations on the morphology and cytology of an undescribed Heterobasidiomycete from Washington state. Mycologia 40, 478–481.

Nyland, G. 1949. Studies on some unusual Heterobasidiomycetes from Washington State. Mycologia 41, 686–701.

Nyland, G. 1950. The genus *Tilletiopsis*. Mycologia 42, 487–496.

Oberwinkler, F. 1985. Anmerkungen zur Evolution und Systematik der Basidiomyceten. Bot. Jahrb. Syst. 107, 541–580.

Oberwinkler, F. 1987. Heterobasidiomycetes with ontogenetic yeast-stages – systematic and phylogenetic aspects. In: G.S. de Hoog, M.Th. Smith and A.C.M. Weijman (Eds), The Expanding Realm of Yeast-like Fungi. Elsevier, Amsterdam, pp. 61–74. (Stud. Mycol. 30, 61–74).

Oberwinkler, F. 1990. New genera of auricularioid heterobasidiomycetes. Rep. Tottori Mycol. Inst. 28, 113–127.

Oberwinkler, F. 1993. Diversity and phylogenetic importance of tropical heterobasidiomycetes. In: S. Isaac, J.C. Frankland, R. Watling and A.J.S. Whalley (Eds), Aspects of Tropical Mycology. Cambridge University Press, Cambridge, pp. 121–147.

Oberwinkler, F., and R.J. Bandoni. 1981. *Tetragoniomyces* gen. nov. and Tetragoniomycetaceae fam. nov. (Tremellales). Can. J. Bot. 59, 1034–1040.

Oberwinkler, F., and R. Bandoni. 1982a. Carcinomycetaceae: a new family in the Heterobasidiomycetes. Nord. J. Bot. 2, 501–516.

Oberwinkler, F., and R.J. Bandoni. 1982b. A taxonomic survey of the gasteroid, auricularioid heterobasidiomycetes. Can. J. Bot. 60, 1726–1750.

Oberwinkler, F., and R.J. Bandoni. 1982c. *Atractogloea*: a new genus in the Hoehnelomycetaceae (heterobasidiomycetes). Mycologia 74, 634–639.

Oberwinkler, F., and R. Bandoni. 1983. *Trimorphomyces*: a new genus in the Tremellaceae. Syst. Appl. Microbiol. 4, 105–113.

Oberwinkler, F., and R. Bauer. 1989. The systematics of gasteroid, auricularioid Heterobasidiomycetes. Sydowia 41, 224–256.

Oberwinkler, F., R.J. Bandoni, P. Blanz, G. Deml and L. Kisimova-Horovitz. 1982. Graphiolales: basidiomycetes parasitic on palms. Plant Syst. Evol. 140, 251–277.

Oberwinkler, F., R.J. Bandoni, P. Blanz and L. Kisimova-Horovitz. 1983. *Cystofilobasidium*: a new genus in the Filobasidiaceae. Syst. Appl. Microbiol. 4, 114–122.

Oberwinkler, F., R.J. Bandoni, R. Bauer, G. Deml and L. Kisimova-Horovitz. 1984. The life-history of *Christiansenia pallida*, a dimorphic mycoparasitic heterobasidiomycete. Mycologia 76, 9–22.

Oberwinkler, F., R. Bauer and R.J. Bandoni. 1990a. *Colacogloea*: a new genus in the auricularioid Heterobasidiomycetes. Can. J. Bot. 68, 2531–2536.

Oberwinkler, F., R. Bauer and R.J. Bandoni. 1990b. Heterogastridiales: a new order of basidiomycetes. Mycologia 82, 48–58.

Oberwinkler, F., R. Bauer and J. Schneller. 1990c. *Phragmoxenidium mycophilum* sp. nov., an unusual mycoparasitic heterobasidiomycete. Syst. Appl. Microbiol. 13, 186–191.

Oberwinkler, F., R. Bauer and J. Tschen. 1999. The mycoparasitism of *Platygloea bispora*. Kew Bull. 54, 763–769.

Obilie, E.M., K. Tano-Debrah and W.K. Amoa-Awua. 2003. Microbial modification of the texture of grated cassava during fermentation into akyeke. Int. J. Food Microbiol. 89, 275–280.

O'Brien, E.A., L.B. Koski, Y. Zhang, L. Yang, E. Wang, M.W. Gray, G. Burger and B.F. Lang. 2007. TBestDB: a taxonomically broad database of expressed sequence tags (ESTs). Nucleic Acids Res. 35, D445–D451.

O'Brien, H.E., J.L. Parrent, J.A. Jackson, J.-M. Moncalvo and R. Vilgalys. 2005. Fungal community analysis by large-scale sequencing of environmental samples. Appl. Environ. Microbiol. 71, 5544–5550.

O'Brien, M., P. O'Kiely, P.D. Forristal and H.T. Fuller. 2005. Fungi isolated from contaminated baled grass silage on farms in the Irish Midlands. FEMS Microbiol. Lett. 247, 131–135.

Odds, F.C. 1988. *Candida* and Candidosis, 2nd edn. Bailliere Tindall, London.

Odds, F.C., and R. Bernaerts. 1994. CHROMagar *Candida*, a new differential isolation medium for presumptive identification of clinically important *Candida* species. J. Clin. Microbiol. 32, 1923–1929.

Odds, F.C., and M.D. Jacobsen. 2008. Multilocus sequence typing of pathogenic *Candida* species. Eukaryot. Cell 7, 1075–1084.

Odds, F.C., M.G. Rinaldi, C.R. Cooper Jr., A. Fothergill, L. Pasarell and M.R. McGinnis. 1997. *Candida* and *Torulopsis*: a blinded evaluation of use of pseudohypha formation as basis for identification of medically important yeasts. J. Clin. Microbiol. 35, 313–316.

Odling-Smee, F.J., K.N. Laland and M.W. Feldman. 2003. Niche Construction: The Neglected Process in Evolution. Princeton University Press, Princeton, NJ.

O'Donnell, K.L. 1992. Ultrastructure of meiosis and the spindle pole body cycle in freeze-substituted basidia of the smut fungi *Ustilago maydis* and *Ustilago avenae*. Can. J. Bot. 70, 629–638.

O'Donnell, K., and E. Cignelnik. 1997. Two divergent intragenomic rDNA ITS2 types within a monophyletic lineage of the fungus *Fusarium* are nonorthologous. Mol. Phylogenet. Evol. 7, 103–116.

O'Donnell, K.L., and D.J. McLaughlin. 1984a. Ultrastructure of meiosis in *Ustilago maydis*. Mycologia 76, 468–485.

O'Donnell, K.L., and D.J. McLaughlin. 1984b. Postmeiotic mitosis, basidiospore development, and septation in *Ustilago maydis*. Mycologia 76, 486–502.

O'Donnell, K., H.C. Kistler, B.K. Tacke and H.H. Casper. 2000. Gene genealogies reveal global phylogeographic structure and reproductive isolation among lineages of *Fusarium graminearum*, the fungus causing wheat scab. Proc. Natl. Acad. Sci. USA 97, 7905–7910.

Odunfa, S.A., S.A. Adeniran, Teniola and J. Nordstrom. 2001. Evaluation of lysine and methionine production in some *Lactobacilli* and yeasts from ogi. Int. J. Food Microbiol. 63, 159–163.

Ogata, K., H. Nishikawa and M. Ohsugi. 1969. A yeast capable of utilizing methanol. Agric. Biol. Chem. 33, 13–19.

Ogawa, J.M., E.I. Zehr, G.W. Bird, D.F. Ritchie, K. Uriu and J.K. Uyemoto (Eds). 1995. Compendium of Stone Fruit Diseases. APS Press, St. Paul, MN, 98pp.

Ogawa, S., and Y. Ota. 2000. Influence of exogenous natural oils on the w-1 and w-2 hydroxy fatty acid moiety of sophorose lipid produced by *Candida bombicola*. Biosci. Biotechnol. Biochem. 64, 2466–2468.

Ogawa, Y., H. Tatsuma, S. Murakami, Y. Ishida, K. Murakami, A. Masaki, H. Kawabe, H. Arimura, E. Nakano and H. Motai. 1990. Secretion of *Aspergillus oryzae* alkaline

protease in an osmophilic yeast, *Zygosaccharomyces rouxii*. Agric. Biol. Chem. 54, 2521–2529.
Ogletree, F.F., A.T. Abdelal and D.G. Ahearn. 1978. Germ-tube formation by atypical strains of *Candida albicans*. Antonie van Leeuwenhoek 44, 15–24.
Ogrydziak, D.M. 1988. Production of alkaline extracellular protease by *Yarrowia lipolytica*. Crit. Rev. Biotechnol. 8, 177–187.
Ohara, Y., and H. Nonomura. 1954a. Yeasts occurring in a mash and koji of tamari-soya. Part 2. A taxonomic study on the four strains of Cryptococcaceae. J. Agric. Chem. Soc. Jpn 28, 717–721. In Japanese.
Ohara, Y., and H. Nonomura. 1954b. A taxonomic study on the yeasts isolated in Japan. Part 1. Genus *Pichia* Hansen. J. Agric. Chem. Soc. Jpn 28, 160–165.
Ohara, Y., H. Nonomura and H. Yunome. 1960a. Dynamic aspects of yeast flora during vinous fermentation. Part 5. Bull. Res. Inst. Ferment. Yamanishi Univ. 7, 3–5.
Ohara, Y., H. Nonomura and H. Yunome. 1960b. New species and varieties of Cryptococcoideae from grape musts. J. Agric. Chem. Soc. Jpn 34, 709–711.
Ohara, Y., H. Nonomura and T. Yamazaki. 1964. *Torulopsis vinacea* sp. nov., a new yeast isolated from grape musts. J. Gen. Appl. Microbiol. 10, 77–78.
Ohara, Y., H. Nonomura and T. Yamazaki. 1965. *Candida incommunis* sp. nov., a new yeast isolated from grape must. J. Gen. Appl. Microbiol. 11, 273–275.
Ohata, M., K. Kohama, Y. Morimitsu, K. Kubota and E. Sugawara. 2007. The formation mechanism by yeast of 4-hydroxy-2-(or 5)-ethyl-5 (or 2)-methyl-3(2H)-furanone in miso. Biosci. Biotechnol. Biochem. 71, 407–413.
Ohki, S.Y., E. Kariya, K. Hiraga, A. Wakamiya, T. Isobe, K. Oda and M. Kainosho. 2001. NMR structure of *Streptomyces* killer toxin-like protein, SKLP: further evidence for the wide distribution of single-domain $\beta\gamma$-crystallin superfamily proteins. J. Mol. Biol. 305, 109–120.
Oho, O. 1919. Über das sogenannte "Inkin". Kyoto Ingaku Zasshi 16, 7–21.
Ohshima, Y., T. Sugaura, M. Horita and T. Sasaki. 1987. Industrial application of artificially induced diploid strains of *Torulaspora delbrueckii*. Appl. Environ. Microbiol. 53, 1512–1514.
Ojima, K., J. Breitenbach, H. Visser, Y. Setoguchi, K. Tabata, T. Hoshino, J. van den Berg and G. Sandmann. 2006. Cloning of the astaxanthin synthase gene from *Xanthophyllomyces dendrorhous* (*Phaffia rhodozyma*) and its assignment as a beta-carotene 3-hydroxylase/4-ketolase. Mol. Genet. Genomics 275, 148–158.
Okabe, Y. 1929. Studien über den Soorpilz. I. Mitteilung: Bakteriologische Eigenschaften und systematische Stellung des Soorpilzes. Zentralbl. Bakteriol. Parasitenkd. Infektionskr., Erste Abteilung 111, 181–187.
Okada, K., T. Kainou, H. Matsuda and M. Kawamukai. 1998. Biological significance of the side chain length of ubiquinone in *Saccharomyces cerevisiae*. FEBS Lett. 43, 241–244.
Okamoto, K., and J.M. Shaw. 2005. Mitochondrial morphology and dynamics in yeast and multicellular eukaryotes. Annu. Rev. Genet. 39, 503–536.
Oki, T., K. Kouno, A. Kitai and A. Ozaki. 1972. New yeast capable of assimilating methanol. J. Gen. Appl. Microbiol. 18, 295–305.
Okoli, I., C.A. Oyeka, K.J. Kwon-Chung, B. Theelen, V. Robert, J. Z. Groenewald, D.C. McFadden, A. Casadevall and T. Boekhout. 2007. *Cryptotrichosporon anacardii* gen. nov., sp. nov., a new Trichosporonoid capsulate basidiomycetous yeast from Nigeria that is able to form melanin on niger seed agar. FEMS Yeast Res. 7, 339–350.
Okuda, T., A. Ikeda and H. Maruyama. 1981. *Holtermannia corniformis*: physiological characterization of the yeast state and mating. Trans. Mycol. Soc. Jpn 22, 153–163.
Okunishi, M., K. Yamada and K. Komagata. 1979. Electrophoretic comparison of enzymes from basidiomycetes in different stages of development. J. Gen. Appl. Microbiol. 25, 329–334.
Okunuki, K. 1931. Beiträge zur Kenntnis der rosafarbigen Sprosspilze. Jpn. J. Bot. 5, 283–322.
Oladiran, A.O., and L.N. Iwu. 1993. Studies on the fungi associated with tomato fruit rots and effects of environment on storage. Mycopathologia 121, 157–161.
Olden, K. 2006. Toxicogenomics – a new systems toxicology approach to understanding of gene–environment interactions. Ann. N. Y. Acad. Sci. 1076, 703–706.
Olemska-Beer, R., I. Merker, D.D. Ditto and M.J. DiNovi. 2006. Food-processing enzymes from recombinant organisms – a review. Regul. Toxicol. Pharmacol. 45, 144–158.
Olive, L.S. 1947. Notes on Tremellales from Georgia. Mycologia 39, 90–108.
Olive, L.S. 1950. A new genus of the Tremellales from Louisiana. Mycologia 42, 385–390.
Olive, L.S. 1951. Taxonomic notes on Louisiana fungi. III. Additions to the Tremellales. Mycologia 43, 677–690.
Olive, L.S. 1952. Studies on the morphology and cytology of *Itersonila perplexans* Derx. Bull. Torrey Bot. Club 72, 120–138.
Olive, L.S. 1968. An unusual Heterobasidiomycete with *Tilletia*-like basidia. J. Elisha Mitchell Sci. Soc. 84, 261–266.
Oliveira, E.S., H. Cardello, E.M. Jeronimo, E.L.R. Souza and G.E. Serra. 2005. The influence of different yeasts on the fermentation, composition and sensory quality of cachaca. World J. Microbiol. Biotechnol. 21, 707–715.
Oliveira, K.F., L. Malovolta, C.S. Souza, E.J. Vicente and C. Laluce. 2006. Pectinolytic activity secreted by yeasts isolated from fermented citrus molasses. J. Appl. Microbiol. 100, 633–640.
Oliver, S.G. 1991. "Classical" yeast biotechnology. In: M.F. Tuite and S.G. Oliver (Eds), *Saccharomyces*. Biotechnology Handbooks, Vol. 4. Plenum Press, New York, pp. 213–248.
Oliver, S.G. 2006. From genomes to systems: the path with yeast. Philos. Trans. R. Soc. B 361, 477–482.
Oliver, S.G. 2007. Introduction to functional analysis in yeast. Methods Microbiol. 36, 1–21.
Olson, H.C., and B.W. Hammer. 1935. Observations on yeasts causing gas in sweetened condensed milk. Iowa State Coll. J. Sci. 10, 37–43.
Olson, H.C., and B.W. Hammer. 1937. The genera *Sporobolomyces* and *Bullera* from the standpoint of dairy products. Iowa State Coll. J. Sci. 11, 207–213.
Olver, W.J., S.A. James, A. Lennard, A. Galloway, I.N. Roberts and T.C.H. Boswell. 2002. Nosocomial transmission of *Saccharomyces cerevisiae* in bone marrow transplant patients. J. Hosp. Infect. 52, 268–272.

Omemu, A.M., O.B. Oyewole and M.O. Bankole. 2007. Significance of yeasts in the fermentation of maize for ogi production. Food Microbiol. 24, 571–576.

O'Neill, E.B., and S.A. Meyer. 2000. Resolution of strain identity of selected *Candida* strains by DNA reassociation and restriction enzyme analysis. 10th Int. Symp. on Yeasts. Arnhem, The Netherlands, p. 334.

Onishi, H. 1957. Studies on osmophilic yeasts. III. Classification of osmophilic soy and miso yeasts. Bull. Agric. Chem. Soc. Jpn 21, 151–156.

Onishi, H. 1963. Osmophilic yeasts. Adv. Food Res. 12, 53–94.

Onishi, H. 1972. *Candida tsukubaensis* sp. n. Antonie van Leeuwenhoek 38, 365–367.

Onishi, H., and T. Suzuki. 1969a. *Torulopsis mannitofaciens* sp. n. isolated from soy-sauce mash. Antonie van Leeuwenhoek 36, 258–260.

Onishi, H., and T. Suzuki. 1969b. Microbial production of xylitol from glucose. Appl. Microbiol. 18, 1031–1035.

Onishi, N., and T. Tanaka. 1998. Galacto-oligosaccharide production using a recycling cell culture of *Sterigmatomyces elviae* CBS 8119. Lett. Appl. Microbiol. 26, 136–139.

Ono, E., Y. Maeda, A. Mori, H. Tanimoto, Y. Fukutomi, C. Oshikawa, K. Sekiya, T. Thuburai, N. Thurikisawa, M. Otomo, M. Taniguchi, M. Hasegawa, E. Miyazaki, T. Kumamoto and K. Akiyama. 2007. Summer-type hypersensitivity pneumonitis – immunological examinations in onset and non-onset members. Nihon Kokyuki Gakkai Zasshi 45, 566–571. In Japanese.

Orlean, P. 1997. Biogenesis of yeast wall and surface components. In: J.R. Pringle, J.R. Broach and J.W. Jones (Eds), The Molecular and Cellular Biology of the Yeast *Saccharomyces*, Vol. 3. Cold Spring Harbor Laboratory Press, Cold Spring Harbor, New York, pp. 229–362.

Orlovich, D.A., and A.E. Ashford. 1994. Structure and development of the dolipore septum in *Pisolithus tinctorius*. Protoplasma 178, 66–80.

Orlowski, M. 1991. *Mucor* dimorphism. Microbiol. Rev. 55, 234–258.

Osanai, Y., K. Toshima and S. Matsumura. 2004. Transformation of biodegradable polyesters into cyclic oligomers under continuous flow using an enzyme-packed column. Macromol. Biosci. 4, 936–942.

Oshima, Y., and I. Takano. 1972. Genetic controlling system for homothallism and a novel method for breeding triploid cells in *Saccharomyces*. Fermentation Technology Today, Proc. 4th Int. Ferment. Symp. pp. 847–852.

Osorio-Cadavid, E., C. Chaves-López, R. Tofalo, A. Pararella and G. Suzzi. 2008. Detection and identification of wild yeasts in Champús, a fermented Colombian maize beverage. Food Microbiol. 25, 771–777.

Ostergaard, S., L. Olsson and J. Nielsen. 2000. Metabolic engineering of *Saccharomyces cerevisiae*. Microbiol. Mol. Biol. Rev. 64, 34–50.

Osterwalder, A. 1912. Eine neue Gärungs *Monilia: Monilia vini* n. sp. Zentralbl. Bakteriol. Parasitenkd, Abt. II, 33, 257–272.

Osterwalder, A. 1924. Neue aus Obst- und Traubensäften gewonnene *Saccharomyces*-Arten. Zentralbl. Bakteriol. Parasitenkd., Abt. II, 60, 481–528.

Osterwalder, A. 1934. Von Kaltgärhefen und Kaltgärung. Zentralbl. Bakteriol. Parasitenkd., Abt. II, 90, 226–249.

Osumi, M. 1998. The ultrastructure of yeast: cell wall structure and formation. Micron 29, 207–233.

Oswald, M., M. Fischer, N. Dirninger and F. Karst. 2007. Monoterpenoid biosynthesis in *Saccharomyces cerevisiae*. FEMS Yeast Res. 7, 413–421.

Ota, M. 1923. Cinq levures du genre *Debaryomyces* considérées comme pathogènes. Ann. Parasitol. Hum. Comp. 1, 124–136.

Ota, M. 1924a. Beiträge zur Morphologie, Biologie und Systematik der pathogenen, asporogenen Sprosspilze. Dermatol. Wochenschr. 78, 216–237, 260–265.

Ota, M. 1924b. Uber vier neue pathogene Hefearten von der Gattung *Debaryomyces* (Klöcker). Dermatol. Wochenschr. 78, 284–289, 312–316.

Ota, M. 1925. Remarques complémentaires sur la levure pathogène de favre (*Myceloblastanon favrei* n. sp.). Ann. Parasitol. Hum. Comp. 3, 181–184.

Ota, M. 1926. Sur quelques champignons pathogènes du type *Trichosporum beigeli* Vuillemin. Ann. Parasitol. Hum. Comp. 4, 1–13.

Ota, M. 1928. Champignons parasites de l'homme. VI (Études morphologiques et systématiques). Jpn. J. Dermatol. Urol. 28, 16–23, 381–424. In Japanese.

Otani, Y. 1931. Yeasts found in fermented Worcester sauce. Zyozogaku Zasshi 9, 645–651. In Japanese.

Otani, Y. 1939. Microbiological studies on the "Nukamiso-pickles". Zentralbl. Bakteriol. Parasitenkd., Abt. II, 101, 139–151.

Ouchi, K. 1981. Breeding of killer yeast strains for sake brewing. Hakkokogaku Kaishi 59, 517–524.

Oura, T., and S. Kajiwara. 2008. Substrate specificity and regioselectivity of delta 12 and omega 3 fatty acid desaturases from *Saccharomyces kluyveri*. Biosci. Biotechnol. Biochem. 72, 3174–3179.

Ozkan, T.B., E. Sahin, G. Edemir and F. Budak. 2007. Effect of *Saccharomyces boulardii* in children with acute gastroenteritis and its relationship to the immune respons. J. Int. Med. Res. 35, 201–212.

Ozyurt, M., and U.D. Deveci. 2004. Conversion of agricultural and industrial wastes for single cell production and pollution potential reduction: a review. Fresenius Environ. Bull. 13, 693–699.

Pache, R.A., A. Zanzoni, J. Naval, J.M. Maas and P. Aloy. 2008. Towards a molecular charterisation of pathological pathways. FEBS Lett. 582, 1259–1265.

Padhye, A.A., S. Verghese, P. Ravichandran, G. Balamurugan, L. Hall, P. Padmaja and M.C. Fernande. 2003. *Trichosporon loubieri* infection in a patient with adult polycystic kidney disease. J. Clin. Microbiol. 41, 479–482.

Pady, S.M. 1974. Sporobolomycetaceae in Kansas. Mycologia 66, 333–338.

Pagano, J., J.D. Levin and W. Trejo. 1957. Diagnostic medium for differentiation of species of *Candida*. Antibiot. Ann. 137–143.

Page, B.T., and C.P. Kurtzman. 2005. Rapid identification of *Candida* and other clinically important yeast species by flow cytometry. J. Clin. Microbiol. 43, 4507–4514.

Page, B.T., C.E. Shields, W.G. Merz and C.P. Kurtzman. 2006. Rapid identification of ascomycetous yeasts from clinical specimens by a molecular method based on flow cytometry and comparison with identifications from phenotypic assays. J. Clin. Microbiol. 44, 3167–3171.

Page, R.D.M., and E.C. Holmes. 1998. Molecular Evolution: A Phylogenetic Approach. Blackwell Science, Cambridge, 346pp.

Pagnocca, F.C., M.F. Legaspe, A. Rodrigues, C.C. Ruivo, N.S. Nagamoto, M. Bacci, Jr. and L.C. Forti. 2010. Yeasts isolated from a fungus-growing ant nest, including the description of *Trichosporon chiarellii* sp. nov., an anamorphic basidiomycetous yeast. Int. J. Syst. Evol. Microbiol. 60, 1454–1459.

Paine, T.D., K.F. Raffa and T.C. Harrington. 1997. Interactions among scolytid bark beetles, their associated fungi, and live host conifers. Annu. Rev. Entomol. 42, 179–206.

Palkova, Z., and L. Vachova. 2006. Life within a community: benefit to yeast long-term survival. FEMS Microbiol. Rev. 30, 806–824.

Pallmann, C.L., J.A. Brown, T.L. Olincka, L. Cocolin, D.A. Mills and L.F. Bisson. 2001. Use of WL Medium to profile native flora fermentations. Am. J. Enol. Viticult. 52, 198–203.

Palmeri, R., and G. Spagna. 2007. beta-Glucosidase in cellular and acellular form for winemaking application. Enzyme Microb. Technol. 40, 382–389.

Palou, E., A. Lopez-Malo, C.U. Barbosa-Canoual, J. Welts-Chanes and B.G. Swanson. 1997. Effect of water activity on high hydrostatic pressure inhibition of *Zygosaccharomyces bailii*. Lett. Appl. Microbiol. 24, 417–420.

Pandey, A., S. Benjamin, C.R. Soccol, P. Nigam, N. Krieger and V.T. Soccol. 1999. The realm of microbial lipases in biotechnology. Biotechnol. Appl. Biochem. 29, 119–131.

Pandey, A., C. Webb, C.R. Coccol and C. Larroche (Eds). 2006. Enzyme Technology. Springer. Asiatech Publishers, New Delhi.

Panepinto, J., L. Liu, J. Ramos, X. Zhu, T. Valyi-Nagy, S. Eksi, J. Fu, H.A. Jaffe, B. Wickes and P.R. Williamson. 2005. The DEAD-box RNA helicase Vad1 regulates multiple virulence-associated genes in *Cryptococcus neoformans*. J. Clin. Invest. 115, 632–641.

Pang, K.R., J.J. Wu, D.B. Huang and S.K. Tyring. 2004. Subcutaneous fungal infections. Dermatol. Ther. 17, 523–531.

Panke, S., M. Held and M. Wubbolts. 2004. Trends and innovations in industrial biocatalysis for the production of fine chemicals. Curr. Opin. Biotechnol. 15, 272–279.

Panon, G. 1997. Influence of oxygen on fermentation pattern in model media containing mixed or sequential cultures of three cider-producing yeasts: *Saccharomyces cerevisiae* var. *uvarum, Hanseniaspora valbyensis* and *Metschnikowia pulcherrima*. Sci. Aliments 17, 193–217.

Pant, N.C., and G. Fraenkel. 1950. The function of the symbiotic yeasts of two insect species, *Lasioderma serricorne* F. and *Stegobium* (sitodrepa) *paniceum* L. Science 112, 498–500.

Papadakis, C.R. 1922. Sur l'existence d'une copulation hétérogamique dans *Pichia farinosa* Lindner. C. R. Soc. Biol. 86, 447–449.

Papadogeorgakis, H., E. Frangoulis, C. Papaefstathioi and A. Katsambas. 1999. *Rhodotorula rubra* fungaemia in an immunosuppressed patient. J. Eur. Acad. Dermatol. Venereol. 12, 169–170.

Papanikolaou, S., I. Chevalot, M. Komaitis, I. Marc and G. Aggelis. 2002. Single cell oil production by *Yarrowia lipolytica* growing on an industrial derivative of animal fat in batch cultures. Appl. Microbiol. Biotechnol. 58, 308–312.

Papouskova, K., and H. Sychrova. 2007. The co-action of osmotic and high temperature stresses results in a growth improvement of *Debaryomyces hansenii* cells. Int. J. Food Microbiol. 118, 1–7.

Pappas, P.G. 2006. Invasive candidiasis. Infect. Dis. Clin. North Am. 20, 485–506.

Paracer, S., and V. Ahmadjian. 2000. Symbiosis, An Introduction to Biological Associations, 2nd edn. Oxford University Press, New York.

Pariza, M.W., and E.A. Johnson. 2001. Evaluating the safety of microbial enzyme preparations used in food processing: update for a new century. Regul. Toxicol. Pharmacol. 33, 173–186.

Park, C.-M., J.A. Bruenn, C. Ganesa, W.F. Flurkey, R.F. Bozarth and Y. Koltin. 1994. Structure and heterologous expression of the *Ustilago maydis* viral toxin KP4. Mol. Microbiol. 11, 155–164.

Park, C.-S, J.-H. Jeong, S.-Y. Hong and W.-S. Choi. 2001. Yeast *Pichia ciferrii*. US Patent 6,194,196.

Park, D., D.-S. Lee, Y.-M. Kim and J.-M. Park. 2008. Bioaugmentation of cyanide-degrading microorganisms in a full-scale cokes wastewater treatment facility. Bioresour. Technol. 99, 2092–2096.

Park, J.-B., B.-Ch. Seo and J.-R. Kim. 1998. Fermentation process for preparing erythritol using *Trichosporonoides madida* DS 911. US Patent 6060291.

Park, J.-N., M.-J. Sohn, D.-B. Oh, O. Kwon, S.-K. Rhee, C.-G. Hur, S.-Y. Lee, G. Gellissen and H.-A. Kang. 2007. Identification of the cadmium-inducible *Hansenula polymorpha* SEO1 gene promoter by transcriptome analysis and its application to whole-cell heavy metal detection. Appl. Environ. Microbiol. 73, 5990–6000.

Park, K.-A., K. Ahn, E.-S. Chung and T.-Y. Chung. 2008. *Pichia anomala* fungal keratitis. Cornea 27, 619–620.

Park, S.-K., C.-T. Kim, J.-W. Lee, O.-H. Jhee, A.-S. Om, J.-S. Kang and T.-W. Moon. 2007. Analysis of ethyl carbamate in Korean soy sauce. Food Control 18, 975–982.

Park, Y.-Ch., D.-Y. Lee, D.-H. Lee, H.-J. Kim, Y.-W. Ryu and J.-H. Seo. 2005. Proteomics and physiology of erythritol-producing strains. J. Chromatogr. B 815, 251–260.

Parker, A., and J.P. Blackeman. 1984. Stimulation of *Uromyces viciae-fabae in vitro* and *in vivo* by the phylloplane yeast *Cryptococcus*. Physiol. Plant Pathol. 24, 119–128.

Parle, J.N. 1957. Yeasts isolated from the mammalian alimentary tract. J. Gen. Microbiol. 17, 363–367.

Parle, J.N., and M.E. di Menna. 1966. The source of yeasts in New Zealand wines. N.Z. J. Agric. Res. 9, 98–107.

Parmasto, E. 1974. *Helicogonium jacksonii* (Dipodascales) found in Caucasus. Folia Cryptog. Eston. 6, 41–48.

Parolis, L.A., H. Parolis, L. Kenne, M. Meidal and K. Bock. 1998. The extracellular polysaccharide of *Pichia* (*Hansenula*) *holstii* NRRL Y–2448: the phosphorylated side chains. Carbohydr. Res. 309, 77–87.

Passoth, V., E. Fredlund, U.A. Druvefors and J. Schnurer. 2006. Biotechnology, physiology and genetics of the yeast *Pichia anomala*. FEMS Yeast Res. 6, 3–13.

Passoth, V., A.-C. Andersson, M. Olstorpe, B. Theelen, T. Boekhout and J. Schnürer. 2009. *Cryptococcus cerealis* sp. nov., a psychrophilic yeast species isolated from fermented cereals. Antonie van Leeuwenhoek 96, 635–643.

Pastinen, O. 2002. Xylose isomerase from *Streptomyces rubiginosus*: stability, novel reactions and applications. Doctoral Thesis, Helsinki University of Technology, Espoo, Finland.

Patel, R., G.D. Robert, D.G. Kelly and R.C. Walker. 1995. Central venous catheter infection due to *Ustilago* species. Clin. Infect. Dis. 21, 1043–1044.

Patel, R.N. 2000. Microbial/enzymatic synthesis of chiral drug intermediates. Adv. Appl. Microbiol. 47, 33–78.

Patel, R.N. 2001. Enzymatic synthesis of chiral intermediates for Omapatrilat, an antihypertensive drug. Biomol. Eng. 17, 167–182.

Patel, R.N. 2004. Biocatalytic synthesis of chiral pharmaceutical intermediates. Food Technol. Biotechnol. 42, 305–325.

Patel, R.N. 2007. Biocatalysis: synthesis of chiral intermediates for pharmaceuticals. In: C.T. Hou and J.-F. Shaw (Eds), Biocatalysis and Biotechnology for Functional Foods and Industrial Products. CRC Press, Boca Raton, FL, pp. 283–322.

Patel, R.N., A. Goswami, L. Chu, M.J. Donovan, V. Nanduri, S. Goldberg, R. Johnston, P.J. Siva, B. Nielsen, J. Fan, W. He, Z. Shi, K.Y. Wang, R. Eiring, D. Cazzulino, A. Singh and R. Mueller. 2004. Enantioselective microbial reduction of substituted acetophenones. Tetrahedron Asymmetry 15, 1247–1258.

Patel, S.S., B.J. Belmont, J.M. Sante and M.F. Rexach. 2007. Natively unfolded nucleoporins gate protein diffusion across the nuclear pore complex. Cell 129, 83–96.

Patil, S.V., V.K. Jayaraman and B.D. Kulkarni. 2002. Optimization of media by evolutionary algorithms for production of polyols. Appl. Biochem. Biotechnol. 102–103 119–128.

Patiño-Vera, M., B. Jiménez, K. Balderas, M. Ortiz, R. Allende, A. Carrillo and E. Galindo. 2005. Pilot-scale production and liquid formulation of *Rhodotorula minuta*, a potential biocontrol agent of mango anthracnose. J. Appl. Microbiol. 99, 540–550.

Patouillard, M. 1900. Essai Taxonomique sur les Families et les Genres des Hyménomycètes. Duclune, Lons-le-Saunier, 184pp.

Patton, A.M., and R. Marchant. 1978. A mathematical analysis of dolipore/parenthesome structure in basidiomycetes. J. Gen. Microbiol. 109, 335–349.

Paula, C.R., M.C. Sampaio, E.G. Birman and A.M. Siqueira. 1990. Oral yeasts in patients with cancer of the mouth, before and during radiotherapy. Mycopathologia 112, 119–124.

Paula, C.R., V.L. Krebs, M.E. Auler, L.S. Ruiz, F.E. Matsumoto, E. H. Silva, E.M. Diniz and F.A. Vaz. 2006. Nosocomial infection in newborns by *Pichia anomala* in a Brazilian intensive care unit. Med. Mycol. 44, 479–484.

Paulitz, T.C., and R.R. Bélanger. 2001. Biological control in greenhouse systems. Annu. Rev. Phytopathol. 39, 103–133.

Pavgi, M.S., and A.N. Mukhopadhyay. 1969. Artificial culture and *in vitro* chlamydospore development of *Protomyces macrosporus* Unger. Pathol. Microbiol. 33, 287–295.

Pavlica, F. 1962. The first observation of congenital pneumocystic pneumonia in a fully developed stillborn child. Ann. Paediatr. 198, 184.

Pavlou, A., and J. Reichert. 2004. Recombinant protein therapeutics – success rates, market trends and values to 2010. Nat. Biotechnol. 22, 1513–1519.

Pavlou, A., and J. Reichert. 2005. The therapeutic antibody market to 2008. Eur. J. Pharm. Biopharm. 59, 389–396.

Pavlova, K., G. Angelova, I. Savova, D. Grigorova and L. Kupenov. 2002. Studies of Antarctic yeast for beta-glucosidase production. World J. Microbiol. Biotechnol. 18, 569–573.

Pawar, S., D. Murray, W. Khalife, B. Robinson-Dunn and M. MacGinnis. 2002. Human infection caused by *Moniliella suaveolens*. Clin. Microbiol. Newslett. 24, 53–55.

Paz, Z., U. Gerson and A. Sztejnberg. 2007a. Assaying three new fungi against citrus mites in the laboratory, and a field trial. Biocontrol 5, 855–862.

Paz, Z., S. Burdman, U. Gerson and A. Sztejnberg. 2007b. Antagonistic effects of the endophytic fungus *Meira geulakonigii* on the citrus rust mite *Phyllocoptruta oleivora*. J. Appl. Microbiol. 103, 2570–2579.

Pedersen, T.A. 1958. *Cryptococcus terricolus* nov. spec. A new yeast isolated from Norwegian soils. C.R. Trav. Lab. Carlsberg 31, 93–103.

Pedersen, T.A. 1961. Lipid formation in *Cryptococcus terricolus*. I. Nitrogen nutrition and lipid formation. Acta Chem. Scand. 15, 651–662.

Pedersen, T.A. 1963. Lipid formation in *Cryptococcus terricolus*. VI. Effect of malonate on respiration. Physiol. Plant. 16, 167–176.

Peláez Campomanes, F., and C. Ramírez Gómez. 1956a. El *Sporobolomyces hispanicus*, nueva especie de Sporobolomycetaceae aislado de extracto de corteza de encina. Microbiol. Esp. 9, 37–41.

Peláez Campomanes, F., and C. Ramírez Gómez. 1956b. Una nueva especie de *Endomyces* Reess: *Endomyces ovetensis* nov. sp. Microbiol. Esp. 9, 191–200.

Pelletier, R., I. Alarie, R. Lagace and T.J. Walsh. 2005. Emergence of disseminated candidiasis caused by *Candida krusei* during treatment with caspofungin: case report and review of literature. Med. Mycol. 43, 559–564.

Peltroche-Llacsahuanga, H., S. Schmidt, M. Seibold, R. Lutticken and G. Haase. 2000. Differentiation between *Candida dubliniensis* and *Candida albicans* by fatty-acid methyl-ester analysis using gas–liquid chromatography. J. Clin. Microbiol. 38, 3696–3704.

Pennycott, T.W., H.M. Ross, I.M. McLaren, A. Park, G.F. Hopkins and G. Foster. 1998. Causes of death of wild birds of the family Fringillidae in Britain. Vet. Rec. 143, 155–158.

Pennycott, T.W., G. Duncan and K. Venugopal. 2003. Marek's disease, candidiasis and megabacteriosis in a flock of chickens (*Gallus gallus domesticus*) and Japanese quail (*Coturnix japonica*). Vet. Rec. 153, 293–297.

Pereira Filho 1927. Macroglossia mycotica. J. Trop. Med. Hyg. 30, 8–10.

Pereira-Dias, S., M.E. Potes, A. Marinho, M. Malfeito-Ferreira and V. Loureiro. 2000. Characterisation of yeast flora isolated from an artisanal Portuguese ewes' cheese. Int. J. Food Microbiol. 60, 55–63.

Perelló, A., M.R. Simón and A.M. Arambarri. 2002. Interactions between foliar pathogens and the saprophytic microflora of the wheat (*Triticum aestivum* L.) phylloplane. J. Phytopathol. 150, 232–243.

Perera, C.O., and G.M. Yen. 2007. Functional properties of carotenoids in human health. Int. J. Food Prop. 10, 201–230.

Perez, F., M. Ramirez and J.A. Regodon. 2001. Influence of killer strains of *Saccharomyces cerevisiae* on wine fermentation. Antonie van Leeuwenhoek 79, 3–4.

Perfect, J.R. 2006. *Cryptococcus neoformans*: the yeast that likes it hot. FEMS Yeast Res. 6, 463–468.

Perkins, G., D. Goodenough and G. Sosinsky. 1997. Three-dimensional structure of the gap junction connexon. Biophys. J. 72, 533–544.

Perniola, R., M.L. Faneschi, E. Manso, M. Pizzolante, A. Rizzo, Sticchi-Damiani and R. Longo. 2006. *Rhodotorula mucilaginosa* outbreak in neonatal intensive care unit: microbiological features, clinical presentation, and analysis of related variables. Eur. J. Microbiol. Infect. Dis. 25, 193–196.

Perparim, K., H. Nagai, A. Hashimoto, Y. Goto, T. Tashiro and M. Nasu. 1996. *In vitro* susceptibility of *Trichosporon beigelii* to antifungal agents. J. Chemother. 8, 445–448.

Perrins, N., F. Gaudinio and R. Bond. 2007. Carriage of *Malassezia* spp. yeasts in cats with diabetes mellitus, hyperthyroidism and neoplasia. Med. Mycol. 45, 541–546.

Petch, T. 1931. Notes on entomogenous fungi. Trans. Br. Mycol. Soc. 16, 209–245.

Péter, G., and T. Deák. 1991. On the false positive urease activity of *Yarrowia lipolytica*. Antonie van Leeuwenhoek 60, 55–59.

Péter, G., J. Tornai-Lehoczki and T. Deák. 1997. *Candida novakii*, sp. nov., a new anamorphic yeast species of ascomycetous affinity. Antonie van Leeuwenhoek 71, 375–378.

Petér, G., J. Tornai-Lehoczki, D. Dlauchy and G. Vitányi. 2000. *Pichia sporocuriosa* sp. nov., a new yeast isolated from rambutan. Antonie van Leeuwenhoek 77, 37–42.

Péter, G., J. Tornai-Lehoczki, L. Fülöp and D. Dlauchy. 2003. Six new methanol assimilating yeast species from wood material. Antonie van Leeuwenhoek 84, 147–159.

Péter, G., D. Dlauchy, R. Vasdinyei, J. Tornai-Lehoczki and T. Deák. 2004. *Candida galli* sp. nov., a new yeast from poultry. Antonie van Leeuwenhoek 86, 105–110.

Péter, G., D. Dlauchy, J. Tornai-Lehoczki and C.P. Kurtzman. 2005a. *Kuraishia molischiana* sp. nov., the teleomorph of *Candida molischiana*. Antonie van Leeuwenhoek 88, 241–247.

Péter, G.J., M. Tornai-Lehoczki, Suzuki and D. Dlauchy. 2005b. *Metschnikowia viticola* sp. nov., a new yeast species from grape. Antonie van Leeuwenhoek 87, 155–160.

Péter, G., D. Dlauchy and J. Tornai-Lehoczki. 2006. *Candida floccosa* sp. nov., a novel methanol-assimilating yeast species. Int. J. Syst. Evol. Microbiol. 56, 2015–2018.

Petér, G., J. Tornai-Lehoczki and D. Dlauchy. 2007a. *Ogataea allantospora* sp. nov., an ascomycetous yeast species from phylloplane. Antonie van Leeuwenhoek 92, 443–448.

Petér, G., J. Tornai-Lehoczki, K.-S. Shin and D. Dlauchy. 2007b. *Ogataea thermophila* sp. nov., the teleomorph of *Candida thermophila*. FEMS Yeast Res. 7, 494–496.

Petér, G., J. Tornai-Lehoczki and D. Dlauchy. 2008. *Ogataea nitratoaversa* sp. nov., a methylotrophic yeast species from temperate forest habitats. Antonie van Leeuwenhoek 94, 217–222.

Péter, G., J. Tornai-Lehoczki and D. Dlauchy. 2009a. *Trichomonascus apis* sp. nov., a heterothallic yeast species from honeycomb. Int. J. Syst. Evol. Microbiol. 59, 1550–1554.

Petér, G., J. Tornai-Lehoczki and D. Dlauchy. 2009b. *Ogataea populialbae* sp. nov., a yeast species from white poplar. FEMS Yeast Res. 9, 936–941.

Peter, M., and Z. Peter. 1988. Experimentelle Studien bezueglich der Persistenz einiger fakulativ pathogener Pilze in flusswasser. Zentralbl. Mikrobiol. 143, 523–528.

Péteri, Z., J. Téren, C. Vágvölgyi and J. Varga. 2007. Ochratoxin degradation and adsorption caused by astaxanthin-producing yeasts. Food Microbiol. 24, 205–210.

Peters, D. 2007. Raw materials. White Biotechnol. Adv. Biochem. Eng./Biotechnol. 105, 1–30.

Peters, F.T., A.E. Schwaninger, C.A. Dragan, M. Bureik and H.H. Maurer. 2007. New fission yeast strains producing human cytochrome P450 enzymes to be used for biotechnological synthesis of drug metabolites. Ther. Drug Monit. 29, 466–467.

Peters, I.I., and F.E. Nelson. 1948. Preliminary characterization of the lipase of *Mycotorula lipolytica*. J. Bacteriol. 55, 593–600.

Petersen, G.R., W.W. Schubert, G.F. Richards and G.A. Nelson. 1990. Yeasts producing exopolysaccharides with drag-reducing activity. Enzyme Microb. Technol. 12, 255–259.

Petersen, R.F., G. Marinoni, M.L. Nielsen and J. Piskur. 2000. Molecular approaches for analyzing diversity and phylogeny among yeast species. Contrib. Microbiol. 5, 15–35.

Peterson, J.C., and M.T. Cushion. 2005. *Pneumocystis*: not just pneumonia. Curr. Opin. Microbiol. 8, 393–398.

Peterson, J.B., and H. Ris. 1976. Electron-microscopic study of the spindle and chromosome movement in the yeast *Saccharomyces cerevisiae*. J. Cell Sci. 22, 219–242.

Peterson, S.W., and C.P. Kurtzman. 1991. Ribosomal RNA sequence divergence among sibling species of yeasts. Syst. Appl. Microbiol. 14, 124–129.

Petersson, S., and J. Schnürer. 1995. Biocontrol of mold growth in high-moisture wheat stored under airtight conditions by *Pichia anomala*, *Pichia guilliermondii* and *Saccharomyces cerevisiae*. Appl. Environ. Microbiol. 61, 1027–1032.

Petersson, S., and J. Schnürer. 1998. *Pichia anomala* as a biocontrol agent of *Penicillium roqueforti* in high-moisture wheat, rye, barley, and oats stored under airtight conditions. Can. J. Microbiol. 44, 471–476.

Petersson, S., N. Jonsson and J. Schnürer. 1998. *Pichia anomala* as a biocontrol agent during storage of high-moisture feed grain under airtight conditions. Postharvest Biol. Technol. 15, 175–184.

Petrescu, I., J. Lamotte-Braaseur, J.P. Chessa, P. Ntarima, M. Claeyssens, B. Devreese, G. Marino and C. Gerday. 2000. Xylanase from the psychrophilic yeast *Cryptococcus adeliae*. Extremophiles 4, 137–144.

Petter, R., B.S. Kang, T. Boekhout, B.J. Davis and K.J. Kwon-Chung. 2001. A survey of heterobasidiomycetous yeasts for the presence of the genes homologous to virulence factors of *Filobasidiella neoformans*, CNLAC1 and CAP59. Microbiology (London) 147, 2029–2036.

Peynaud, E., and S. Domercq. 1956. Sur les *Brettanomyces* isolés de raisins et de vins. Arch. Mikrobiol. 24, 266–280.

Pfaller, M.A., A. Houston and S. Coffmann. 1996. Application of CHROMagar *Candida* for rapid screening of clinical specimens for *Candida albicans, Candida tropicalis, Candida* krusei, and *Candida* (*Torulopsis*) *glabrata*. J. Clin. Microbiol. 34, 58–61.

Pfaller, M.A., D.J. Diekema, M. Mendez, C. Kibbler, P. Erzsebet, S.C. Chang, D.L. Gibbs and V.A. Newell. 2006. *Candida guilliermondii*, an opportunistic fungal pathogen with decreased susceptibility to fluconazole: geographic and temporal trends from the ARTEMIS DISK antifungal surveillance program. J. Clin. Microbiol. 44, 3551–3556.

Pfeiffer, I., Z. Farkas and W.I. Golubev. 2004a. dsRNA viruses in *Nadsonia fulvescens*. J. Gen. Appl. Microbiol. 50, 97–100.

Pfeiffer, I., W.I. Golubev, Z. Farkas, J. Kucsera and N. Golubev. 2004b. Mycocin productin in *Cryptococcus aquaticus*. Antonie van Leeuwenhoek 86, 374–396.

Phaff, H.J. 1956. A proposal for amendment of the diagnosis of the genus *Pichia* Hansen. Antonie van Leeuwenhoek 22, 113–116.

Phaff, H.J., and E.P. Knapp. 1956. The taxonomy of yeasts found in exudates of certain trees and other natural breeding sites of some species of *Drosophila*. Antonie van Leeuwenhoek 22, 117–130.

Phaff, H.J. 1970a. *Hanseniaspora* Zikes. In: J. Lodder (Ed.), The Yeasts, A Taxonomic Study, 2nd edn. North-Holland, Amsterdam, pp. 209–225.

Phaff, H.J. 1970b. *Sporidiobolus* Nyland. In: J. Lodder (Ed.), The Yeasts, A Taxonomic Study, 2nd edn. North-Holland, Amsterdam, pp. 822–830.

Phaff, H.J. 1970c. *Sporobolomyces* Kluyver et van Niel. In: J. Lodder (Ed.), The Yeasts, A Taxonomic Study, 2nd edn. North-Holland, Amsterdam, pp. 831–862.

Phaff, H.J. 1970d. *Bullera* Derx. In: J. Lodder (Ed.), The Yeasts, A Taxonomic Study, 2nd edn. North-Holland, Amsterdam, pp. 815–821.

Phaff, H.J. 1985. Biology of some yeasts other than *Saccharomyces*. In: A.L. Demain and N.A. Solomon (Eds), Biology of Industrial Microorganisms, Benjamin/ Cummings, Menlo Park, CA, pp. 537–562.

Phaff, H.J. 1990. Isolation of yeasts from natural sources. In: D.P. Labeda (Ed.), Isolation of Biotechnological Organisms from Nature. McGraw-Hill Publishing Co., New York, pp. 53–79.

Phaff, H.J., and D.G. Ahearn. 1970. *Rhodotorula* Harrison. In: J. Lodder (Ed.), The Yeasts, A Taxonomic Study, 2nd edn. North-Holland, Amsterdam, pp. 1187–1223.

Phaff, H.J., and L. do Carmo-Sousa. 1962. Four new species of yeast isolated from insect frass in bark of *Tsuga heterophylla* (Raf.) Sargent. Antonie van Leeuwenhoek 28, 193–207.

Phaff, H.J., and J.W. Fell. 1970. *Cryptococcus* Kützing emend. Phaff et Spencer. In: J. Lodder (Ed.), The Yeasts, A Taxonomic Study, 2nd edn. North-Holland, Amsterdam, pp. 1088–1145.

Phaff, H.J., and C.P. Kurtzman. 1984. *Lipomyces* Lodder et Kreger-van Rij. In: N.J.W. Kreger-van Rij (Ed.), The Yeasts, A Taxonomic Study, 3rd edn. Elsevier, Amsterdam, pp. 252–262.

Phaff, H.J., and M.W. Miller. 1961. A specific microflora associated with the fig wasp, *Blastophaga psenes* Linnaeus. J. Insect. Pathol. 3, 233–243.

Phaff, H.J., and M.W. Miller. 1984. *Schwanniomyces* Klöcker. In: N.J.W. Kreger-van Rij (Ed.), The Yeasts, A Taxonomic Study, 3rd edn. Elsevier, Amsterdam, pp. 423–426.

Phaff, H.J., and M.W. Miller. 1998a. *Wickerhamia* Soneda. In: C.P. Kurtzman and J.W. Fell (Eds), The Yeasts, A Taxonomic Study. Elsevier, Amsterdam, pp. 409–410.

Phaff, H., and M. Miller. 1998b. *Cyniclomyces* van der Walt & D.B. Scott. In C.P., Kurtzman and J.W. Fell (Eds), The Yeasts, A Taxonomic Study. Elsevier, Amsterdam, pp. 154–156.

Phaff, H.J., and J.F.T. Spencer. 1969. Improved parameters in the separation of species in the genera *Rhodotorula* and *Cryptococcus*. Proc. II Int. Symp. Yeasts. Bratislava, 1966, pp. 59–67.

Phaff, H.J., and W.T. Starmer. 1980. Specificity of natural habitats for yeasts and yeast-like organisms. In: F.A. Skinner, S.M. Passmore and R.R. Davenport (Eds), Biology and Activities of Yeasts. Society for Applied Bacteriology Symposium Series No. 9. Academic Press, London, pp. 79–102.

Phaff, H.J., and W.T. Starmer. 1987. Yeasts associated with plants, insects and soil. In: A.H. Rose and J.S. Harrison (Eds), The Yeasts, Vol. I, Biology of Yeasts, 2nd edn. Academic Press, London, pp. 123–180.

Phaff, H.J., and M. Yoneyama. 1961. *Endomycopsis scolyti*, a new heterothallic species of yeast. Antonie van Leeuwenhoek 27, 196–202.

Phaff, H.J., E.M. Mrak and O.B. Williams. 1952. Yeasts isolated from shrimp. Mycologia 44, 431–451.

Phaff, H.J., M.W. Miller and M. Shifrine. 1956. The taxonomy of yeasts isolated from *Drosophila* in the Yosemite region of California. Antonie van Leeuwenhoek 22, 145–161.

Phaff, H.J., M.W. Miller and W.B. Cooke. 1960. A new species of *Schwanniomyces*: *Schwanniomyces alluvius*. Antonie van Leeuwenhoek 26, 182–188.

Phaff, H.J., M. Yoneyama and L. do Carmo-Sousa. 1964a. A one-year, quantitative study of the yeast flora in a single slime flux of *Ulmus carpinifolia* Gled. Riv Pat Veg 4, 485–497.

Phaff, H.J., M.W. Miller and J.F.T. Spencer. 1964b. Two new species of *Pichia* isolated from slime fluxes of deciduous trees. Antonie van Leeuwenhoek 30, 132–140.

Phaff, H.J., M.W. Miller, M. Yoneyama and M. Soneda. 1972. A comparative study of the yeast florae associated with trees from the Japanese islands and on the west coast of North America. In: G. Terui (Ed.), Fermentation Technology Today. Society of Fermentation Technology, Osaka.

Phaff, H.J., M.W. Miller, M. Miranda, W.B. Heed and W.T. Starmer. 1974. *Cryptococcus cereanus*, a new species of the genus *Cryptococcus*. Int. J. Syst. Bacteriol. 24, 486–490.

Phaff, H.J., M.W. Miller and M. Miranda. 1976. *Pichia scutulata*, a new species from tree exudates. Int. J. Syst. Bacteriol. 26, 326–331.

Phaff, H.J., M.W. Miller and E.M. Mrak. 1978a. The Life of Yeasts, 2nd edn. Harvard University Press, Cambridge, MA.

Phaff, H.J., W.T. Starmer, M. Miranda and M.W. Miller. 1978b. *Pichia heedii*, a new species of yeast indigenous to necrotic cacti in the North American Sonoran Desert. Int. J. Syst. Bacteriol. 28, 326–331.

Phaff, H.J., M.W. Miller and M. Miranda. 1979. *Hansenula alni*, a new heterothallic species of yeast from exudates of alder trees. Int. J. Syst. Bacteriol. 29, 60–63.

Phaff, H.J., W.T. Starmer, M. Miranda and M.W. Miller. 1980. *Candida mucilagina*, a new species of yeast found in decaying cladodes of *Opuntia inermis* and in necrotic tissue of Cereoid cacti. Int. J. Syst. Bacteriol. 30, 596–600.

Phaff, H.J., Y. Yamada, J. Tredick and M. Miranda. 1983. *Hansenula populi*, a new homothallic species of yeast from exudates of cottonwood trees. Int. J. Syst. Bacteriol. 33, 375–380.

Phaff, H.J., W.T. Starmer, J. Tredick and M. Miranda. 1985. *Pichia deserticola* and *Candida deserticola*, two new species of yeasts associated with necrotic stems of cacti. Int. J. Syst. Bacteriol. 35, 211–216.

Phaff, H.J., M. Miranda, W.T. Starmer, J. Tredick and J.S.F. Barker. 1986. *Clavispora opuntiae*, a new heterothallic yeast occurring in necrotic tissue of *Opuntia* species. Int. J. Syst. Bacteriol. 36, 372–379.

Phaff, H.J., W.T. Starmer, J. Tredick-Kline and V. Aberdeen. 1987a. *Pichia barkeri*, a new yeast species occurring in necrotic tissue of *Opuntia stricta*. Int. J. Syst. Bacteriol. 37, 386–390.

Phaff, H.J., W.T. Starmer and J. Tredick-Kline. 1987b. *Pichia kluyveri* sensu lato – a proposal for two new varieties and a new anamorph. In: G.S. de Hoog, M.Th. Smith and A.C. M. Weijman (Eds), The Expanding Realm of Yeast-like Fungi. Elsevier, Amsterdam, pp. 403–414. (Stud. Mycol. 30, 403–414).

Phaff, H.J., W.T. Starmer, M.A. Lachance, V. Aberdeen and J. Tredick-Kline. 1992. *Pichia caribaea*, a new species of yeast occurring in necrotic tissue of cacti in the Caribbean area. Int. J. Syst. Bacteriol. 42, 459–462.

Phaff, H.J., W.T. Starmer, M.-A. Lachance and P.F. Ganter. 1994. *Candida caseinolytica* sp. nov., a new species of yeast occurring in necrotic tissue of *Opuntia* and *Stenocereus* species in the southwestern United States and Baja California, Mexico. Int. J. Syst. Bacteriol. 44, 641–645.

Phaff, H.J., J. Blue, A.N. Hagler and C.P. Kurtzman. 1997. *Dipodascus starmeri* sp. nov., a new species of yeast occurring in cactus necroses. Int. J. Syst Bacteriol. 47, 307–312.

Phaff, H.J., A. Vaughan-Martini and W.T. Starmer. 1998. *Debaryomyces prosopidis* sp. nov., a yeast from exudates of mesquite trees. Int. J. Syst. Bacteriol. 48, 1419–1424.

Phaff, H.J., W.T. Starmer and C.P. Kurtzman. 1999. *Pichia lachancei* sp. nov., associated with several Hawaiian plant species. Int. J. Syst. Bacteriol. 49, 1295–1299.

Phaff, H.J., W.T. Starmer and C.P. Kurtzman. 2000. *Pichia hawaiiensis* sp. nov., occurring in decaying bark of Charpentiera trees in the Hawaiian archipelago. Int. J. Syst. Evol. Microbiol. 50, 1683–1686.

Philippe, H., F. Delsuc, H. Brinkmann and N. Lartillot. 2005. Phylogenomics. Annu. Rev. Ecol. Evol. Syst. 36, 519–539.

Phillips, M.J., F. Delsuc and D. Penny. 2004. Genome-scale phylogeny and the detection of systematic biases. Mol. Biol. Evol. 21, 1455–1458.

Phillips, R.M. 1993. The gall-causing fungus of sloes. Cecidology 8, 84–86.

Phister, G.T., and D.A. Mills. 2003. Real-time PCR assay for detection and enumeration of *Dekkera bruxellensis* in wine. Appl. Environ. Microbiol. 69, 7430–7434.

Piano, S., V. Neyrotti, Q. Migheli and M.L. Gullino. 1997. Biocontrol capability of *Metschnikowia pulcherrima* against *Botrytis* post-harvest rot of apple. Postharvest Biol. Technol. 11, 131–140.

Pich, U., and G. Kunze. 1992. Genome organization of mitrochondrial DNA from the non-saccharomycete yeast *Arxula adeninivorans* LS3. Curr. Genet. 22, 505–506.

Pickett, K.M., and C.P. Randle. 2005. Strange Bayes indeed: uniform topological priors imply non-uniform clade priors. Mol. Phylogenet. Evol. 34, 203–211.

Pielou, E.C. 1975. Ecological Diversity. Wiley, New York.

Pien, F.D., R.L. Thompson, D. Deye and G.D. Roberts. 1980. *Rhodotorula septicemia*: two cases and review of the literature. Mayo Clin. Proc. 55, 258–260.

Pierard, G.E., E. Xhauflaire-Uhoda and C. Pierard-Franchimont. 2006. The key role of corneocytes in pityrosporoses. Dermatology 212, 23–26.

Pierini, L.M., and T.L. Doering. 2001. Spatial and temporal sequence of capsule construction in *Cryptococcus neoformans*. Mol. Microbiol. 41, 105–115.

Pifer, L.L., W.T. Hughes and M.J. Murphy Jr. 1977. Propagation of *Pneumocystis carinii* in vitro. Pediatr. Res. 11, 305–316.

Pignal, M.-C. 1967. Une nouvelle espèce de levure isolée de larves d'insectes: *Pichia stipitis*. Bull. Mens. Soc. Linn. Lyon 36, 163–168.

Pignal, M.-C. 1968. Quelques levures associées a des insectes xylophages de la République Centrafricaine. Cahiers de la Maboké 6, 5–15.

Pignal, M.-C. 1970. A new species of yeast isolated from decaying insect-invaded wood. Antonie van Leeuwenhoek 36, 525–529.

Pignal, M.-C., C. Chararas and M. Bourgeay-Causse. 1988. Yeasts from *Ips sexdentatus* (Scolytidae). Mycopathologia 103, 43–48.

Pijper, A. 1928. Een nieuwe *Hanseniaspora*. Verh. K. Ned. Akad. Wet. Afd. Natuurk. 37, 868–871.

Pilat, A. 1957. Übersicht der europaïschen Auriculariales und Tremellales unter besonderer Berücksichtigung der tschechoslowakischen Arten. Acta Mus. Nat. Pragae 13, B(4), 115–210.

Pimenta, R.S., P.D.D. Alves, A. Corrêa, M.-A. Lachance, G.S. Prasad, B.R.R.P. Rajaram, Sinha and C.A. Rosa. 2005. *Geotrichum silvicola* sp. nov., a novel asexual arthroconidial yeast species related to the genus *Galactomyces*. Int. J. Syst. Evol. Microbiol. 55, 497–501.

Pimentel, J.D., M. Baker, A.J. Woodgyer and O.C. Harris. 2005. Fatal disseminated *Blastoschizomyces capitatus* (*Geotrichum capitatum*) in a patient with relapse of acute lymphoblastic leukaemia. Pathol. 37, 319–321.

Pimentel, M., Y. Antonini, R. Martins, M.-A. Lachance and C.A. Rosa. 2005. *Candida riodocensis* and *Candida cellae*, two new yeast species from the *Starmerella* clade associated with solitary bees in the Atlantic Rain Forest of Brazil. FEMS Yeast Res. 5, 875–879.

Pincus, D.H., S. Orenga and S. Chatellier. 2007. Yeast identification – past, present, and future methods. Med. Mycol. 45, 97–121.

Pinjon, E., D. Sullivan, I. Salkin, D. Shanley and D. Coleman. 1998. Simple, inexpensive, reliable method for differentiation of *Candida dubliniensis* from *Candida albicans*. J. Clin. Microbiol. 36, 2093–2095.

Pinna, A., F. Carta, S. Zanetti, S. Sanna and L.A. Sechi. 2001. Endogenous *Rhodotorula minuta* and *Candida albicans* endophthalmitis in an injecting drug user. Br. J. Ophthalmol. 85, 759.

Pintar, J., and W.T. Starmer. 2003. The costs and benefits of killer toxin production by the yeast *Pichia kluyveri*. Antonie van Leeuwenhoek 83, 89–98.

Piper, P.W. 2006. Long-lived yeast as a model for ageing research. Yeast 23, 215–226.

Piper, P.W., C.O. Calderon, K. Hatzixanthis and M. Mollapour. 2001. Weak acid adaptation: the stress response that

confers yeasts with resistance to organic food preservatives. Microbiology 147, 2635–2642.
Pirttilä, A.M., H. Pospiech, H. Laukkanen, R. Myllylä and A. Hohtola. 2003. Two endophytic fungi in different tissues of Scots pine buds (*Pinus sylvestris* L.). Microb. Ecol. 45, 53–62.
Piškur, J., and R.B. Langkjaer. 2004. Yeast genome sequencing: the power of comparative genomics. Mol. Microbiol. 53, 381–389.
Piškur, J., S. Smole, C. Groth, R.F. Petersen and M.B. Pedersen. 1998. Structure and genetic stability of mitochondrial genomes vary among yeasts of the genus *Saccharomyces*. Int. J. Syst. Bacteriol. 48, 1015–1024.
Pitt, J.I. 1974. Resistance of some food spoilage yeasts to preservatives. Food Technol. Aust. 26, 238–241.
Pitt, J.I., and A.D. Hocking. 1997. Fungi and Food Spoilage, 2nd edn. Blackie Academic & Professional, London.
Pitt, J.I., and M.W. Miller. 1968. Sporulation in *Candida pulcherrima, Candida reukaufii* and *Chlamydozyma* species: their relationships with *Metschnikowia*. Mycologia 60, 663–685.
Pitt, J.I., and M.W. Miller. 1970a. Speciation in the yeast genus *Metschnikowia*. Antonie van Leeuwenhoek 36, 357–381.
Pitt, J.I., and M.W. Miller. 1970b. The parasexual cycle in yeasts from the genus *Metschnikowia*. Mycologia 62, 462–473.
Pizarro, F., F.A. Vargas and E. Agosin. 2007. A systems biology perspective of wine fermentations. Yeast 24, 977–991.
Plahutaa, P., and P. Raspor. 2007. Comparison of hazards: current vs. GMO wine. Food Control 18, 492–502.
Plaut, H.C. 1885. Beitrag zur Systematischen Stellung des Soorpilzes in der Botanik. Voigt, Leipzig.
Plaut, H.C. 1887. Neue Beiträge zur Systematischen Stellung des Soorpilzes in der Botanik. Voigt, Leipzig.
Plazas, J., J. Portilla, V. Boix and M. Perez-Mateo. 1994. *Sporobolomyces salmonicolor* lymphadenitis in an AIDS patient. Pathogen or passenger? AIDS 8, 387–388.
Plevako, E.A., and M.E. Cheban. 1935. Biological observations on yeasts utilizing pentoses. Mikrobiologiia 4, 86–95. In Russian.
Pneumocystis Workshop. 1994. Revised nomenclature for *Pneumocystis carinii*. J. Eukaryot. Microbiol. 41, 121S–122S.
Podar, M., and A.L. Reysenbach. 2006. New opportunities revealed by biotechnological explorations of extremophiles. Curr. Opin. Biotechnol. 17, 250–255.
Pohl, C.H., J.L.F. Kock, P.W.J. van Wyk and J. Albertyn. 2006. *Cryptococcus anemochoreius* sp. nov., a novel anamorphic basidiomycetous yeast isolated from the atmosphere in central South Africa. Int. J. Syst. Evol. Microbiol. 56, 2703–2706.
Polacheck, I., and K.J. Kwon-Chung. 1980. Creatinine metabolism in *Cryptococcus neoformans* and *Cryptococcus bacillisporus*. J. Bacteriol. 142, 15–20.
Polacheck, I., and K.J. Kwon-Chung. 1986. Canavanine resistance in *Cryptococcus neoformans*. Antimicrob. Agents Chemother. 29, 468–473.
Polacheck, I., and K.J. Kwon-Chung. 1988. Melanogenesis in *Cryptococcus neoformans*. J. Gen. Microbiol. 134, 1037–1041.
Polacheck, I., V.I. Hearing and K.J. Kwon-Chung. 1982. Biochemical studies of phenoloxidase and utilization of catecholamines in *Cryptococcus neoformans*. J. Bacteriol. 150, 1212–1220.
Poláková, S., C. Blume, J.Á. Zárate, M. Mentela, D. Jørck-Ramberg, J. Stenderup and J. Piškur. 2009. Formation of new chromosomes as a virulence mechanism in yeast *Candida glabrata*. Proc. Natl. Acad. Sci. USA 106, 2688–2693.
Pollacci, G., and A. Nannizzi. 1926. I Miceti Patogeni dell'Uomo e degli Animali, Vol. 5. Capelli, Bologna.
Pollacci, G., and A. Nannizzi. 1928. I Miceti Patogeni dell'Uomo e degli Animali, Vol. 7. Siena, San Bernardino.
Pollacci, G., and A. Nannizzi. 1929. I Miceti Patogeni dell'Uomo e degli Animali, Vol. 9. Siena, San Bernardino.
Polonelli, L., and G. Morace. 1986. Reevaluation of the yeast killer phenomenon. J. Clin. Microbiol. 24, 866–869.
Polonelli, L., G. Dettori, C. Cattel and G. Morace. 1987. Biotyping of mycelial fungus cultures by the killer system. Eur. J. Epidemiol. 3, 237–242.
Polonelli, L., S. Conti, L. Campani, G. Morace and F. Fanti. 1989. Yeast killer toxins and dimorphism. J. Clin. Microbiol. 27, 1423–1425.
Polonelli, L., S. Conti, M. Gerloni, W. Magliani, M. Castagnola, G. Morace and C. Chezzi. 1991. "Antibiobodies," antibiotic-like anti-idiotypic antibodies. J. Med. Vet. Mycol. 29, 235–242.
Polonelli, L., R. Lorenzini, F. de Bernardis, M. Gerloni, S. Conti, G. Morace, W. Magliani and C. Chezzi. 1993. Idiotypic vaccination, immunoprotection mediated by anti-idiotypic antibodies with antibiotic activity. Scand. J. Immunol. 37, 105–110.
Polonelli, L., F. de Bernardis, S. Conti, M. Boccanera, M. Gerloni, G. Morace, W. Magliani, C. Chezzi and A. Cassone. 1994. Idiotypic intravaginal vaccination to protect against *Candida 1* vaginitis by secretory, yeast killer toxin-like anti-idiotypic antibodies. J. Immunol. 152, 3175–3182.
Polonelli, L., F. de Bernardis, S. Conti, M. Boccanera, W. Magliani, M. Gerloni, C. Cantelli and A. Cassone. 1996. Human natural yeast killer toxin-like candidacidal antibodies. J. Immunol. 156, 1880–1885.
Polonelli, L., N. Séguy, S. Conti, M. Gerloni, D. Bertolotti, C. Cantelli, W. Magliani and J.C. Cailliez. 1997. Monoclonal yeast killer toxin-like candidacidal anti-idiotypic antibodies. Clin. Diagn. Lab. Immunol. 4, 142–146.
Polonelli, L., W. Magliani, S. Conti, L. Bracci, L. Lozzi, P. Neri, D. Adriani, F. de Bernardis and A. Cassone. 2003. Therapeutic activity of an engineered synthetic killer anti-idiotypic antibody fragment against experimental mucosal and systemic candidiasis. Infect. Immun. 71, 6205–6212.
Polyakova, A.V., and I.Yu. Chernov. 2002. A new yeast species, *Candida aurita* sp. nov., from oligotrophic bogs of Western Siberia. Microbiology (Moscow) (Mikrobiologiia) 71, 331–334.
Polyakova, A.V., I.Y. Chernov and N.W.S. Panikov. 2001. Yeast diversity in hydromorphic soils with reference to a grass-sphagnum wetland in western Siberia and hummocky Tundra Region at Cape Barrow (Alaska). Mikrobiologiia 70, 714–720. In Russian.
Pompon, D., B. Louerat, A. Bronine and P. Urban. 1996. Yeast expression of animal and plant P450's in optimized redox environments. Methods Enzymol. 272, 51–64.
Poncet, S. 1973a. Incidence de l'introduction d'espèces nouvelles sur les groupes établis dans le genre *Hansenula*

(Ascomycètes, Cryptococcacées) par l'application d'une méthode d'analyse factorielle. Ann. Microbiol. (Inst. Pasteur, Paris) 124A, 95–108.
Poncet, S. 1973b. Taxonomie numérique du genre *Kluyveromyces*. Mycopathol. Mycol. Appl. 51, 267–281.
Poon, N.H., and A.W. Day. 1976a. Somatic nuclear division in the sporidia of *Ustilago violaceae*. III. Ultrastructural observations. Can. J. Microbiol. 22, 495–506.
Poon, N.H., and A.W. Day. 1976b. Somatic nuclear division in the sporidia of *Ustilago violaceae*. IV. Microtubules and the spindle-pole body. Can. J. Microbiol. 22, 507–522.
Popolo, L., and M. Vai. 1999. The Gas1 glycoprotein, a putative wall polymer cross-linker. Biochim. Biophys. Acta 1426, 385–400.
Popolo, L., D. Gilardelli, P. Bonfante and M. Vai. 1997. Increase in chitin as an essential response to defects in assembly of cell wall polymers in the ggp1delta mutant of *Saccharomyces cerevisiae*. J. Bacteriol. 179, 463–469.
Popta, C.M.L. 1899. Beitrag zur Kenntniss der Hemiasci. Flora Allgem. Bot. Ztg. 5–50.
Porat, R., A. Daus, B. Weiss, L. Cohen and S. Droby. 2002. Effect of combining hot water, sodium bicarbonate and biocontrol on postharvest decay of citrus fruit. J. Hort. Sci. Biotechnol. 77, 441–445.
Pore, R.S. 1972. Nutritional basis for relating *Prototheca* and *Chlorella*. Can. J. Microbiol. 18, 1175–1177.
Pore, R.S. 1973. Selective medium for the isolation of *Prototheca*. Appl. Environ. Microbiol. 26, 648–649.
Pore, R.S. 1984. Detoxification of chlordecone poisoned rats with *Chlorella* and *Chlorella* derived sporopollenin. Drug Chem. Toxicol. 7, 57–71.
Pore, R.S. 1985a. *Prototheca* taxonomy. Mycopathologia 90, 129–139.
Pore, R.S. 1985b. *Prototheca* associated with banana. Mycopathologia 90, 187–189.
Pore, R.S. 1986. The association of *Prototheca* spp. with slime flux in *Ulmus americana* and other trees. Mycopathologia 94, 67–73.
Pore, R.S. 1998. *Prototheca* Krüger. In: C.P. Kurtzman and J.W. Fell (Eds), The Yeasts, A Taxonomic Study, 4th edn. Elsevier, Amsterdam, pp. 883–887.
Pore, R.S. 2005. Protothecosis. In: W.G. Merz and R.J. Hay (Eds), Medical Mycology, Vol. 4, Topley and Wilson's Microbiology and Microbial Infections, 10th edn. Hodder Arnold, London, pp. 396–411.
Pore, R.S., and T.A. Shahan. 1988. *Prototheca zopfii*: natural, transient, occurrence in pigs and rats. Mycopathologia 101, 85–88.
Pore, R.S., and W.G. Sorenson. 1981. Kepone removal from aqueous solution by immobilized algae. J. Environ. Sci. Health A16, 51–63.
Pore, R.S., and W.G. Sorenson. 1990. *Reniforma strues*, a new yeast from wastewater. Mycologia 82, 549–553.
Pore, R.S., R.F. d'Amato and L. Ajello. 1977. *Fissuricella* gen. nov.: a new taxon for *Prototheca filamenta*. Sabouraudia 15, 69–78.
Pore, R.S., E.A. Barnett, W.C. Barnes and J.D. Walker Jr. 1983. *Prototheca* ecology. Mycopathologia 81, 49–62.
Pore, R.S., D.F. Boehm and E.A. Barnett. 1986. *Prototheca* (achloric alga) in wastewater. Water Air Soil Pollut. 27, 355–362.
Pore, R.S., T.A. Shahan, M.D. Pore and R. Blauwiekel. 1987. Occurrence of *Prototheca zopfii*, a mastitis pathogen, in milk. Vet. Microbiol. 15, 315–323.
Porro, D. 2004. Process for expression and secretion of proteins by the non-conventional yeast *Zygosaccharomyces bailii*. International Patent Application Number WO 2004/042036 A2.
Porro, D., M.M. Bianchi, L. Brambilla, R. Menghini, D. Bolzani, V. Carrera, J. Livevense, C.L. Liu, B.M. Ranzi, L. Frontali and L. Alberhhina. 1999. Replacement of a metabolic pathway for large-scale production of lactic acid from engineered yeasts. Appl. Environ. Microbiol. 65, 4211–4215.
Porro, D., M. Sauer, P. Branduardi and D. Mattanovich. 2005. Recombinant protein production in yeasts. Mol. Biotechnol. 31, 245–259.
Posada, D., and T.R. Buckley. 2004. Model selection and model averaging in phylogenetics: advantages of the AIC and Bayesian approaches over likelihood ratio tests. Syst. Biol. 53, 793–808.
Posada, D., and K.A. Crandall. 1998. Modeltest: testing the model of DNA substitution. Bioinformatics 14, 817–818.
Posada, D., and K.A. Crandall. 2001. Selecting the best-fit model of nucleotide substitution. Syst. Biol. 50, 580–601.
Posada, F., and F.E. Vega. 2005. Coffee endophytes pathogenic to the coffee berry borer. Abstr. 38th Ann. Meeting Soc. Invert. Pathol., Aug. 7–11, 2005, Anchorage, Alaska, USA.
Pottier, I., S. Gente, J.-P. Vernoux and M. Guéguen. 2008. Safety assessment of dairy microorganisms: *Geotrichum candidum*. Int. J. Food Microbiol. 126, 327–332.
Pou, J., X. Figarella, M.J. Fernández and J. Garrido. 1985a. Obtención de proteinas a partir de bagacillo de caña. I. Estudio de hidrólisis de bagacillo i selección de especies de levaduras. Microbiol. Esp. 38, 81–88.
Pou, J., M.J. Fernàndez and J. Garrido. 1985b. Obtencion de proteinas de bagacillo de caña. II. Estudio de la multiplicacion de *Trichosporon penicillatum* en cultivo semi-solido en bandejas. Microbiol. Esp. 38, 89–95.
Poza, M., T. de Miguel, C. Sieiro and T.G. Villa. 2001. Characterization of a broad pH range protease of *Candida caseinolytica*. J. Appl. Microbiol. 91, 916–921.
Prakitchaiwattana, C., G.H. Fleet and G.M. Heard. 2004. Application and evolution of denaturing gradient gel electrophoresis to analyse the yeast ecology of wine grapes. FEMS Yeast Res. 4, 865–877.
Praphailong, W., and G.H. Fleet. 1997. The effect of pH, sodium chloride, sucrose, sorbate and benzoate on the growth of food spoilage yeasts. Food Microbiol. 14, 459–468.
Praphailong, W., and G.H. Fleet. 2000. *Debaryomyces*. In: R.K. Robinson, C.A. Batt and P. Patel (Eds), Encyclopedia of Food Microbiology. Academic Press, London, pp. 515–520.
Praphailong, W., M. von Gestel, G.H. Fleet and G.M. Heard. 1997. Evaluation of the Biolog system for the identification of food and beverage yeasts. Lett. Appl. Microbiol. 24, 455–459.
Prasad, G.S., S. Mayilraj, N. Sood, V. Singh, K. Biswas and L. Banwari. 2005. *Candida digboiensis* sp. nov., a novel anamorphic yeast species from an acidic tar sludge-contaminated oilfield. Int. J. Syst. Evol. Microbiol. 55, 967–972.
Prescott, S.C., and C.G. Dunn. 1940. Industrial Microbiology, 1st edn. McGraw Hill, New York.

Pretorius, E.E., F. Spaaij, G. Weber and J.P. van der Walt. 1993. *Myxozyma monticola* sp. nov. (Candidaceae), a new species from South African soil. Syst. Appl. Microbiol. 16, 261–265.

Pretorius, I.S. 2000. Tailoring wine yeast for the new millennium, novel approaches to the ancient art of winemaking. Yeast 16, 675–729.

Pretorius, I.S., and F.F. Bauer. 2002. Meeting the consumer challenge through genetically customized yeast strains. Trends Biotechnol. 20, 426–432.

Pretorius, I.S., M. du Toit and P. Rensburg. 2003. Designer yeasts for the 21st century. Food Technol. Biotechnol. 41, 3–10.

Price, C.W., and H.J. Phaff. 1979. *Debaryomyces polymorphus* and *D. pseudopolymorphus*, new taxonomic combinations. Mycologia 71, 444–445.

Price, C.W., G.B. Fuson and H.J. Phaff. 1978. Genome comparison in yeast systematics: delimitation of species within the genera *Schwanniomyces*, *Saccharomyces*, *Debaryomyces* and *Pichia*. Microbiol. Rev. 42, 161–193.

Pridham, T.G., and K.B. Raper. 1950. *Ashbya gossypii* – its significance in nature and in the laboratory. Mycologia 42, 603–623.

Prieto, J.A., B.R. Bort, J. Martínez, F. Randez-Gil, C. Buesa and P. Sanz. 1995. Purification and characterization of a new alpha-amylase of intermediate thermal stability from the yeast *Lipomyces kononenkoae*. Biochem. Cell Biol. 73, 41–49.

Prillinger, H. 1987. Are there yeasts in Homobasidiomycetes? Stud. Mycol. 30, 33–59.

Prillinger, H., C. Dörfler, G. Laaser, B. Eckerlein and L. Lehle. 1990a. Ein Beitrag zur Systematik und Entwicklungsbiologie höherer Pilze: Hefe-Typen der Basidiomyceten. Teil I: Schizosaccharomycetales, *Protomyces*-Typ. Z. Mykol. 56, 219–250.

Prillinger, H., C. Dörfler, G. Laaser and G. Hauska. 1990b. Ein Beitrag zur Systematik und Entwicklungsbiologie höherer Pilze. Hefe-Typen der Basidiomyceten. Teil III: *Ustilago*-Typ. Z. Mykol. 56, 251–278.

Prillinger, H., G. Deml, C. Dörfler, G. Laaser and W. Lockau. 1991a. Ein Beitrag zur Systematik und Entwicklungsbiologie höherer Pilze. Hefe-Typen der Basidiomyceten. Teil II: *Microbotryum*-Typ. Bot. Acta 104, 5–17.

Prillinger, H., G. Laaser, C. Dörfler and K. Ziegler. 1991b. Ein Beitrag zur Systematik und Entwicklungsbiologie hoherer Pilze. Hefe-Typen der Basidiomyceten. Teil IV: *Dacrymyces*-Typ, *Tremella*-Typ. Sydowia 53, 170–218.

Prillinger, H., F. Oberwinkler, C. Umile, K. Tlachac, R. Bauer, C. Dörfler and E. Taufratzhofer. 1993a. Analysis of cell wall carbohydrates (neutral sugars) from ascomycetous and basidiomycetous yeasts with and without derivatization. J. Gen. Appl. Microbiol. 39, 1–34.

Prillinger, H., J. Altenbuchner, G. Laaser and C. Dörfler. 1993b. Yeasts isolated from homobasidiomycetes (*Asterophora, Collybia*): new aspects for sexuality, taxonomy, and speciation. Exp. Mycol. 17, 24–45.

Prillinger, H., E. Staudacher, K. Lopandic, F. Altmann, C. Umile and R. Messner. 1994. Cell wall neutral sugars of yeasts as a tool to clarify phylogenetic relationships of higher fungi. In: RIKEN Symposium, Wako, Saitama, Japan, pp. 15–17.

Prillinger, H., R. Messner, H. Koenig, R. Bauer, K. Lopandic, O. Molnar, P. Dangel, F. Weigang, T. Kirisits, T. Nakase and L. Sigler. 1996. Yeasts associated with termites: a phenotypic and genotypic characterization and use of coevolution for dating evolutionary radiations in asco- and basidiomycetes. Syst. Appl. Microbiol. 19, 265–283.

Prillinger, H., G. Kraepelin, K. Lopandic, W. Schweigkofler, O. Molnár, F. Weigang and M.M. Dreyfuss. 1997a. New species of *Fellomyces* isolated from epiphytic lichen species. Syst. Appl. Microbiol. 20, 572–584.

Prillinger, H., W. Schweigkofler, M. Breitenbach, P. Briza, E. Staudacher, K. Lopandic, O. Molnár, F. Weigang, M. Ibl and A. Ellinger. 1997b. Phytopathogenic filamentous (*Ashbya*, *Eremothecium*) and dimorphic fungi (*Holleya*, *Nematospora*) with needleshaped ascospores as new members within the Saccharomycetaceae. Yeast 13, 945–960.

Prillinger, H., O. Molnár, F. Eliskases-Lechner and K. Lopandic. 1999. Phenotypic and genotypic identification of yeasts from cheese. Antonie van Leeuwenhoek 75, 267–283.

Prillinger, H., K. Bacigálová, K. Lopandic and M. Binder. 2000. *Taphrina padi* in Bayern und der Slowakei. Hoppea Denkschr. Regensb. Bot. Ges. 61, 275–294.

Prillinger, H., K. Lopandic, M. Suzuki, K. Sterflinger, E. Weber and F. Oberwinkler. 2001. Molecular phylogeny and systematics of yeasts and yeast-like fungi with special reference to the Asco- and Basidiomycota. Yeast Newslett. 50, 75–76.

Prillinger, H., K. Lopandic, W. Schweigkofler, R. Deak, H.J.M. Aarts, R. Bauer, K. Sterflinger, G.F. Kraus and A. Maraz. 2002. Phylogeny and systematics of the Fungi with special reference to the Ascomycota and Basidiomycota. In: M. Breitenbach, R. Crameri and S.B. Lehrer (Eds), Fungal Allergy and Pathogenicity. Chem. Immunol. 81, 207–295.

Prillinger, H., K. Lopandic, T. Sugita and M. Wuczkowski. 2007. *Asterotremella* gen. nov. *albida*, an anamorphic tremelloid yeast isolated from the agarics *Asterophora lycoperdoides* and *Asterophora parasitica*. J. Gen. Appl. Microbiol. 53, 167–175.

Pringle, A., S.N. Patek, M. Fischer, J. Stolze and N.P. Money. 2005. The captured launch of a ballistospore. Mycologia 97, 866–871.

Pringsheim, E., and H. Bilewsky. 1911. Über Rosahefe. Beitr. Biol. Pflanz. 10, 118–133.

Pringsheim, E.G. 1963. Farblose Algen. G. Fischer Verlag, Stuttgart.

Prista, C., M.C. Loureiro-Dias, V. Montiel, R. García and J. Ramos. 2005. Mechanisms underlying the halotolerant way of *Debaryomyces hansenii*. FEMS Yeast Res. 5, 693–701.

Pritchard, F.J., and W.S. Porte. 1923. Watery-rot of tomato fruits. J. Agric. Res. 24, 895–906.

Propísek, M., Z. Palková, J. Korb and D. Vaněk. 1996. Isolation and characterization of a new dsRNA virus from *Wickerhamia fluorescens*. Folia Microbiol. 41, 223–227.

Prostoserdov, N.N., and R. Afrikian. 1933. Jerezwein in Armenien. Weinland 5, 389 (cited by Kudryavtsev 1960).

Puchkov, E.O., U. Zahringer, B. Lindner, T.V. Kulakovskaya, U. Seydel and A. Wiese. 2002. The mycocidal, membrane-active complex of *Cryptococcus humicola* is a new type of cellobiose lipid with detergent features. Biochim. Biophys. Acta 1558, 161–170.

Puel, F., C. Largeau and G. Giraud. 1987. Occurrence of a resistant biopolymer in the outer walls of the parasitic alga *Prototheca wickerhamii* (Chlorococcales): ultrastructural and chemical studies. J. Phycol. 23, 649–656.

Pugh, G.J.F., and J.L. Mulder. 1971. Mycoflora associated with *Typha latifolia*. Trans. Br. Mycol. Soc. 57, 273–282.

Pulverer, C., and H. Korth. 1971. *Cryptococcus neoformans*: Pigmentbildung aus verschiedenen Polyphenolen. Med. Microbiol. Immunol. 175, 46–51.

Puntoni, V. 1935. Manuale d. Microbiol., Studio, Edit. d. Ist. Univ. Roma, 2nd edn (cited by Lodder and Kreger-van Rij 1952).

Puntoni, V. 1938. Studio sul genere *Trichosporon*. Mycopathol. Mycol. Appl. 1. 169–181.

Pusey, P.L. 1999. Effect of nectar on microbial antagonists evaluated for use in control of fire blight of pome fruits. Phytopathology 89, 39–46.

Put, H.M.C., J. de Jong, F.E.M.J. Sand and A.M. van Grinsven. 1976. Heat resistance studies on yeasts spp. causing spoilage in soft drinks. J. Appl. Bacteriol. 40, 135–152.

Pyke, M. 1958. The technology of yeast. In: A.H. Cook (Ed.), The Chemistry and Biology of Yeasts. Academic Press, New York, pp. 535–586.

Qi, J., B. Wang and B.I. Hao. 2004. Whole proteome prokaryote phylogeny without sequence alignment: a K-string composition approach. J. Mol. Evol. 58, 1–11.

Qin, G.Z., and S.P. Tian. 2004. Biocontrol of postharvest diseases of jujube fruit by *Cryptococcus laurentii* combined with a low dosage of fungicides under different storage conditions. Plant Dis. 5, 497–501.

Qin, G., S. Tian and Y. Xu. 2004. Biocontrol of postharvest diseases on sweet cherries by four antagonistic yeasts in different storage conditions. Postharvest Biol. Technol. 31, 51–58.

Qin, G.Z., S.P. Tian, Y. Xu, Z.L. Chan and B.Q. Li. 2006. Combination of antagonistic yeasts with two food additives for control of brown rot caused by *Monilinia fructicola* on sweet cherry fruit. J. Appl. Microbiol. 100, 508–515.

Qiu, Y.L., Y.R. Cho, J.C. Cox and J.D. Palmer. 1998. The gain of three mitochondrial introns identifies liverworts as the earliest land plants. Nature 394, 671–674.

Querol, A., and G.H. Fleet, (Eds). 2006. Yeasts in Food and Beverages. Springer-Verlag, Berlin.

Querol, A., M.T. Fernandez- Espinar, M. del Olmo and E. Barrio. 2003. Adaptive evolution of wine yeast. Int. J. Food Microbiol. 86, 3–10.

Queyrat, L., and G. Laroche. 1909. Sur une mycose vaginale (*Parendomyces albus*). Étude microbiologique, expérimentale et thárapeutique. Bull. Mem. Soc. Med. Hôp. Paris 28, 111–136.

Quinquaud, M. 1868. Nouvelles recherches sur le muguet. Classification et conditions de développement du *Syringospora robinii* (dit *Oidium albicans*). Arch. Phys. Norm. Pathol. 1, 290–305.

Quirin, N., M. Desnos-Ollivier, J.F. Cantin, J.C. Valery, Y. Doussy, R. Goursaud, F. Dromer and J.M. Tivollier. 2007. Peritonitis due to *Blastobotrys proliferans* in a patient undergoing continuous ambulatory peritoneal dialysis. J. Clin. Microbiol. 45, 3453–3455.

Quirós, M., P. Martorell, M.-J. Valderrama, A. Querol, J.M. Peinado and M.-I. de Silóniz. 2006. PCR-RFLP analysis of the IGS region of rDNA: a useful tool for the practical discrimination between species of the genus *Debaryomyces*. Antonie van Leeuwenhoek 90, 211–219.

Rabenhorst, L. 1867. Zwei Parasiten an den todten Haaren der Chignons. Hedwigia 6, 49.

Rabosto, X., M. Carrau, A. Paz, E. Boido, E. Dellacassa and F.M. Carrau. 2006. Grapes and vineyard soils as sources of microorganisms for biological control of *Botrytis cinerea*. Am. J. Enol. Vitic. 57, 332–338.

Radler, F. 1993. Yeasts – metabolism of organic acids. In: G.H. Fleet (Ed.), Wine Microbiology and Biotechnology. Harwood Academic Publishers, Chur, Switzerland, pp. 165–182.

Radler, F., M.J. Schmitt and B. Meyer. 1990. Killer toxin of *Hanseniaspora uvarum*. Arch. Microbiol. 154, 175–178.

Radler, F., S. Herzberger, I. Schoenig and P. Schwarz. 1993. Investigation of a killer strain of *Zygosaccharomyces bailii*. J. Gen. Microbiol. 139, 495–500.

Radoi, F., M. Kishida and H. Kawasaki. 2005. Endo-polygalacturonase in *Saccharomyces* wine yeasts; effect of carbon source on enzyme production. FEMS Yeast Res. 5, 663–668.

Ragaert, P., F. Devlieghere, S. Loos, J. Dewulf, H. van Langenhove and J. Debevere. 2006. Metabolite production of yeasts on a strawberry-agar during storage at 7°C in air and low oxygen atmosphere. Food Microbiol. 23, 154–161.

Ragan, M.A. 1992. Phylogenetic inference based on matrix representation of trees. Mol. Phylogenet. Evol. 1, 53–58.

Ragauskas, A.J., C.K. Williams, B.H. Davison, G. Britovsek, J. Cairney, C.A. Eckert, W.J. Frederick Jr., J.P. Hallett, D.J. Leak, C.L. Liotta, J.R. Mielenz, R. Murphy, R. Templer and T. Tschaplinski. 2006. The path forward for biofuels and biomaterials. Science 311, 484–489.

Raitvir, A.G. 1967. Key to the Heterobasidiomycetidae of the U.S.S.R. Academy of Sciences of the U.S.S.R. Academy of Sciences of Estonian S.S.R., Leningrad. In Russian.

Rajagopala, S.V., B. Titz and P. Uetz. 2007. Array-based yeast two-hybrid screening for protein–protein interactions. Methods Microbiol. 36, 139–163.

Rajasingh, H., D.I. Vage, S.A. Pavey and S.W. Omholt. 2007. Why are salmonids pink? Can. J. Fish. Aquat. Sci. 64, 1614–1627.

Ram, A.F., J.C. Kapteyn, R.C. Montijn, L.H. Caro, J.E. Douwes, W. Baginsky, P. Mazur, H. van den Ende and F.M. Klis. 1998. Loss of the plasma membrane-bound protein Gas1p in *Saccharomyces cerevisiae* results in the release of beta1,3-glucan into the medium and induces a compensation mechanism to ensure cell wall integrity. J. Bacteriol. 180, 1418–1424.

Ramage, G., S.P. Saville, B.L. Wickes and J.L. Lopez-Ribot. 2002. Inhibition of *Candida albicans* biofilm formation by farnesol, a quorum-sensing molecule. Appl. Environ. Microbiol. 68, 5459–5463.

Ramani, R., B.T. Kahn and V. Chaturvedi. 1997. *Tilletiopsis minor*, a new etiologic agent of human subcutaneous mycosis in an immunocompromised host. J. Clin. Microbiol. 35, 2992–2995.

Ramírez, C. 1954. Note sur deux nouvelles espèces de levures isolées de divers milieux. Rev. Mycol. 19, 98–102.

Ramírez, C. 1974. A compilation of descriptions of new *Candida* species with keys to all species of the genus described up to date. Microbiol. Esp. 27, 15–78.

Ramírez, C. 1988. Emendation of yeasts isolated from decayed wood in the evergreen rainy Valdivian forest of southern Chile. Mycopathologia 103, 95–101.

Ramírez, C. 1989. A new species of *Trichosporonoides* isolated from sweetened orange/mango drink in Australia. Mycopathologia 108, 25–30.

Ramírez, C., and J. Boidin. 1953a. Trois nouvelles espèeces de levures isolées de liqueurs tannantes. Rev. Mycol. 18, 149–156.

Ramírez, C., and J. Boidin. 1953b. Nuevas especies de levaduras aisladas de liquidos curtientes. Microbiol. Esp. 4, 405–414.

Ramírez, C., and J. Boidin. 1954. *Saccharomyces chambardi*, nouvelle espèce de levure isolée de liqueur tannante. Bull. Mens. Soc. Linn. Lyon 23, 151–152.

Ramírez, C., and J. Boidin. 1955. Nueva especie de levadura aislada de liquido curtiente *Saccharomyces chambardi* nov. sp. Microbiol. Esp. 8, 225–228.

Ramírez, C., and C. González. 1972. *Candida iberica* sp. n. A new species isolated from Spanish sausages. Can. J. Microbiol. 18, 1778–1780.

Ramírez, C., and A. González. 1984a. Three new, nonfermenting, and nitrate-negative *Candida* species isolated from decayed wood in the evergreen rainy Valdivian forest of southern Chile. Mycopathologia 87, 175–180.

Ramírez, C., and A. González. 1984b. *Rhodotorula grinbergsii* sp. nov. isolated from decayed wood in the evergreen rainy Valdivian forest of southern Chile. Mycopathologia 88, 51–53.

Ramírez, C., and A. González. 1984c. Two new species and one variety of nitrate-utilizing mycelial *Candida* isolated from decayed wood in the evergreen rainy Valdivian forest of southern Chile. Mycopathologia 88, 55–60.

Ramírez, C., and A. González. 1984d. Four new species of *Apiotrichum* isolated from decayed wood in the evergreen rainy Valdivian forest of southern Chile. Mycopathologia 88, 71–78.

Ramírez, C., and A. González. 1984e. *Pichia scaptomyzae* sp. nov., isolated from *Scaptomyza multispinosa* Malloch (Diptera) in southern Chile. Mycopathologia 88, 79–81.

Ramírez, C., and A. González. 1984f. Five new filamentous, glucose-fermenting *Candida* isolated from decayed wood in the evergreen rainy Valdivian forest of southern Chile. Mycopathologia 88, 83–92.

Ramírez, C., and A. González. 1984g. Three new filamentous, fermenting *Candida* isolated from decayed wood in the evergreen rainy Valdivian forest of southern Chile. Mycopathologia 88, 93–98.

Ramírez, C., and A. González. 1984h. Two new amycelial *Candida* isolated from decayed wood in the evergreen rainy Valdivian forest of southern Chile. Mycopathologia 88, 99–103.

Ramírez, C., and A. González. 1984i. *Candida santjacobensis* and *Candida ancudensis*, two new species of yeasts isolated from decayed wood in the evergreen rainy Valdivian forest of southern Chile. Mycopathologia 88, 105–109.

Ramírez, C., and A. González. 1984j. Two new filamentous, non-fermenting *Candida* and a new *Schizoblastosporion* isolated from decayed wood in the evergreen rainy Valdivian forest of southern Chile. Mycopathologia 88, 165–171.

Ramírez, C., and A.T. Martinez. 1978. *Torulopsis pampelonensis* sp. nov. A new species of yeast isolated from beech forest soil. Can. J. Microbiol. 24, 433–435.

Ramírez, C., C. González and C. Gutierrez. 1981. *Rhodotorula matritense* sp. nov., isolated from powdered red pepper (*Capsicum frutescens* L.). Mycopathologia 74, 433–435.

Ramírez Gómes, C. 1953. Estudio sobre nuevas especies de levaduras aisladas de differentes sustratos. Microbiol. Esp. 6, 249–253.

Ramírez Gómez, C. 1957. Contribucion al estudio de la ecologia de las levaduras. I. Estudio de levaduras aisladas de hongos carnosos. Microbiol. Esp. 10, 215–247.

Ramírez Gómez, C. 1959. Nouvelle diagnose d'une levure isolée d'une *Amanita lividopallescens, Geotrichum zambettakesii* n. comb. Rev. Mycol. 24, 434–436.

Ramírez Gómez, C., and G. Sierra Rico. 1956. Una nueva variedad de *Torulopsis holmii* (Jörgensen) y estudio de sus productos metabolicos. Microbiol. Esp. 9, 147–162.

Ramirez-Orozco, M., N.Y. Hernandez-Saavedra and J.-L. Ochoa. 2001. *Debaryomyces hansenii* growth in nonsterile seawater ClO_2-peptone-containing medium. Can. J. Microbiol. 47, 676–679.

Ramos, A., and I. Spencer-Martins. 1983. Extracellular glucose producing exodextranase of the yeast *Lipomyces lipofer*. Antonie van Leeuwenhoek 49, 183–190.

Ramos, J.M., M. Cuenca-Estrella, F. Gutierrez, M. Elia and J.L. Rodriguez-Tudela. 2004. Clinical case of endocarditis due to *Trichosporon inkin* and antifungal susceptibility profile of the organism. J. Clin. Microbiol. 42, 2341–2344.

Ramos, L.P., and H.M. Wilhelm. 2005. Current status of biodiesel development in Brazil. Appl. Biochem. Biotechnol. 121–124, 807–819.

Randez-Gil, F., P. Sanz and J.A. Prieto. 1999. Engineering baker's yeast: room for improvement. TIBTECH 17, 237–244.

Randhawa, H.S., T. Kowshik and Z.U. Khan. 2003. Decayed wood of *Syzygium cumini* and *Ficus religiosa* living trees in Delhi/New Delhi metropolitan area as natural habitat of *Cryptococcus neoformans*. Med. Mycol. 41, 199–209.

Ranieri, S., Y. Kodama, Y. Kaneko, K. Mikata, Y. Nakao and T. Ashikari. 2006. Pure and mixed genetic lines of *Saccharomyces bayanus* and *Saccharomyces pastorianus* and their contribution to the lager brewing strain genome. Appl. Environ. Microbiol. 72, 3968–3974.

Rankine, B.C., and D.A. Pilone. 1974. Yeast spoilage of bottled table wine and its prevention. Aust. Wine Brew. Spirit Rev. 92, 36–40.

Rankine, B.C., and J.C.M. Fornachon. 1964. *Schizosaccharomyces malidevorans* sp. n., a yeast decomposing L-malic acid. Antonie van Leeuwenhoek 30, 73–75.

Rao, R.S., B. Bhadra, N.N. Kumar and S. Shivaji. 2007. *Candida hyderabadensis* sp. nov., a novel ascomycetous yeast isolated from wine grapes. FEMS Yeast Res. 7, 489–493.

Rao, V., and G.S. de Hoog. 1975. Some notes on *Torula*. Persoonia 8, 199–206.

Raper, J.R. 1966. Genetics of Sexuality in Higher Fungi. Ronald Press, New York.

Raso, J., and G.U. Barbosa-Canovas. 2003. Nonthermal preservation of foods using combined processing techniques. Crit. Rev. Food Sci. Nutr. 43, 265–285.

Raspor, P., and J. Zupan. 2006. Yeasts in extreme environments. In: G. Peter and C.A. Rosa (Eds), Biodiversity and Ecophysiology of Yeasts. Springer, Berlin, pp. 371–417.

Rath, P.M. 2004. First isolation of *Sporopachydermia cereana* in humans. 14th European Congress of Clinical

Microbiology and Infectious Diseases, Prague, Czech Republic, May 1–4, 2004. Abstract number 902, p. 1773.
Rathbone, D.A., and N.C. Bruce. 2002. Microbial transformation of alkaloids. Curr. Opin. Microbiol. 5, 274–281.
Ratledge, C. 2002. Regulation of lipid accumulation in oleaginous microorganisms. Biochem. Soc. Trans. 30, 1047–1050.
Rattray, J.B.M. 1988. Yeasts. In: C. Ratledge and S.G. Wilkinson (Eds), Microbial Lipids, Vol. 1. Academic Press, London, pp. 555–697.
Rau, U., L.A. Nguyen, H. Roeper and S. Lang. 2005a. Fed-batch bioreactor production of mannosylerythritol lipids secreted by *Pseudozyma aphidis*. Appl. Microbiol. Biotechnol. 68, 607–613.
Rau, U., L.A. Nguyen, S. Schulz, V. Wray, M. Nimtz, H. Roeper, H. Koch and S. Lang. 2005b. Formation and analysis of mannosylerythritol lipids secreted by *Pseudozyma aphidis*. Appl. Microbiol. Biotechnol. 66, 551–559.
Ravelhofer, K., R. Rotheneder, M. Gareis, R. Suttner, O. Wolf, R. Matiello and J. Kösters. 1998. Megabakteriosen bei verscheidenen Vogelspezies. DVG Tag. Vogelkr. 9, 95–104.
Ravelhofer-Rotheneder, K., H. Engelhardt, O. Wolf, R. Amann, W. Breuer and J. Kösters. 2000. Taxonomic classification of "megabacteria" isolates originating from budgerigars (*Melopsittacus undulatus*). Tierärztl. Prax. 28, 415–420.
Ravella, S.R., S.A. James, C.J. Bond, I.N. Roberts, K. Cross, A. Retter and P.J. Hobbs. 2010. *Cryptococcus shivajii* sp. nov.: a novel basidiomycetous yeast isolated from biogas reactor. Curr. Microbiol. 60, 12–16.
Rawsthorne, H., and T.G. Phister. 2006. A real-time PCR assay for the enumeration and detection of *Zygosaccharomyces bailii* from wine and fruit juices. Int. J. Food Microbiol. 112, 1–7.
Ray, W.W. 1939. Contributions to knowledge of the genus *Taphrina* in North America. Mycologia 31, 56–75.
Raymond, C.K., T. Bukowski, S.D. Holderman, A.F. Ching, E. Vanaja and M.R. Stamm. 1998. Development of the methylotrophic yeast *Pichia methanolica* for the expression of the 65 kilodalton isoform of human glutamate decarboxylase. Yeast 14, 11–23.
Rayner, R.W. 1970. A Mycological Colour Chart. Commonwealth Mycological Institute, Kew, Surrey, and British Mycological Society.
Razanskiene, A.J., A. Schmidt, A. Geldmacher, M. Ritzi, Å. Niedrig, D.H. Lundkvist, H. Krüger, K. Meisel Sasnauskas and R. Ulrich. 2004. High yields of stable and highly pure nucleocapsid proteins of different hantaviruses can be generated in the yeast *Saccharomyces cerevisiae*. J. Biotechnol. 111, 319–333.
Re, S. 1925. Observations on the cultural and biochemical characters of *Monilia castellanii* (*Cryptococcus castellani*) and *Monilia macroglossiae* (*Cryptococcus macroglossiae*). J. Trop. Med. Hyg. 28, 317–319.
Rebholz, S.L., and M.T. Cushion. 2001. Three new karyotype forms of *Pneumocystis carinii* f. sp. *carinii* identified by contoured clamped homogeneous electrical field (CHEF) electrophoresis. J. Eukaryot. Microbiol. (Suppl.), 109S–110S.
Recca, J., and E.M. Mrak. 1952. Yeasts occurring in citrus products. Food Technol. 6, 450–454.
Redaelli, P. 1925. I miceti come associazione microbica nelle tubercolosi polmonare cavitaria. Osservazioni micopatologiche, istopatologiche e sperimentali. Mem. Prem. R. Ist. Lombardo Sci. Lett., Pavia, pp. 1–99.
Redaelli, P. 1931. Il problema della Torulopsidaceae e dei loro rapporti con l'uomo e con la patologia umana studiato particolarmente in Italia. (Blastomiceti e blastomicosi.) Riv. Biol. 13, 171–235.
Redaelli, P., and R. Ciferri. 1941. Nuovi reperti di *Trichosporon* ed osservazioni interno a questo genere. Mycopathologia 3, 203–224.
Redaelli, P., and R. Ciferri. 1947. Un quadriennio di attivita del Centro di Micologia Umana e comparata di Pavia. Mycopathologia 4, 25–47.
Redaelli, P., R. Ciferri and A. Giordano. 1937. *Debaryomyces neoformans* (Sanfelice) *nobis* n. comb. pour les espèces du groupe *Saccharomyces hominis–Cryptococcus neoformans–Torula histolytica*. Boll. Sez. Ital. Soc. Int. Microbiol. 9, 24–28.
Redaelli, P., R. Ciferri and C. Cavallero. 1938. Sul presento *Endomyces albicans* Vuillemin. Mycopathologia 2, 116–121.
Reddy, M.S., and C.L. Kramer. 1975. A taxonomic revision of the Protomycetales. Mycotaxon 3, 1–50.
Redhead, S.A. 1977. The genus *Neolecta* (Neolectaceae fam. nov., Lecanolales, Ascomycetes) in Canada. Can. J. Bot. 55, 301–306.
Redhead, S.A., and D. Malloch. 1977. The Endomycetaceae: new concepts, new taxa. Can. J. Bot. 55, 1701–1711.
Redhead, S.A., M.T. Cushion, J.K. Frenkel and J.R. Stringer. 2006. *Pneumocystis* and *Trypanosoma cruzi*: nomenclature and typifications. J. Eukaryot. Microbiol. 53, 2–11.
Redmond, J.D., J.J. Marois and J.D. MacDonald. 1987. Biological control of *Botrytis cinerea* on roses with epiphytic microorganisms. Plant Dis. 71, 799–802.
Redzepovic, S., S. Orlic, S. Sikora, A. Majdak and I.S. Pretorius. 2002. Identification and characterization of *Saccharomyces cerevisiae* and *Saccharomyces paradoxus* strains isolated from Croatian vineyards. Lett. Appl. Microbiol. 35, 305–310.
Reeb, V., F. Lutzoni and C. Roux. 2004. Contribution of RPB2 to multilocus phylogenetic studies of the Pezizomycotina (Euascomycetes, Fungi) with special emphasis on the lichen-forming Acarosporaceae and evolution of polyspory. Mol. Phylogenet. Evol. 32, 1036–1060.
Reeleder, R.D. 2004. The use of yeasts for biological control of the plant pathogen *Sclerotinia sclerotiorum*. BioControl 49, 583–594.
Reese, A.J., and T.L. Doering. 2003. Cell wall α-1,3-glucan is required to anchor the *Cryptococcus neoformans* capsule. Mol. Microbiol. 50, 1401–1409.
Reess, M. 1877. Über den Soorpilz. Sitzungsber. Phys. Med. Soc. Erlangen 9, 190–195.
Rehm, H.-J., and G. Reed (Eds). 1996. Biotechnology. A Multi-Volume Comprehensive Treatise. 2nd, completely revised edn. VCH, New York.
Reichert, A.S., and W. Neupert. 2004. Mitochondriomics or what makes us breathe. Trends Genet. 20, 555–562.
Reid, D.A. 1970. New or interesting records of British Hymenomycetes, IV. Trans. Br. Mycol. Soc. 55, 413–441.
Reid, I.D. 1974. Properties of conjugation hormones (erogens) from the basidiomycete *Tremella mesenterica*. Can. J. Bot. 52, 521–524.
Reiersöl, S. 1955. Species of *Rhodotorula* isolated from laryngeal swabs. Antonie van Leeuwenhoek 21, 286–289.
Reiersöl, S. 1958. *Torulopsis norvegica* nov. sp. Antonie van Leeuwenhoek 24, 111–112.
Reiersöl, S., and M. di Menna. 1958. A new *Cryptococcus* species. Antonie van Leeuwenhoek 24, 27–30.

Reiss, E. 1854. J.F. Klotzsch, Herbarium vivum mycologicum, No. 1885.

Reiss, F. 1935. Eine neue pathogene Hefe des Genus *Mycotorula*. Zentralbl. Bakteriol. Parasitenkd. Infekt. Abt. 1, 134, 189–191.

Remak, R. 1845. Diagnostische und pathogenetische Untersuchungen. A. Hirschwald, Berlin.

Renker, C., J. Alphei and F. Buscot. 2003. Soil nematodes associated with the mammal pathogenic fungal genus *Malassezia* (Basidiomycota: Ustilaginomycetes) in Central European forests. Biol. Fertil. Soils 37, 70–72.

Renker, C., V. Blanke, B. Börstler, J. Heinrichs and F. Buscot. 2004. Diversity of *Cryptococcus* and *Dioszegia* yeasts (Basidiomycota) inhabiting arbuscular mycorrhizal roots or spores. FEMS Yeast Res. 4, 597–603.

Rennerfelt, E. 1937. Undersökningar över svampinfektionen i slipmassa occii des utveckling däri. Sven. Skogsvardsfoerb. Tidskr. 47, 159.

Renouf, V., and A. Lonvaud-Funel. 2007. Development of an enrichment medium to detect *Dekkera*/*Brettanomyces bruxellensis*, a spoilage wine yeast, on the surface of grape berries. Microbiol. Res. 162, 154–167.

Renter, C.W.M., M.A. Morgan, F.C. Barge, F. Gunzer, M. Eder, B. Hertenstein and A. Ganser. 2005. *Candida kefyr* as an emerging pathogen causing nosocomial bloodstream infections in neutropenic leukemia patients. Clin. Infect. Dis. 41, 1365–1366.

Reuter, M., G. Bell and D. Greig. 2007. Increased outbreeding in yeast in response to dispersal by an insect vector. Curr. Biol. 17, R81–R83.

Rezaei, K., F. Temelli and E. Jenab. 2007. Effect of pressure and temperature on enzymatic reactions in supercritical fluids. Biotechnol. Adv. 25, 272–280.

Rezende, R.P., J.C.T. Dias, C.A. Rosa, F. Carazza and V.R. Linardi. 1999. Utilization of nitriles by yeasts isolated from a Brazilian gold mine. J. Gen. Appl. Microbiol. 45, 185–192.

Rezusta, A., C. Aspiroz, T. Boekhout, J. Cano, B. Theelen, J. Guarro and M.C. Rubio. 2008. Cholesterol-dependent and amphotericin B-resistant *Candida glabrata* from an ICU patient. Med. Mycol. 46, 265–268.

Rhee, S.-K., J.-H. Bae, E.-S. Choi, J.-H. Sohn, H.-A. Kang and C.-S Park. 2003. Plasmid for gene expression in *Pichia ciferrii* and transformation method using the same. US Patent 6,638,735.

Rhode, O.H.J. 2006. Intraspecies diversity of *Cryptococcus laurentii* (Kufferath) C.E. Skinner and *Cryptococcus podzolicus* (Bab'eva & Reshetova) originating from a single soil sample. MSc Thesis, Stellenbosch University, South Africa.

Rhodes, J.C., and K.J. Kwon-Chung. 1985. Production and regeneration of protoplasts from *Cryptococcus*. Sabouraudia 23, 81–83.

Rhodes, J.C., K.J. Kwon-Chung and T.J. Popkin. 1981. Ultrastructure of the septal complex in hyphae of *Cryptococcus laurentii*. J. Bacteriol. 145, 1410–1412.

Rhodes, J.C., I. Polacheck and K.J. Kwon-Chung. 1982. Phenoloxidase activity and virulence in isogenic strains of *Cryptococcus neoformans*. Infect. Immun. 36, 1175–1184.

Ribeiro, E. 1995. Genomic comparisons of strains of selected species of *Candida* and *Pichia*. MSc Thesis, Georgia State University, Atlanta, GA.

Ribéreau-Gayon, P. 2006. Handbook of Enology, 2nd edn. Wiley, Chichester.

Ricca, E., V. Calabro, S. Curcio and G. Iorio. 2007. The state of the art in the production of fructose from inulin enzymatic hydrolysis. Crit. Rev. Biotechnol. 27, 129–145.

Richardson, J.D., S.F. Queener, M. Bartlett and J. Smith. 1989. Binary fission of *Pneumocystis carinii* trophozoites grown *in vitro*. J. Protozool. 36, 27S–29S.

Richet, H.M., M.M. McNeil, M.C. Edwards and W.R. Jarvis. 1989. Cluster of *Malassezia furfur* pulmonary infections in a neonatal intensive care unit. J. Clin. Microbiol. 27, 1197–1200.

Ricklefs, R.E. 1987. Community diversity: relative roles of local and regional processes. Science 235, 167–171.

Rigby, S., G.W. Procop, G. Haase, D. Wilson, G. Hall, C. Kurtzman, K. Oliveira, S. Von Oy, J.J. Hyldig-Nielsen, J. Coull and H. Stender. 2002. Fluorescence *in situ* hybridization with peptide nucleic acid probes for rapid identification of *Candida albicans* directly from blood culture bottles. J. Clin. Microbiol. 40, 2182–2186.

Rimek, D., G. Haase, A. Lück, J. Casper and A. Podbielski. 2004. First report of a case of meningitis caused by *Cryptococcus adeliensis* in a patient with acute myeloid leukemia. J. Clin. Microbiol. 42, 481–483.

Rippon, J.W. 1988. Medical Mycology: The Pathogenic Fungi and the Pathogenic Actinomycetes, 3rd edn. Saunders, Philadelphia, PA.

Riquelme, A.J., M.A. Calvo, A.M. Guzmán, M.S. Depix, P. Gacía, C. Pérez, M. Arrese and J.A. Labaraca. 2003. *Saccharomyces cerevisiae* fungemia after *Saccharomyces boulardii* treatment in immunocompromised patients. J. Clin. Gastroenterol. 36, 41–43.

Rischin, M. 1921. Über einen Fall von bisher noch nicht beschreibener *Parendomyces*-Erkrankung, die unter dem Bilde der tiefen (Sycosis parasitaria) und oberflächlichen Trichophytie verlief. Arch. Dermatol. Syph. 134, 232–242.

Ritterband, D.C., J.A. Seedor, M.K. Shah, S. Waheed and I.A. Schorr. 1998. A unique case of *Cryptococcus laurentii* keratitis spread by a rapid gas permeable contact lens in a patient with onychomycosis. Cornea 17, 115–118.

Ro, D.K., and C.J. Douglas. 2004. Reconstitution of the entry point of plant phenylpropanoid metabolism in yeast (*Saccharomyces cerevisiae*) – implications of metabolic flux into the phenylpropanoid pathway. J. Biol. Chem. 279, 2600–2607.

Ro, D.K., E.M. Paradise, M. Ouellet, K.J. Fisher, K.L. Newman, J. M. Ndungu, K.A. Ho, R.A. Eachus, T.S. Ham, J. Kirby, M.C. Chang, S.T. Withers, Y. Shiba, R. Sarpong and J.D. Keasling. 2006. Production of the antimalarial drug precursor artemisinic acid in engineered yeast. Nature 440, 940–943.

Robbertse, B., J.B. Reeves, C.L. Schoch and J.W. Spatafora. 2006. A phylogenomic analysis of the Ascomycota. Fungal Genet. Biol. 43, 715–725.

Robbins, W.J., and R. Ma. 1944. A *Rhodotorula* deficient for para-amino-benzoic acid. Science 100, 85–86.

Roberson, R.W., and E.S. Luttrell. 1987b. Dolipores in *Tilletia*. Mycologia 81, 650–652.

Robert, V. 2003. Data processing. In: T. Boekhout and V. Robert (Eds), Yeasts in Food: Beneficial and Detrimental Aspects. Behrs Verlag, Hamburg, pp. 139–169.

Robert, V. 2007. Data integration and multi-factorial analyses, the yeasts and the BioloMICS software as a case study. In: N. MacLeod (Ed.), Automated Object Identification in Systematics: Theory, Approaches, and Applications. Taylor & Francis, London, pp. 277–288.

Robert, V., P. Evrard and G.L. Hennebert. 1997. BCCM/Allev 2.00, an automated system for the identification of yeasts. Mycotaxon 64, 455–463.

Robert, V., B. Bonjean, M. Karutz, H. Paschold, W. Peeters and M.G. Wubbolts. 2001. *Candida bituminiphila*, a novel anamorphic species of yeast. Int. J. Syst. Evol. Microbiol. 51, 2171–2176.

Roberts, C. 1960. On the occurrence of yeasts in the mountainous soils of the Jotunheimen, Norway. Compt. Rend. Trav. Lab. Carlsberg 32, 75–87.

Roberts, C., and J.P. van der Walt. 1958. The life cycle of *Kluyveromyces polysporus*. C.R. Lab. Carlsberg 31, 129–148.

Roberts, G.D., C.D. Horstmeier, G.A. Land and J.H. Foxworth. 1978. Rapid urea broth test for yeasts. J. Clin. Microbiol. 7, 584–588.

Roberts, P. 1995. British *Tremella* species 1: *Tremella aurantia* and *T. mesenterica*. Mycologist 9, 110–114.

Roberts, P. 1996. Heterobasidiomycetes from Majorca & Cabrera (Balearic Islands). Mycotaxon 60, 111–123.

Roberts, P. 1997. New heterobasidiomycetes from Great Britain. Mycotaxon 63, 195–216.

Roberts, P. 2001. British *Tremella* species III: *Tremella caulunicola* sp. nov., *T. invasa, T. sarnensis* sp. nov., *T. simplex* and *T. versicolor*. Mycologist 15, 146–150.

Roberts, P. 1998a. British *Tremella* spp. II. *Tremella encephala, T. steidleri* and *T. foliacea*. Mycologist 13, 127–131.

Roberts, P. 1998b. New British Records 164. *Cystobasidium fimetarium* (Shum.) P. Roberts comb. nov. Mycologist 13, 171–172.

Roberts, P.J., and A.A.R. de Meijer. 1997. Macromycetes from the state of Paraná, Brazil. 6, Sirobasidiaceae & Tremellaceae. Mycotaxon 64, 261–283.

Roberts, P.J., and B.M. Spooner. 1998. Heterobasidiomycetes from Darussalam. Kew Bull. 53, 631–650.

Roberts, P., S. Moshitch-Moshkovitz, E. Kvam, E. O'Toole, M. Winey and D.S. Goldfarb. 2003. Piecemeal microautophagy of nucleus in *Saccharomyces cerevisiae*. Mol. Biol. Cell 14, 129–141.

Roberts, R.G. 1990a. Postharvest biological control of gray mold of apples by *Cryptococcus laurentii*. Phytopathology 80, 526–530.

Roberts, R.G. 1990b. Biological control of Mucor rot of pear by *Cryptococcus laurentii*. Phytopathology 80, 10–51.

Roberts, S.M. 2001. Preparative biotransformations. J. Chem. Soc. Perkin Trans. 1, 1475–1499.

Robertson, L.A. 2003. The Delft School of Microbiology, the nineteenth to the twenty-first century. Adv. Appl. Microbiol. 52, 357–388.

Robin, C. 1853. Histoire naturelle des végétaux parasites qui croissent sur l'homme et sur les animaux vivants. Baillière, Paris.

Robinow, C.F. 1961. Mitosis in the yeast *Lipomyces lipofer*. J. Biophys. Biochem. Cytol. 9, 879–892.

Robinow, C.F., and A. Bakerspigel. 1965. Somatic nuclei and forms of mitosis in fungi. In: G.C. Ainsworth and A.S. Sussman (Eds), The Fungi, An Advanced Treatise, Vol. 1. The Fungal Cell. Academic Press, New York, pp. 119–142.

Röder, C., H. König and J. Frölich. 2007. Species-specific identification of *Brettanomyces*/*Dekkera* yeasts by fluorescently labeled DNA probes targeting the 26S rRNA. FEMS Yeast Res. 7, 1013–1026.

Rodriges, F., G. Goncalves, S. Pereira-da-Silva, M. Malfeito-Ferreira and V. Loureiro. 2001. Development and use of a new medium to detect yeasts of the genera *Brettanomyces/Dekkera*. J. Appl. Microbiol. 90, 588–599.

Rodrigues, C., D. Yarrow and I. Spencer-Martins. 1996. Nuclear DNA comparisons among strains of *Pichia membranifaciens*. Abstr. 9th Int. Symp. on Yeasts, Sydney, Australia, p. 31.

Rodrigues, F., M. Corte-Real, C. Leao, J.P. van Dijken and J.T. Pronk. 2001. Oxygen requirements of the food spoilage yeast *Zygosaccharomyces bailii* in synthetic and complex media. Appl. Environ. Microbiol. 67, 2123–2128.

Rodrigues, F., P. Ludovico and C. Leao. 2006. Sugar metabolism in yeasts: an overview of aerobic and anaerobic glucose catabolism. In: C.A. Rosa and G. Peters (Eds), Biodiversity and Ecophysiology of Yeasts. Springer-Verlag, Berlin, pp. 101–122.

Rodrigues, M.G., and Á. Fonseca. 2003. Molecular systematics of the dimorphic ascomycete genus *Taphrina*. Int. J. Syst. Evol. Microbiol. 53, 607–616.

Rodrigues, R.C., L. Sene, G.S. Matos, I.C. Roberto, A. Pessoa Jr. and M.G. Felipe. 2006. Enhanced xylitol production by precultivation of *Candida guilliermondii* cells in sugarcane bagasse hemicellulosic hydrolysate. Curr. Microbiol. 53, 53–59.

Rodrigues de Miranda, L. 1972. *Filobasidium capsuligenum* nov. comb. Antonie van Leeuwenhoek 38, 91–99.

Rodrigues de Miranda, L. 1975. Two new species of the genus *Sterigmatomyces*. Antonie van Leeuwenhoek 45, 193–199.

Rodrigues de Miranda, L. 1978. A new genus: *Sporopachydermia*. Antonie van Leeuwenhoek 44, 439–450.

Rodrigues de Miranda, L. 1979. *Clavispora*, a new yeast genus of the Saccharomycetales. Antonie van Leeuwenhoek 45, 479–483.

Rodrigues de Miranda, L. 1984a. *Sporopachydermia* Rodrigues de Miranda. In: N.J.W. Kreger-van Rij (Ed.), The Yeasts, A Taxonomic Study, 3rd edn. Elsevier, Amsterdam, pp. 427–430.

Rodrigues de Miranda, L. 1984b. *Cryptococcus* Kützing emend. Phaff et Spencer. In: N.J.W. Kreger-van Rij (Ed.), The Yeasts, A Taxonomic Study, 3rd edn. Elsevier, Amsterdam, pp. 845–872.

Rodrigues de Miranda, L. 1984c. *Bullera* Derx. In: N.J.W. Kreger-van Rij (Ed.), The Yeasts, A Taxonomic Study, 3rd edn. Elsevier, Amsterdam, pp. 577–584.

Rodrigues de Miranda, L., and W. Batenburg-van der Vegte. 1981. *Cryptococcus mollis* Kützing, type species of the genus *Cryptococcus*. Antonie van Leeuwenhoek 47, 65–72.

Rodrigues de Miranda, L., and H.G. Diem. 1974. Deux nouvelles espèces de levures isolées de la phyllosphère de l'Orge. Can. J. Bot. 52, 279–282.

Rodrigues de Miranda, L., and B. Norkrans. 1968. *Candida suecica* sp. n. isolated from marine environment. Antonie van Leeuwenhoek 34, 115–118.

Rodrigues de Miranda, L., and T. Török. 1976. *Pichia humboldtii* sp. nov., the perfect state of *Candida ingens*. Antonie van Leeuwenhoek 42, 343–348.

Rodriguez, M.E., C. Lopes, S. Valles, M.R. Giraudo and A. Caballero. 2007. Selection and preliminary characterization of betaglycosidases producer Patagonian wild yeasts. Enzyme Microb. Technol. 41, 812–820.

Rodríguez-Peña, J.M., V.J. Cid, J. Arroyo and C. Nombela. 2000. A novel family of cell wall-related proteins regulated differently during the yeast life cycle. Mol. Cell Biol. 20, 3245–3255.

Rodriguez-Tudela, J.L., T.M. Diaz-Guerra, E. Mellado, V. Cano, C. Tapia, A. Perkins, A. Gomez-Lopez, L. Rodero and M. Cuenca-Estrella. 2005. Susceptibility patterns and molecular identification of *Trichosporon* species. Antimicrob. Agents Chemother. 49, 4026–4034.

Roehr, M. (Volume Ed.). 1996. Products of primary metabolism, Vol. 6. In: H.-J. Rehm, and G. Reed (Eds), Biotechnology. 2nd revised edn. VCH-Wiley, Weinheim.

Roeijmans, H.J., G.W. van Eijk and D. Yarrow. 1989. Some name changes necessitated by redefinition of the genus *Candida*. Mycotaxon 35, 405–406.

Roesler, U., H. Scholz and A. Hensel. 2003. Emended phenotypic characterization of *Prototheca zopfii*: a proposal for three biotypes and standards for their identification. Int. J. Syst. Evol. Microbiol. 53, 1195–1199.

Roesler, U., A. Möller, A. Hensel, D. Baumann and U. Truyen. 2006. Diversity within the current algal species *Prototheca zopfii*: a proposal for two *Prototheca zopfii* genotypes and description of a novel species, *Prototheca blaschkeae* sp. nov. Int. J. Syst. Evol. Microbiol. 56, 1419–1425.

Rogers, D.P. 1947. A new gymnocarpous Heterobasidiomycete with gasteromycetous basidia. Mycologia 39, 556–563.

Rogowska-Szadkowska, D., A. Wiercinska-Drapalo, A. Borzuchowska and D. Prokopowicz. 1997. *Candida humicola* infection of the central nervous system in an HIV-infected patient: a case report. Przegl. Epidemiol. 51, 465–469. In Polish.

Rojas, V., J.V. Gil, F. Pinaga and P. Manzanares. 2001. Studies on acetate ester production by non-*Saccharomyces* wine yeasts. Int. J. Food Microbiol. 70, 283–289.

Rokas, A., and S.B. Carroll. 2005. More genes or more taxa? The relative contribution of gene number and taxon number to phylogenetic accuracy. Mol. Biol. Evol. 22, 1337–1344.

Rokas, A., B.L. Williams, N. King and S.B. Carroll. 2003. Genome-scale approaches to resolving incongruence in molecular phylogenies. Nature 425, 798–804.

Rokas, A., D. Kruger and S.B. Carroll. 2005. Animal evolution and the molecular signature of radiations compressed in time. Science 310, 1933–1938.

Rokem, J.S., A.E. Lantz and J. Nielsen. 2007. Systems biology on antibiotic production by microorganisms. Nat. Prod. Rep. 24, 1262–1287.

Rolle, M., and B. Mehnert. 1957. Symbiotic yeasts in mammals. Zentralbl. Bakteriol. Parasitenkd. I. Orig. 168, 268–277.

Roller, S., and N. Corvill. 1999. The antifungal properties of chitosan in laboratory media and apple juice. Int. J. Food Microbiol. 47, 67–77.

Romano, P., and G. Suzzi. 1996. Origin and production of acetoin during wine yeast fermentation. Appl. Environ. Microbiol. 62, 309–315.

Romano, P., A. Ricciardi, G. Salzano and G. Suzzi. 2001. Yeasts from water buffalo mozzarella, a traditional cheese of the Mediterranean area. Int. J. Food Microbiol. 69, 45–51.

Romano, P., G. Suzzi, R. Zironi and G. Comi. 1993. Biometric study of acetoin production in *Hanseniaspora guilliermondii* and *Kloeckera apiculata*. Appl. Environ. Microbiol. 59, 1838–1841.

Romano, P., G. Suzzi, G. Comi, R. Zironi and M. Maifreni. 1997a. Glycerol and other fermentation products of apiculate wine yeasts. J. Appl. Microbiol. 82, 615–618.

Romano, P., G. Suzzi, P. Domizio and F. Fatichenti. 1997b. Secondary products formation as a tool for discriminating non-*Saccharomyces* wine strains. Strain diversity in non-*Saccharomyces* wine yeasts. Antonie van Leeuwenhoek 71, 239–242.

Romano, P., V. Brandolini, C. Ansaloni and E. Menziani. 1998. The production of 2,3-butanediol as a differentiating character in wine yeasts. World J. Microbiol. Biotechnol. 14, 649–653.

Romano, P., C. Fiore, M. Paraggio, M. Caruso and A. Capece. 2003. Function of yeast species and strains in wine flavor. Int. J. Food Microbiol. 86, 169–180.

Romano, P., A. Capece and L. Jespersen. 2006. Taxonomic and ecological diversity of food and beverage yeasts. In: A. Querol and G.H. Fleet (Eds), Yeasts in Food and Beverages. Springer-Verlag, Berlin, pp. 13–53.

Romanos, M.A., C.A. Scorer and J.J. Clare. 1992. Foreign gene expression in yeast: a review. Yeast 8, 423–488.

Romer, M., E. Hammer, M.C. Cazau and A.M. Arambarri. 2002. Isolation and characterization of biarylic structure-degrading yeasts: hydroxylation potential of dibenzofuran. Environ. Pollut. 118, 379–382.

Romero, M., L. Calvo, C. Alba, M. Habulin, M. Primozic and Z. Knez. 2005. Enzymatic synthesis of isoamyl acetate with immobilized *Candida antarctica* lipase in supercritical carbon dioxide. J. Supercrit. Fluid. 33, 77–84.

Romero, M.C., E. Hammer, M.C. Cazau and A.M. Arambarri. 2001. Selection of autochthonous yeast strains able to degrade biphenyl. World J. Microbiol. Biotechnol. 17, 591–594.

Romero, P., B. Patiño, M. Quirós, M.-T. González-Jaén, M.-J. Valderrama, M.-I. de Silóniz and J.M. Peinado. 2005. Differential detection of *Debaryomyces hansenii* isolated from intermediate-moisture foods by PCR-RFLP of the IGS region of rDNA. FEMS Yeast Res. 5, 455–461.

Römisch, K., N. Collie, N. Soto, J. Logue, M. Lindsay, W. Scheper and C.-H.C. Cheng. 2003. Protein translocation across the endoplasmic reticulum membrane in cold-adapted organisms. J. Cell Sci. 116, 2875–2883.

Rooney, L., and P.B. Moens. 1973a. Nuclear divisions at meiosis in the ascomycetous yeast *Wickerhamia fluorescens*. Can. J. Microbiol. 19, 1383–1387.

Rooney, L., and P.B. Moens. 1973b. The fine structure of ascospore delimitation in the yeast *Wickerhamia fluorescens*. Can. J. Microbiol. 19, 1389–1392.

Roostita, R., and G.H. Fleet. 1996a. Growth of yeasts in milk and associated changes to milk composition. Int. J. Food Microbiol. 31, 205–219.

Roostita, R., and G.H. Fleet. 1996b. The occurrence and growth of yeasts in Camembert and blue-veined cheeses. Int. J. Food Microbiol. 28, 393–404.

Roostita, R., and G.H. Fleet. 1999. Growth of yeasts isolated from cheeses on organic acids in the presence of sodium chloride. Food Technol. Biotechnol. 37, 73–79.

Rosa, C.A., and M.A. Lachance. 1998. The yeast genus *Starmerella* gen. nov. and *Starmerella bombicola* sp. nov., the teleomorph of *Candida bombicola* (Spencer, Gorin & Tulloch) Meyer & Yarrow. Int. J. Syst. Bacteriol. 48, 1413–1417.

Rosa, C.A., and M.A. Lachance. 2005. *Zygosaccharomyces machadoi* sp. n., a yeast species isolated from a nest of the stingless bee *Tetragonisca angustula* Lundiana. Int. J. Biodivers. 6 (Suppl.), 27–29.

Rosa, C., and G. Péter. 2006. Biodiversity and Ecophysiology of Yeasts. Springer, Berlin.

Rosa, C.A., A.N. Hagler, L.C.S. Mendonça-Hagler, P.B. Morais, N.C.M. Gomes and R.F. Moneiro. 1992. *Clavispora opuntiae* and other yeasts associated with the moth *Sigelgaita* sp, in the cactus *Pilosocereus arrabidae* of Rio de Janeiro, Brasil. Antonie van Leeuwenhoek 62, 267–272.

Rosa, C.A., S. Jindamorakot, S. Limtong, T. Nakase, M.A. Lachance, A. Fidalgo-Jiménez, H.M. Daniel, F.C. Pagnocca, J. Inacio and P.B. Morais. 2009. Synonymy of the yeast genera Moniliella and Trichosporonoides and proposal of Moniliella fonsecae sp. nov. and five new species combinations. Int. J. Syst. Evol. Microbiol. 59, 425–429.

Rosa, C.A., P.B. Morais, A.N. Hagler, L.C. Mendonça-Hagler and R.F. Monteiro. 1994. Yeast communities of the cactus *Pilosocereus arrabidae* and associated insects in the sandy coastal plains of southeastern Brazil. Antonie van Leeuwenhoek. 65, 55–62.

Rosa, C.A., P.B. Morais, S.R. Santos, P.R. Peres Neto, L.C. Mendonça-Hagler and A.N. Hagler. 1995. Yeast communities associated with different plant resources in sandy coastal plains of southeastern Brazil. Mycol. Res. 99, 1047–1054.

Rosa, C.A., M.A. Lachance, W.T. Starmer, J.F. Barker, J.M. Bowles and B. Schlag-Edler. 1999. *Kodamaea nitidulidarum*, *Candida restingae*, and *Kodamaea anthophila*, three new related yeast species from ephemeral flowers. Int. J. Syst. Bacteriol. 49, 309–318.

Rosa, C.A., M.A. Lachance, J. Silva, A. Teixeira, M.M. Marini, Y. Antonini and R.P. Martins. 2003. Yeast communities associated with stingless bees. FEMS Yeast Res. 4, 271–275.

Rosa, C.A., M.A. Lachance, L.C.R.S. Teixeira, R.S. Pimenta and P.B. Morais. 2007a. *Metschnikowia cerradonensis* sp. nov., a yeast species isolated from ephemeral flowers and their nitidulid beetles in Brazil. Int. J. Syst. Evol. Microbiol. 57, 161–165.

Rosa, C.A., F.C. Pagnocca, M.A. Lachance, C.C.C. Ruivo, A.O. Medeiros, M.R.C. Pimentel, J.C.R. Fontenelle and R.P. Martins. 2007b. *Candida flosculorum* and *Candida floris*, two novel yeast species associated with tropical flowers. Int. J. Syst. Evol. Microbiol. 57, 2970–2974.

Rosa, C.A., S. Jindamorakot, S. Limtong, T. Nakase, M.A. Lachance, A. Fidalgo-Jiménez, H.M. Daniel, F.C. Pagnocca, J. Inácio and P.B. Morais. 2009. Synonymy of the yeast genera *Moniliella* and *Trichosporon*ides and proposal of *Moniliella fonsecae* sp. nov. and five new species combinations. Int. J. Syst. Evol. Microbiol. 59, 425–429.

Rosa, E.A.R., C.V. Pereira, R.T. Rosa and J.F. Hofling. 2000. Grouping oral *Candida* species by multilocus enzyme electrophoresis. Int. J. Syst. Evol. Microbiol. 50, 1343–1349.

Rosa, C.A., S. Jindamorakot, S. Limtong, T. Nakase, F.C. Pagnocca and M.A. Lachance. 2010. *Candida golubevii* sp. nov., an asexual yeast related to *Metschnikowia lunata*. Int. J. Syst. Evol. Microbiol. 60, 704–706.

Rosales, C.M., M.A. Jackson and D. Zwick. 2004. *Malassezia furfur* meningitis associated with total parenteral nutrition subdural effusion. Pediatr. Dev. Pathol. 7, 86–90.

Rosario, I., M. Hermoso de Mendoza, S. Déniz, G. Soro, I. Álamo and B. Acosta. 2005. Isolation of *Cryptococcus* species including *C. neoformans* from cloaca of pigeons. Mycoses 48, 421–424.

Rosche, B., M. Breuer, B. Hauer and P. Rogers. 2005. Cells of *Candida utilis* for in vitro (R)phenylacetylcarbinol production in an aqueous/octanol two-phase reactor. Biotechnol. Lett. 27, 575–581.

Rose, A.H., and J.S. Harrison. 1987. The Yeasts, 2nd edn. Academic Press, London.

Rose, A.H., and J.S. Harrison. 1993. The Yeasts, Yeast Technology, Vol. 5. Academic Press, London.

Rosell, C.M., and M. Gomez. 2007. Frozen dough and partially baked bread: an update. Food Rev. Int. 23, 303–319.

Roselli, G., C. Cantini and P. Mariotti. 1997. Susceptibility to peach leaf curl (*Taphrina deformans* (Berk.) Tul.) in a peach germplasm collection. J. Hort. Sci. 72, 863–872.

Rosenberg, M., H. Mikovà and L. Krištofikovà. 1999. Formation of L-malic acid by yeasts of the genus *Dipodascus*. Lett. Appl. Microbiol. 29, 221–223.

Rosi, I., M. Vinella and P. Domizio. 1994. Characterization of betaglucosidase activity in yeasts of enological origin. J. Appl. Bacteriol. 77, 519–527.

Rosing, W.C. 1987. Ultrastructure of septa, asci, and ascospores of *Eremothecium ashbyi*. Mycologia 79, 857–865.

Rosini, G. 1984. Assessment of dominance of added yeast in wine fermentation and origin of *Saccharomyces cerevisiae* in wine-making. J. Gen. Appl. Microbiol. 30, 249–256.

Rosini, G., F. Federici and A. Martini. 1982a. Yeast flora of grape berries during ripening. Microbiol. Ecol. 8, 83–89.

Rosini, G., F. Federici, A.E. Vaughan and A. Martini. 1982b. Systematics of species of the yeast genus *Saccharomyces* associated with the fermentation industry. Eur. J. Appl. Microbiol. Biotechnol. 15, 188–193.

Rossi, G. 2000a. Histological and immunohistochemical findings in proventricular mucosa of chickens experimentally infected with “megabacterium”. Proc. 18th Meeting Eur. Soc. Vet. Pathol., p. 156.

Rossi, G. 2000b. Possibility of infecting mammals with megabacteria from birds. Vet. Rec. 146, 444.

Rossignol, T., L. Dulau, A. Julien and B. Blondin. 2003. Genome-wide monitoring of wine yeast gene expression during alcoholic fermentation. Yeast 20, 1369–1385.

Rost, K., and H. Venner. 1964. Untersuchungen an Nucleinsäuren. X. Isolierung und Untersuchung von Deoxyribonucleinsäure aus Hefe. Z. Physiol. Chem. 339, 230–237.

Rostrup, E. 1883. Fortsatte undersogelser over snyltesvampes angreb paa skovtraene. Tiddskrift for Skovbrug 6, 199–300. In Danish.

Rostrup, E. 1885. Om nogle af Snyltesvampe foraarsagede misdannelser hos blomsterplanter. Bot. Tidsskr. 14, 230–243. In Danish.

Roth, A., J. Wecke, V. Karsten and K. Janitschke. 1997. Light and electron microscopy study of carbohydrate antigens found in the electron-lucent layer of *Pneumocystis carinii* cysts. Parasitol. Res. 83, 177–184.

Rout, M.P., and J.D. Aitchison. 2001. The nuclear pore complex as a transport machine. J. Biol. Chem. 276, 6593–6596.

Rout, M.P., J.D. Aitchison, A. Suprapto, K. Hjertaas, Y. Zhao and B.T. Chait. 2000. The yeast nuclear pore complex: composition, architecture, and transport mechanism. J. Cell Biol. 148, 635–651.

Routien, J.B. 1949. *Crebrothecium ashbyi*. Mycologia 41, 183–185.

Roy, A., B.N. Manjula and C.P.J. Glaudemans. 1981. The interaction of two polysaccharides containing β-1,6-linked galactopyranosyl residues with two monoclonal antigalactan immunoglobulin Fab′ fragments. Mol. Immunol. 18, 79–84.

Roy, B., and S.A. Meyer. 1998. Confirmation of the distinct genotype groups within the form species *Candida parapsilosis*. J. Clin. Microbiol. 36, 216–218.

Royse, D.J., and B. May. 1982. Use of isozyme variation to identify genotypic classes of *Agaricus brunnescens*. Mycologia 74, 93–102.

Rozpędowska, E., J. Piškur and K.H. Wolfe. 2010. Yeast genome sequences: resources and applications in phylogenomics. In: Kurtzman, C.P., J.W. Fell and T. Boekhout (Eds), The Yeasts, A Taxonomic Study. 5th edn, pp. 145–157.

Rozzell, J.D. 1999. Commercial scale biocatalysis: myths and realities. Biorg. Med. Chem. 7, 2253–2261.

Rubio-Texeira, M. 2006. Endless versatility in the biotechnological applications of *Kluyveromyces* LAC genes. Biotechnol. Adv. 24, 210–223.

Ruderfer, D.M., S.C. Pratt, H.S. Seidel and L. Kruglyak. 2006. Population genomic analysis of outcrossing and recombination in yeast. Nat. Genet. 38, 1077–1081.

Ruinen, J. 1963. The phyllosphere. II. Yeasts from the phyllosphere of tropical foliage. Antonie van Leeuwenhoek 29, 425–438.

Ruivo, C.C.C., M.A. Lachance, M. Bacci Jr., S.C. Carreiro, C.A. Rosa and F.C. Pagnocca. 2004. *Candida leandrae* sp. nov., an asexual ascomycetous yeast species isolated from tropical plants. Int. J. Syst. Evol. Microbiol. 54, 2405–2408.

Ruivo, C.C.C., M.A. Lachance, C.A. Rosa, M. Bacci and F.C. Pagnocca. 2005. *Candida bromeliacearum* sp. nov. and *Candida ubatubensis* sp. nov., two yeast species isolated from the water tank of *Canistropsis seidelii* (Bromeliaceae). Int. J. Syst. Evol. Microbiol. 55, 2213–2217.

Ruivo, C.C.C., M.-A. Lachance, C.A. Rosa, M. Bacci Jr. and F.C. Pagnocca. 2006. *Candida heliconiae* sp. nov., *Candida picinguabensis* sp. nov. and *Candida saopauloensis* sp. nov., three ascomycetous yeasts from *Heliconia velloziana* (Heliconiaceae). Int. J. Syst. Evol. Microbiol. 56, 1147–1151.

Ruiz, M. 1938. Contribucion al conocimiento de las levaduras del aguamiel y del pulque. I. *Saccharomyces carbajali*. Ann. Inst. Biol. (México) 9, 49–80.

Ruiz-Herrera, J., C.G. Leon, A. Carabez-Trejo and E. Reyes-Salinas. 1996. Structure and chemical composition of the cell walls from the haploid yeast and mycelial forms of *Ustilago maydis*. Fungal Genet. Biol. 20, 133–142.

Running, J.A., D.K. Severson and K.J. Schneider. 2002. Extracellular production of L-ascorbic acid by *Chlorella protothecoides*, *Prototheca* species, and mutants of *P. moriformis* during aerobic culturing at low pH. J. Ind. Microbiol. Biotechnol. 29, 93–98.

Running, J.A., R.P. Burlingame and A. Berry. 2003. The pathway of L-ascorbic acid biosynthesis in the colourless microalga *Prototheca moriformis*. J. Exp. Bot. 54, 1841–1849.

Ruokola, A.-L., and A. Salonen. 1970. A new fungus, *Aureomyces mirabilis* gen. et sp. nov., from pine-timber. Mycopathol. Mycol. Appl. 42, 273–276.

Rupcić, J., and V. Marić. 2004. Cerebrosides of *Candida lipolytica* yeast. Appl. Microbiol. Biotechnol. 64, 416–420.

Russo, G., D. Libkind, R.J. Ulloa, V. de García, J.P. Sampaio and M.R. van Broock. 2010. *Cryptococcus agrionensis* sp. nov., a basidiomycetous yeast of the acidic rock drainage ecoclade, isolated from acidic aquatic environment of volcanic origin (River Agrio, Argentina). Int. J. Syst. Evol. Microbiol. 60, 996–1000.

Rybářová, J., F. Štros and A. Kocková-Kratochvílová. 1980. *Candida ethanolica* n. sp. Z. Allg. Mikrobiol. 20, 579–581.

Rybářová, J., F. Štros and A. Kocková-Kratochvílová. 1981. *Torulopsis ethanolitolerans* n. sp. and *T. ethanolitolerans* var. *minor* n. var. Z. Allg. Mikrobiol. 21, 739–742.

Saëz, H. 1960. *Debaryomyces coudertii*, nouvelle espèce de levure isolée chez un manchot royal (*Aptenodytes patagonica* Miller). Bull. Mens. Soc. Linn. Lyon 29, 288–289.

Saadatzadeh, M.R., H.R. Ashbee, K.T. Holland and E. Ingham. 2001. Production of the mycelial phase of *Malassezia* in vitro. Med. Mycol. 39, 487–493.

Sabouraud, R. 1904. Maladies du Cuir Chevelu. II. Les Maladies Desquamatives. Masson & Cie, Paris.

Saccardo, P.A. 1895. Sylloge Fungorum, Vol. 2, pars III. Patavii, p. 457.

Saccardo, P.A. 1886. Sylloge Fungorum, Vol. 4. Patavii, p. 16.

Saccardo, P.A. 1889. Sylloge Fungorum 8, 816.

Saccardo, P.A. 1889. Sylloge Fungorum, Vol. 8. Patavii, p. 1042.

Saccardo, P.A. 1892. Sylloge Fungorum 10, 67.

Saccardo, P.A. 1892. Sylloge Fungorum, Vol. 10, Typis Seminarii. Patavii.

Saccardo, P.A. 1906. Sylloge Fungorum, Vol. 18, pars VII. Patavii.

Saccardo, P.A., and D. Saccardo. 1906. Sylloge Fungorum, Vol. 18. Patavii.

Saccardo, P.A., and P. Sydow. 1902. Sylloge Fungorum, Vol. 16, pars V. Patavii.

Saccardo, P.A., and J.B. Traverso. 1910. Sylloge Fungorum, Vol. 19. Patavii, p. 871.

Saccardo, P.A., and A. Trotter. 1911. Sylloge Fungorum, Vol. 22. Patavii.

Sacchetti, M. 1932a. Contributo alla conoscenza della flora microbica di alcuni formaggi italiani. Arch. Mikrobiol. 3, 650–662.

Sacchetti, M. 1932b. Interno ad alcuni *Zygosaccharomyces*. Rend. R. Accad. Naz. Lincei 15, 762–765.

Sacchetti, M. 1932c. I lieviti della fermentazione del miele italiano. Mem. R. Accad. Sci. Ist. Bologna, Ser. VIII 9, 2–11.

Sacchetti, M. 1932d. Ricerche sulla fermentazione di un mosto d'uva concentrato. Arch. Mikrobiol. 3, 473–491.

Sacchetti, M. 1933. Contributo alla conoscenza della flora microbica di alcuni formaggi italiani. Arch. Mikrobiol. 4, 427–446.

Sadebeck, R. 1890. Kritische Untersuchungen uber die durch *Taphrina*-arten hervorgebrachten Baumkrankheiten. Jahrb. d. Hamburg. Wiessensch. Anst. 8, 61–95.

Sadebeck, R. 1895. Einige neue Beobachtungen und kritische Bemerkungen uber die Exoasceen. Bericht. d. Deutsch. Bot. Ges. 13, 265–280.

Sadowsky, M.J., W.C. Koskinen, M. Bischoff, B.L. Barber, J.M. Becker and R.F. Turco. 2009. Rapid and complete degradation of the herbicide picloram by *Lipomyces kononenkoae*. J. Agric. Food Chem. 57, 4878–4882.

Saeki, A. 1990. Studies on acetic acid fermentation, 3: Continuous production of vinegar with immobilized *Saccharomycodes ludwigii* cell and immobilized *Acetobacter aceti* cells entrapped in calcium alginate gel beads. J. Jpn. Soc. Food Sci. Technol. 37, 722–725.

Saëz, H. 1964. *Geotrichum vanriji* nouvelle espèce de champignon arthrosporé isolé chez une sarcelle d'été (*Anas querquedula* L.). Bull. Mens. Soc. Linn. Lyon 33, 263–267.

Saëz, H. 1965. *Candida krusei* (Castellani) Berkhout var. *transitoria*, nouvelle varïeté de levure isolée chez divers mammifères et oiseaux. Bull. Mens. Soc. Linn. Lyon 34, 265–270.

Saëz, H. 1967. *Rhodotorula vuilleminii* n. sp., isolée chez un ibis rouge: *Guara rubra* (L.). Bull. Soc. Mycol. Fr. 83, 953–958.

Saëz, H. 1968a. Étude de quatre champignons arthrospores, formant des endospores. Microbiol. Esp. 21, 193–204.

Saëz, H. 1968b. *Geotrichum pseudocandidum* n. sp., isolé chez un cerf d'eld – *Rucervus eldi* (Guthrie). Mycopathol. Mycol. Appl. 34, 359–363.

Saëz, H. 1973a. *Candida nouvelii*, nouvelle espèce de levure rencontrée chez deux mammifères sauvages morts en captivité. Bull. Trimest. Soc. Mycol. Fr. 89, 79–82.

Saëz, H. 1973b. *Cryptococcus hungaricus* var. *gallicus*, nouvelle variete de levure rencontree chez deux cerfs *Axis-Axis axis* (Erxleben). Bull. Mens. Soc. Linn. Lyon 42, 216–220.

Saëz, H. 1977. *Trichosporon lutetiae*, nouvelle espèce de levure isolée chez un cerf d'eld de Thaïlande. Bull. Mens. Soc. Linn. Lyon 46, 365–367.

Saëz, H., and T.L. Nguyen. 1989. *Leucosporidium lari-marini*, nouvelle especе de levure isolee chez un oiseau aquatique. Cryptog. Mycol. 10, 81–85.

Saëz, H., and J. Rinjard. 1973. *Trichosporon capitatum*, un constituent de la flore fongique du tube digestif de certains Suidés. Ann. Med. Vet. 117, 177–182.

Saëz, H., and L. Rodrigues de Miranda. 1984. The yeast *Candida sequanensis* sp. nov. Antonie van Leeuwenhoek 50, 379–381.

Saëz, H., and L. Rodrigues de Miranda. 1988. Deux nouvelles espèces de levure, d'origine animale, isolées au Parc Zoologique de Paris: *Cryptococcus feraegula* et *Candida nanaspora*. Bull. Soc. Mycol. Fr. 104, 213–215.

Safran, E., and Y. Levy. 1995. Tentative development of a prediction model for peach leaf curl. Agronomie 15, 49–57.

Saggese, V. 1934. Contributo allo studio delle microsi. Un caso clinico di infezione da *Mycotorula* (*Monilia*) *pinoyi* (Cast.) e relative richerche sperimentali. Riv. Clin. Pediatr. 32, 941–971.

Saha, P., and G.S. Bothast. 1999. Production of xylitol by *Candida peltata*. J. Ind. Microbiol. Biotechnol. 22, 633–636.

Saha, B.C. 2003. Hemicellulose bioconversion. J. Ind. Microbiol. Biotechnol. 30, 279–291.

Saha, B.C., and R.J. Bothast. 1996. Production, purification, and characterization of a highly glucose-tolerant novel beta-glucosidase from *Candida peltata*. Appl. Environ. Microbiol. 62, 3165–3170.

Saito, K. 1907. Mikrobiologische Studien über die Zubereitung des Batatenbranntweines auf der Insel Hachijo (Japan). Zentralbl. Bakteriol. Parasitenkd., Abt. II, 18, 30–37.

Saito, K. 1909. Preliminary notes on the spore formation of the so-called "Soya-kahmhefe". Bot. Mag. Tokyo 23, 96. In Japanese.

Saito, K. 1910. Notizen über einige koreanische Gärungsorganismen. Zentralbl. Bakteriol. Parasitenkd., Abt. II 26, 369–374.

Saito, K. 1914. Mikrobiologische Studien über die Bereitung des mandschurischen Branntweins. Rep. Centr. Lab. S. Manchurian Railway Co. 1, 1–60. (Rev. in: Bull. Inst. Pasteur, 13, 1, 1915; Zentralbl. Bakteriol. Parasitenkd., Abt. II, 55, 323, 1922).

Saito, K. 1922. Untersuchungen über die atmosphärischen Pilzkeime. Mitt. Jpn. J. Bot. 1, 1–54.

Saito, K. 1923. Beschreibung von zwei neuen Hefearten, nebst Bemerkungen über die Sporenbildung bei *Torulaspora delbrücki* Lindner. Bot. Mag. Tokyo 37, 63–66.

Saito, K. 1932. Über die in dem in Gärung begriffenen Saft vom Cocoanuss befindlichen Pilze. J. Brew. Sci. 10, 11–15. In Japanese.

Saito, K., and M. Oda. 1932. Studien über die Saccharomyceten in Saké-Moto. I, III. J. Brew. Sci. 10, 787–802. In Japanese.

Saito, K., and M. Oda. 1934. Investigation of the yeasts in sake-moto. III. J. Brew. Sci. 12, 159–174. In Japanese.

Saito, K., and Y. Ohtani. 1931. On some fermentative yeasts isolated from sap exuded from bark of a tree. Jozogaku Zasshi 9, 6–11. In Japanese.

Saito, S., N. Ishida, T. Onishi, K. Tokuhiro, E. Nagamori, K. Kitamoto and Takahshi. 2004. Genetically engineered wine yeast produces a high concentration of L-lactic acid of extremely high purity. Appl. Environ. Microbiol. 64, 3831–3837.

Saitou, N., and M. Nei. 1987. The neighbor-joining method: a new method for reconstructing phylogenetic trees. Mol. Biol. Evol. 4, 406–425.

Sakagami, Y., A. Isogai, A. Suzuki, S. Tamura, E. Tsuchiya and S. Fukui. 1978a. Isolation of a novel sex hormone, Tremerogen A-10, controlling conjugation tube formation in *Tremella mesenterica* Fries. Agric. Biol. Chem. 42, 1093–1094.

Sakagami, Y., A. Isogai, A. Suzuki, S. Tamura, E. Tsuchiya and S. Fukui. 1978b. Amino acid sequence of Tremerogen A-10, a peptidal hormone inducing conjugation tube formation in *Tremella mesenterica* Fries. Agric. Biol. Chem. 42, 1301–1302.

Sakagami, Y., A. Isogai, A. Suzuki, S. Tamura, C. Kitada and M. Fujino. 1979. Structure of Tremerogen A-10, a peptidal hormone inducing conjugation tube formation in *Tremella mesenterica*. Agric. Biol. Chem. 43, 2643–2645.

Sakai, H., and G.A. Caldo. 1985. Microbiological studies on Bubod, a fermentation starter in the Philippines III. A new yeast species, *Endomycopsis bubodii* Sakai and Caldo sp. nov., and some enzymological properties of *Endomycopsis* strains. Philipp. Agric. 68, 181–188.

Sakai, T., and M. Okushima. 1982. Purification and crystallization of a protopectin-solubilizing enzyme from *Trichosporon penicillatum*. Agric. Biol. Chem. 46, 667–676.

Sakai, T., M. Sawada, T. Katsuragi and K. Tonomura. 1989. Possible role of cell wall mannan in the secretion of the pectin-solubilizing enzyme of *Trichosporon penicillatum* SNO-3. Agric. Biol. Chem. 53, 9–18.

Sakai, Y., M. Oku, I.J. van der Klei and J.A. Kiel. 2006. Pexophagy: autophagic degradation of peroxisomes. Biochim. Biophys. Acta 1763, 1767–1775.

Sakamoto, Y., R. Kano, Y. Nakamura, S. Watanabe, H. Kamata, Y. Fukuda and A. Hasegawa. 2001. First isolation of *Trichosporon domesticum* from a cat. Mycoses 44, 518–520.

Salas, S.D., J.E. Bennett, K.J. Kwon-Chung, J.R. Perfect and P.R. Williamson. 1996. Effect of the laccase gene, CNLACI, on virulence of *Cryptococcus neoformans*. J. Exp. Med. 184, 377–386.

Saligkarias, I.D., F.T. Gravanis and H.A.S. Epton. 2002a. Biological control of *Botrytis cinerea* on tomato plants by the use of epiphytic yeasts *Candida guilliermondii* strains 101 and US 7 and *Candida oleophila* strain I-182: I. In vivo studies. Biol. Control 25, 143–150.

Saligkarias, I.D., F.T. Gravanis and H.A.S. Epton. 2002b. Biological control of *Botrytis cinerea* on tomato plants by the use of epiphytic yeasts *Candida guilliermondii* strains 101 and US 7 and *Candida oleophila* strain I-182: II. A study on mode of action. Biol. Control 25, 151–161.

Salkin, I.F., and M.A. Gordon. 1977. Polymorphism of *Malassezia furfur*. Can. J. Microbiol. 23, 471–475.

Salvat, P., and M. Fontoynont. 1922. Contribution à l'étude des mycoses malgaches. Abcès sous-dermiques dus à l'*Endomyces molardi* (n. sp.). Bull. Soc. Pathol. Exotique 15, 311–320.

Saluja, P., and G.S. Prasad. 2007a. *Debaryomyces singareniensis* sp. nov., a novel yeast species isolated from a coal mine soil in India. FEMS Yeast Res. 7, 482–488.

Saluja, P., and G.S. Prasad. 2007b. *Cryptococcus rajasthanensis* sp. nov., an anamorphic yeast species related to *Cryptococcus laurentii*, isolated from Rajasthan, India. Int. J. Syst. Evol. Microbiol. 57, 414–418.

Saluja, P., and G.S. Prasad. 2008. *Candida ruelliae* sp. nov., a novel yeast species isolated from flowers of *Ruellia* sp. (Acanthaceae). FEMS Yeast Res. 8, 660–666.

Samelis, J., and J.N. Sofos. 2003. Yeasts in meat and meat products. In: T. Boekhout and V. Robert (Eds), Yeasts in Food: Beneficial and Detrimental Aspects. Behrs Verlag, Hamburg, pp. 239–265.

Samonis, G., M. Anatoliotaki, H. Apostolakou, S. Maraki, D. Mavroudis and V. Georgoulias. 2001. Transient fungaemia due to *Rhodotorula rubra* in a cancer patient: case report and review of literature. Infection 29, 173–176.

Sampaio, J.P. 1994. Utilization of low molecular weight lignin-related aromatic compounds for the selective isolation of yeasts: *Rhodotorula vanillica*, a new basidiomycetous yeast species. Syst. Appl. Microbiol. 17, 613–619.

Sampaio, J.P. 1999. Utilization of low molecular weight aromatic compounds by heterobasidomycetous yeasts: taxonomic implications. Can. J. Microbiol. 45, 491–512.

Sampaio, J.P. 2004. Diversity, phylogeny and classification of basidiomycetous yeasts. In: R. Agerer, M. Piepenbring and P. Blanz (Eds), Frontiers in Basidiomycote Mycology. IHW-Verlag, Eching, pp. 49–80.

Sampaio, J.P., and A. Fonseca. 1995. Physiological aspects in the systematics of heterobasidiomycetous yeasts. Stud. Mycol. 38, 29–46.

Sampaio, J.P., and P. Gonçalves. 2008. Natural populations of *Saccharomyces kudriavzevii* in Portugal are associated with oak bark and are sympatric with S. *cerevisiae* and S. *paradoxus*. Appl. Environ. Microbiol. 74, 2144–2152.

Sampaio, J.P., and N. van Uden. 1991. *Rhodotorula ferulica* sp. nov., a yeast that degrades ferulic acid and other phenolic compounds. Syst. Appl. Microbiol. 14, 146–149.

Sampaio, J.P., R. Bauer, D. Begerow and F. Oberwinkler. 1999a. *Occultifur externus* sp. nov., a new species of simple-pored auricularioid heterobasidiomycetes from plant litter in Portugal. Mycologia 91, 1094–1101.

Sampaio, J.P., J.W. Fell, M. Gadanho and R. Bauer. 1999b. *Kurtzmanomyces insolitus* sp. nov., an anamorphic heterobasidiomycetous yeast species. Syst. Appl. Microbiol. 22, 619–625.

Sampaio, J.P., M. Gadanho and R. Bauer. 2001a. Taxonomic studies on the genus *Cystofilobasidium*: description of *Cystofilobasidium ferigula* sp. nov., and clarification of the status of *Cystofilobasidium lari-marini*. Int. J. Syst. Evol. Microbiol. 51, 221–229.

Sampaio, J.P., M. Gadanho, S. Santos, F. Duarte, C. Pais, A. Fonseca and J.W. Fell. 2001b. Polyphasic taxonomy of the genus *Rhodosporidium*: *R. kratochvilovae* and related anamorphic species. Int. J. Syst. Evol. Microbiol. 51, 687–697.

Sampaio, J.P., M. Weiβ, M. Gadanho and R. Bauer. 2002. New taxa in the Tremellales: *Bulleribasidium oberjochense* gen. et sp. nov., *Papiliotrema bandonii* gen. et sp. nov. and *Fibulobasidium murrhardtense* sp. nov. Mycologia 94, 873–887.

Sampaio, J.P., M. Gadanho, R. Bauer and M. Weiβ. 2003. Taxonomic studies in the Microbotryomycetidae: *Leucosporidium golubevii* sp. nov., *Leucosporidiella* gen. nov. and the new orders Leucosporidiales and Sporidiobolales. Mycol. Prog. 2, 53–68.

Sampaio, J.P., J. Inacio, A. Fonseca, M. Gadanho, I. Spencer-Martins, G. Scorzetti and J.W. Fell. 2004a. *Auriculibuller fuscus* gen. nov., sp. nov. and *Bullera japonica* sp. nov., novel taxa in the Tremellales. Int. J. Syst. Evol. Microbiol. 54, 987–993.

Sampaio, J.P., W.I. Golubev, J.W. Fell, M. Gadanho and N.W. Golubev. 2004b. *Curvibasidium cygneicollum* gen. nov., sp. nov. and *Curvibasidium pallidicorallinum* sp. nov., novel taxa in the Microbotryomycetidae (Urediniomycetes), and their relationship with *Rhodotorula fujisanensis* and *Rhodotorula nothofag*i. Int. J. Syst. Evol. Microbiol. 54, 1401–1407.

Sampedro, I., E. Aranda, J.M. Scervino, S. Fracchia, I. Garcia-Romera, J.A. Ocampo and A. Godeas. 2004. Improvement by soil yeasts of arbuscular mycorrhizal symbiosis of soybean (*Glycine max*) colonized by *Glomus mosseae*. Mycorrhiza 14, 229–234.

Samson, R.A., J.A. Stalpers and A.C.M. Weijman. 1983. On the taxonomy of the entomogenous fungus

Filobasidiella arachnophila. Antonie van Leeuwenhoek 49, 447–456.
Samson, R.A., E.S. Hoekstra, J.C. Frisvad and O. Filtenborg. 2000. Introduction to Food and Airborne Fungi. Centraalbureau voor Schimmelcultures, Utrecht, 389pp.
Samsonova, I.A., G. Kunze, R. Bode and F. Böttcher. 1996. A set of genetic markers for the chromosomes of the imperfect yeast *Arxula adeninivorans*. Yeast 12, 1209–1217.
San-Blas, G., and R.A. Calderone. 2004. Pathogenic Fungi: Host Interactions and Emerging Strategies for Control. Caister, Norfolk.
San-Blas, G., G. Nino-Vega and T. Iturriaga. 2002. *Paracoccidioides brasiliensis* and paracoccidioidomycosis: molecular approaches to morphogenesis, diagnosis, epidemiology, taxonomy and genetics. Med. Mycol. 40, 225–242.
San-Blas, F., G. San-Blas and L.J. Cova. 1976. A morphological mutant of *Paracoccidioides brasiliensis* strain IVIC Pb9. Isolation and wall characterization. J. Gen. Microbiol. 93, 209–218.
San Millán, R.M., L.C. Wu, I.F. Salkin and P.F. Lehmann. 1997. Clinical isolates of *Candida guilliermondii* include *Candida fermentati*. Int. J. Syst. Bacteriol. 47, 385–393.
Sancak, B., J.H. Rex, V. Paetznick, E. Chen and J. Rodriguez. 2003. Evaluation of a method for identification of *Candida dubliniensis* bloodstream isolates. J. Clin. Microbiol. 41, 489–491.
Sanche, S.E., D.A. Sutton and M.R. Rinaldi. 2003. Dematiaceous fungi. In: E.J. Anaissie, M.R. McGinnis and M.A. Pfaller (Eds), Clinical Mycology. Churchill Livingstone, Philadelphia, PA, pp. 325–351.
Sánches-Torres, P., L. González-Candelas and D. Ramón. 1998. Heterologous expression of a *Candida molischiana* anthocyanin-β-glucosidase in a wine yeast strain. J. Agric. Food. Chem. 46, 354–360.
Sancholle, M., and A. Schneider. 1979. Composition en lipides et acides gras de deux especes de *Taphrina* parasites de *Prunus domestica*. Biochem. Syst. Ecol. 7, 257–261.
Sand, F.E.M.J. 1973. Recent investigations on the microbiology of fruit juice concentrates. Proc. Int. Fruit Juice Union, Vienna, pp. 185–216.
Sandhu, R.S., and H.S. Randhawa. 1962. On the reisolation and taxonomic study of *Candida viswanathii* Viswanathan et Randhawa 1959. Mycopathol. Mycol. Appl. 18, 179–183.
Sandhya, C., and A. Pandey. 2006. Inulinases. In: A. Pandey, C. Webb, C.R. Soccol and C. Larroche (Eds), Enzyme Technology. Springer-Asiatech, New Delhi, pp. 347–358.
Sandmann, G., and N. Misawa. 2002. Fungal carotenoids. In: K. Esser and J.W. Bennett (Eds), The Mycota, Vol. X. Industrial Applications. Springer, Berlin, pp. 247–262.
Sandula, J., G. Krogar, M. Kacurakova and E. Machova. 1999. Microbial (1-3)-β-D-glucans, their preparation, physicochemical characterization and immunomodulatory activity. Carbohydr. Polym. 38, 247–258.
Sanfelice, F. 1894. Contributo alla morphologia e biologia dei blastomiceti che si sviluppano nei succhi di alcuni frutti. Ann. Ist. Ig. R. Univ. Roma 4, 463–469.
Sanfelice, F. 1895a. Sull'azione patogene dei blastomiceti. Ann. Ist. Ig. R. Univ. Roma 5, 239–262.
Sanfelice, F. 1895b. Über einen neuen pathogenen Blastomyceten, welcher innerhalb der Gewebe unter Bildung kalkartig aussehender Massen degeneriert. Zentralbl. Bakteriol. Parasitenkd., Abt. I, 18, 521–526.
Sang, J.H. 1956. The quantitative nutritional requirements of *Drosophila melanogaster*. J. Exp. Biol. 33, 45–72.
Sang, J.H. 1978. The nutritional requirements of *Drosophila*. In: M. Ashburner and T.R.F. Wright (Eds), The Genetics and Biology of *Drosophila*, Vol 2. Academic Press, New York, pp. 159–192.
Sangorrin, M., I. Zajonskovsky, M. van Broock and A. Caballero. 2002. The use of killer biotyping in an ecological survey of yeast in an old Patagonian winery. World J. Microbiol. Biotechnol. 18, 115–120.
Sansone, G., I. Rezz, V. Calvente, D. Benuzzi and M.I. Sanz de Tosetti. 2005. Control of *Botrytis cinerea* strains resistant to iprodione in apple with rhodotorulic acid and yeasts. Postharvest Biol. Technol. 35, 245–251.
Santa María, J. 1956a. *Hansenula matritensis* nov. spec. An. Inst. Nac. Invest. Agron. 5, 151–162.
Santa María, J. 1956b. *Saccharomyces fragilis* Jörgensen var. *bulgaricus* nov. var. An. Inst. Nac. Invest. Agron. 5, 163–165.
Santa María, J. 1956c. *Pichia membranaefaciens* Hansen var. *sicereum* nov. var. An. Inst. Nac. Invest. Agron. 5, 167–170.
Santa María, J. 1957. Un nuevo género de levaduras: *Citeromyces*. Inst. Nac. Invest. Agron., Seccion Bioquimica, Cuaderno no. 258, 269–276.
Santa María, J. 1958a. Ecología de las levaduras. I. Nuevas especies aisladas de alpechin. Bol. Inst. Nac. Invest. Agron. 38, 301–313.
Santa María, J. 1958b. *Sporobolomyces marcillae* nov. spec., isolated from the air. Arch. Mikrobiol. 32, 29–31.
Santa María, J. 1959a. Oxidación de alcohol etilico a acido acetico por levaduras vivas. I. *Saccharomyces aceti* nov. spec. y *Saccharomyces oxidans* nov. spec., nuevas especies aisladas de vino. An. Inst. Nac. Invest. Agron. 8, 715–735.
Santa María, J. 1959b. Ecología de las levaduras. II. Levaduras del asucar, de la ciche condensada y de la remolache. An. Inst. Nac. Invest. Agron. 8, 779–796.
Santa María, J. 1959c. *Candida atmosphaerica*, nov. spec., aislada del aire. An. Inst. Nac. Invest. Agron. 8, 799–802.
Santa María, J. 1960. Taxonomy of yeasts. Nature 185, 781–782.
Santa María, J. 1962. *Saccharomyces hienipiensis*, a new melibiose-fermenting yeast, unable to assimilate raffinose. J. Gen. Microbiol. 28, 375–378.
Santa María, J. 1963a. New melibiose-utilizing yeasts isolated from "alpechin". Antonie van Leeuwenhoek 29, 329–343.
Santa María, J. 1963b. Sobre la validez del género "*Torulaspora*" (Lindner) en las levaduras ascosporigenas. Bol. Inst. Nac. Invest. Agron. 49, 257–266.
Santa María, J. 1964. *Saccharomyces onubensis*, nov. spec., aislada de mosto de uva, y su relación con *Sacch. capensis* (synom. *Sacch. oviformis*). Bol. Inst. Nac. Invest. Agron. 51, 527–536.
Santa María, J. 1966. Characteristics delimiting the genus *Pichia* Hansen. Antonie van Leeuwenhoek 32, 197–201.
Santa María, J. 1968. *Saccharomyces hispanica* nov. spec. Nueva especie de levadura de "Flor". Bol. Inst. Nac. Invest. Agron. 58, 21–32.
Santa María, J. 1970. *Saccharomyces gaditensis* y *Saccharomyces cordubensis*, dos nuevas especies de levaduras de "flor". Bol. Inst. Nac. Invest. Agron. 62, 57–66.
Santa María, J. 1971. *Candida ergatensis* nov. spec. An. Inst. Nac. Invest. Agron. 1, 85–88.
Santa María, J. 1978. Biotaxonomic studies on yeast. Common. Inst. Nac. Invest. Agron., Serie General 3, 1–61.

Santa María, J., and C. García Aser. 1970. *Pichia castillae*, nov. spec., aislada de insectos. Bol. Inst. Nac. Invest. Agron. 62, 51–55.

Santa María, J., and C. García Aser. 1971. *Debaryomyces yarrowii* nov. spec. An. Inst. Nac. Invest. Agron., Serie General 1, 89–92.

Santa María, J., and C. García Aser. 1977. *Pichia segobiensis*, sp. nov. An. Inst. Nac. Invest. Agron., Serie General 5, 45–50.

Santa María, J., and C. Sanchez. 1970. Significacion taxonomica de las propriedades fisiologicas de las especies incluidas en el genero *Kluyveromyces*. Bol. Inst. Nac. Invest. Agron. 62, 23–36.

Santos, A., and D. Marquina. 2004. Killer toxin of *Pichia membranifaciens* and its possible use as a biocontrol agent against gray mold disease of grapevine. Microbiology 150, 2527–2534.

Santos, A., D. Marquina, J.A. Leal and J.M. Peinado. 2000. (1→6)-beta-D-glucan as cell wall receptor for *Pichia membranifaciens* killer toxin. Appl. Environ. Microbiol. 66, 1809–1813.

Sanwal, K. 1960. *Panagrellus dubius* n. sp. (Nematode: Turbatricinae Goodey, 1943.), from frass of beetle *Sternochetus lapathi* (L.), with remarks on redescriptions of *Anguillula rediviva* (L., 1767). Can. J. Zool. 38, 1041–1046.

Sapardo, D.R., S. Vola, S. Pianoand and M.L. Gullino. 2002. Mechanism of action and efficacy of tour isolates of the yeast *Metschnikowia pulcherrima* active against postharvest pathogens on apple. Postharvest Biol. Technol. 24, 123–134.

Sariasiani, F.S. 2007. Development of a combined biological and chemical process for production of industrial aromatics from renewable resources. Annu. Rev. Microbiol. 61, 51–69.

Sartory, A. 1923. Champignons parasites de l'homme et des animaux. In: National Union Catalog Pre-1956. Imprints, Vol. 521, p. 247.

Sartory, A., G. Petges and H. Claque. 1923. Laryngite chronique pseudo-tuberculeuse d'origine mycosique due à une levure nouvelle, *Cryptococcus laryngitidis* n. sp. C. R. Seances Mem. Soc. Biol. 84, 179–180.

Sartory, A., R. Sartory, G. Hufschmitt and J. Meyer. 1930. Etude d'un *Cryptococcus* nouveau (*Cryptococcus corallinus*) isolé de lésions rappelant les lésions trichophytiques. C. R. Soc. Biol. 104, 1316–1319.

Sartory, A., R. Sartory and J. Meyer. 1931. Etude botanique d'une nouvelle levure rose (*Cryptococcus radiatus* n. sp.). C. R. Soc. Biol. 106, 597–600.

Sartory, A., R. Sartory, J. Weill and J. Meyer. 1932a. Un cas de blastomycose invéterèe transmissible au cobaye, due aun *Saccharomyces* pathogene (*Saccharomyces jadini* n. sp.). C. R. Acad. Sci. 194, 1688–1690.

Sartory, A., R. Sartory, F. Sternon and J. Meyer. 1932b. Une dermatomycose causée par une levure nouvelle du genre *Saccharomyces*: "*Saccharomyces sternoni*" n. sp. Bull. Acad. Méd. 107, 120–121.

Sartory, R., G. Hufschmitt and J. Meyer. 1930. Une mycose nouvelle provoquée par une levure du genre *Debaryomyces*: *Debaryomyces mucosus* n. sp. C.R. Hebd. Séances Acad. Sci. 191, 281–283.

Sarukhanyan, F.G. 1957. New species and strains of sporogenous and asporogenous yeasts. Izv. Akad. Nauk Armyanskoi SSR. Ser. Biol. Sel'skokhozyaistvennye Nauki 10, 61–67.

Sasakawa, M. 1922. Zur Systematik pathogener und parasitischer Hefen. Morphologisch-biochemische Studie. Zentralbl. Bakteriol. Parasitenkd., Abt. I, Orig. 88, 269–285.

Sasaki, T., M. Kawamura and H. Ishikawa. 1996. Nitrogen recycling in the brown planthopper, *Nilaparvata lugens*: involvement of yeast-like endosymbionts in uric acid metabolism. J. Insect Physiol. 42, 125–129.

Sasaki, Y., and T. Yoshida. 1958. *Hansenula misumaiensis* Sasaki et Yoshida. Abstr. Hokkaido Branch Mtg., Agric. Chem. Soc. Jpn.

Sasaki, Y., and T. Yoshida. 1959. A taxonomic reconsideration of lactose fermenting yeast preserving in Japan. Mem. Fac. Agric. Hokkaido Univ. 3, 178–184.

Sasaki, Y., and T. Yoshida. 1966. Microbiological studies of soya mashes in Hokkaido. (I) A taxonomic study and distribution of yeasts. J. Ferment. Technol. 44, 61–71.

Sato, I., H. Kobayashi, Y. Hanya, K. Abe, S. Murakami, G. Scorzetti and J.W. Fell. 1999. *Cryptococcus nodaensis* sp. nov., a yeast isolated from soil in Japan that produces salt-tolerant and thermostable glutaminase. J. Ind. Biotechnol. 22, 127–132.

Satoh, K., K. Makimura, Y. Hasumi, Y. Nishiyama, K. Uchida and H. Yamaguchi. 2009. *Candida auris* sp. nov., a novel ascomycetous yeast isolated from the external ear canal of an inpatient in a Japanese hospital. Microbiol. Immunol. 53, 41–44.

Satoh, K., K. Ooe, H. Nagayama and K. Makimura. 2010. *Prototheca cutis* sp. nov., a newly discovered pathogen of protothecosis isolated from inflamed human skin. Int. J. Syst. Evol. Microbiol. 60, 1236–1240.

Sauer, M., D. Porro, D. Mattanovich and P. Branduardi. 2008. Microbial production of organic acids: expanding the markets. Trends Biotechnol. 26, 100–108.

Sauerwein, H., S. Schmitz and S. Hiss. 2007. Effect of a dietary application of a yeast cell wall extract on innate and acquired immunity, on oxidative status and growth performance in weanling piglets and on ileal epithelium in fattened pigs. J. Anim. Physiol. Anim. Nutr. 91, 369–380.

Sawada, K. 1922. Descriptive Catalogue of the Formosan Fungi 3, 53.

Sawada, K. 1929. Fungi from Taiwan (No. 27). Trans. Nat. Hist. Soc. Formosa 19, 31–39.

Sawada, K. 1931. Reports on Formosan fungi. Part 5. Rep. Central Res. Inst. Formosan Gov. 51, 11–12.

Scanlan, C.M., and D.L. Graham. 1990. Characterization of a Gram-positive bacterium from the proventriculus of budgerigars (*Melopsittacus undulatus*). Avian Dis. 34, 779–786.

Scannell, D.R., and K.H. Wolfe. 2008. A burst of protein sequence evolution and a prolonged period of asymmetric evolution follow gene duplication in yeast. Genome Res. 18, 137–147.

Scannell, D.R., K.P. Byrne, J.L. Gordon, S. Wong and K.H. Wolfe. 2006. Multiple rounds of speciation associated with reciprocal gene loss in polyploid yeasts. Nature 440, 341–345.

Scannell, D.R., A.C. Frank, G.C. Conant, K.P. Byrne, M. Woolfit and K.H. Wolfe. 2007. Independent sorting-out of thousands of duplicated gene pairs in two yeast species descended from a whole-genome duplication. Proc. Natl. Acad. Sci. USA 104, 8397–8402.

Scaramella, P. 1928. Richerche preliminari su una nuova forma di "*Mycotorula*" a pigmento rosa-rosso. Nuovo G. Bot. Ital. Ser. 5, 35, 546–554.

Scarr, M.P., and D. Rose. 1966. Study of osmophilic yeasts producing invertase. J. Gen. Microbiol. 45, 9–16.

Schachner, J. 1929. *Trigonopsis variabilis* nov. gen. et spec. Z. Ges. Brauwes 52, 137–142.

Schade, D., A. Walther and J. Wendland. 2003. The development of a transformation system for the dimorphic plant pathogen *Holleya sinecauda* based on *Ashbya gossypii* DNA elements. Fungal Genet. Biol. 40, 65–71.

Schaefer, A., R. Konrad, T. Kuhnigk, P. Kaempfer, H. Hertel and H. Koenig. 1996. Hemicellulose-degrading bacteria and yeasts from the termite gut. J. Appl. Bacteriol. 80, 471–478.

Schaffrath, R., and F. Meinhardt. 2005. *Kluyveromyces lactis* zymocin and other plasmid-encoded yeast killer toxins. In: M. Schmitt and R. Schaffrath (Eds), Topics in Current Genetics, Microbial Protein Toxins, Vol. 11. Springer-Verlag, Berlin, pp. 133–155.

Schanus, E.G., and M. McPherson. 1994. Yeast extract from *Candida utilis*, production and use as emulsifier of same. US Patent 5362869.

Scheda, R. 1966. Merkmalsveränderungen bei Hefen der Gattung *Saccharomyces*. Monatsschr. Brau. 19, 256–258.

Scheffers, W.A. 1966. Stimulation of fermentation in yeasts by acetoin and oxygen. Nature 210, 533–534.

Schehl, B., T. Senn, D.W. Lachenmeir, R. Rodicio and J.J. Henisch. 2007. Contribution of the fermenting yeast strain to ethyl carbamate generation in stone fruit spirits. Appl. Microbiol. Biotechnol. 74, 843–850.

Schiemann, R., A. Glasmacher, E. Bailly, R. Horré, E. Molitor, C. Leutner, M.T. Smith, R. Kleinschmidt, G. Marklein and T. Sauerbruch. 1998. *Geotrichum capitatum* septicaemia in neutropenic patients: case report and review of the literature. Mycose 41, 113–116.

Schimon, O. 1911. Beiträge zur Kenntnis rot gefärbter niederer Pilze. Thesis, München.

Schiönning, H. 1903. Nouveau genre de la famille des Saccharomycètes. C.R. Trav. Lab. Carlsberg 6, 101–125.

Schippers-Lammertse, A.F., and C. Heyting. 1962 Physiological properties, conjugation and taxonomy of *Cephaloascus fragrans* Hanawa 1920. (Syn.: *Asscoybe grovesii* Wells 1954). Antonie van Leeuwenhoek 28, 5–16.

Schisler, D.A., C.P. Kurtzman, R.J. Bothast and P.J. Slininger. 1995. Evaluation of yeasts for biological control of Fusarium dry rot of potatoes. Am. Potato J. 72, 339–353.

Schisler, D.A., N.I. Khan, M.J. Boehm and P.J. Slininger. 2002. Greenhouse and field evaluation of biological control of Fusarium head blight on durum wheat. Plant Dis. 86, 1350–1356.

Schisler, D.A., N.I. Khan, and M.J. Boehm. 2003. *Bacillus* species NRRL B-30212 for reducing Fusarium head blight in cereals. US Patent Application 20030165470.

Schmatz, D.M., M.A. Romancheck, L.A. Pittarelli, R.E. Schwartz, R.A. Fromtling, K.H. Nollstadt, F.L. Vanmiddlesworth, K.E. Wilson and M.J. Turner. 1990. Treatment of *Pneumocystis carinii* pneumonia with 1,3-beta-glucan synthesis inhibitors. Proc. Natl. Acad. Sci. USA 87, 5950–5954.

Schmitt, A.L., C.R. Curtis and G.A. Bean. 1977. Electrophoretic comparison of mycelial enzymes from aflatoxin-producing and non-producing strains and *Aspergillus flavus* and *Aspergillus parasiticus*. Can. J. Microbiol. 23, 60–67.

Schmidt, F.R. 2004. Recombinant expression systems in the pharmaceutical industry. Appl. Microbiol. Biotechnol. 65, 363–372.

Schmitt, M.J., and F. Radler. 1987. Mannoprotein of the yeast cell wall as primary receptor for the killer toxin of *Saccharomyces cerevisiae* strain 28. J. Gen. Microbiol. 133, 3347–3354.

Schmitt, M.J., and F. Radler. 1988. Molecular structure of the cell wall receptor for killer toxin KT28 in *Saccharomyces cerevisiae*. J. Bacteriol. 170, 2192–2196.

Schmitt, M.J., M. Brendel, R. Schwarz and F. Radler. 1989. Inhibition of DNA synthesis in *Saccharomyces cerevisiae* by yeast killer toxin KT28. J. Gen. Microbiol. 135, 1529–1535.

Schmitt, M.J., and F. Breinig. 2002. The viral killer system in yeast, from molecular biology to application. FEMS Microbiol. Rev. 26, 257–276.

Schmitt, M.J., and F. Breinig. 2006. Yeast viral killer toxins: lethality and self protection. Nat. Rev. Microbiol. 4, 212–221.

Schmitt, M.J., and F. Neuhausen. 1994. Killer toxin-secreting double-stranded RNA mycoviruses in the yeasts *Hanseniaspora uvarum* and *Zygosaccharomyces bailii*. J. Virol. 68, 1765–1772.

Schmitt, M.J., O. Poravou, K. Trenz and K. Rehfeldt. 1997. Unique double-stranded RNAs responsible for the anti-*Candida* activity of the yeast *Hanseniaspora uvarum*. J. Virol. 71, 8852–8855.

Schmitz, C., I. Goebel, S. Wagner, A. Vomberg and U. Klinner. 2000. Competition between *n*-alkane-assimilating yeasts and bacteria during colonization of sandy soil microcosms. Appl. Microbiol. Biotechnol. 54, 126–132.

Schnabel, G., W. Chai and K.D. Cox. 2006. Identifying and characterizing summer diseases on "Babygold" peach in South Carolina. Plant Health Prog. Doi: 10.1094./PHP2006030101RS.

Schnegg, H., and F. Oehlkers. 1922. *Saccharomyces odessa* nov. spec. Z. Gesamte Brauwes 45, 92–96, 106–107, 111–113.

Schneider, A. 1917. Further note on a parasitic Saccharomycete of the tomato. Phytopathology 7, 52–53.

Schneider, A. 1971. Mise en evidence de deux variétés de *Taphrina deformans*, parasites l'une du pêcher, l'autre de l'amandier. C. R. Acad. Sci. Paris Ser. D. 273, 685–688.

Schneider, H.P., Y. Wang, Y.K. Chan and R. Maleszka. 1981. Conversion of D-xylose into ethanol by the yeast *Pachysolen tannophilus*. Biotechnol. Lett. 3, 89–92.

Schneider, J.D., R. Hänsel, R. Hedlich and M. Jechorek. 1983. Growth characteristics of a thermotolerant strain of *Lodderomyces elongisporus* grown on sucrose. Acta Biotechnol. 3, 13–19.

Schoellhorn, K. 1919. Sur la fermentation de quelques levures des nectars des plantes d'hiver. Bull. Soc. Bot. Genève 11, 154–190.

Schollenberger, M., H.M. Muller, M. Rufle, H. Terry-Jara, S. Suchy, S. Plank and W. Drochner. 2007. Natural occurrence of *Fusarium* toxins in soy food marketed in Germany. Int. J. Food Microbiol. 113, 142–146.

Schrader, J., M.M.W. Etschmann, D. Sell, J.-M. Hilmer and J. Rabenhorst. 2004. Applied biocatalysis for the synthesis

of natural flavour compounds – current industrial processes and future prosects. Biotechnol. Lett. 26, 463–472.
Schroeder, W.A., and E.A. Johnson. 1993a. Antioxidant role of carotenoids in *Phaffia rhodozyma*. J. Gen. Microbiol. 139, 907–912.
Schroeder, W.A., and E.A. Johnson. 1993b. Carotenoids protect *Phaffia rhodozyma* against singlet oxygen damage. J. Ind. Microbiol. 14, 502–507.
Schroeder, W.A., and E.A. Johnson. 1995. Singlet oxygen and peroxyl radicals regulate carotenoid biosynthesis in *Phaffia rhodozyma*. J. Biol. Chem. 270, 18374–18379.
Schroeder, W.A., P. Calo, M.L. DeClercq and E.A. Johnson. 1996. Selection for carotenogenesis in the yeast *Phaffia rhodozyma* by dark-generated singlet oxygen. Microbiology 142, 2923–2929.
Schröter, J. 1908. Pilze. In: F. Cohn (Ed.), Kryptogamen-Flora von Schlesien, Vol. 3, Zweite Hälfte. J.U. Kern, Breslau, pp. 1–59.
Schröter, J. 1887. Pilze. In: F. Cohn (Ed.), Kryptogamen-Flora von Schlesien, Vol. 3. Ersde Hälfte. J.U. Kern, Breslau, pp. 257–384.
Schuler, M.A., and D. Werck-Reichart. 2003. Functional genomics of P450s. Annu. Rev. Plant Biol. 54, 629–667.
Schuller, D., and M. Casal. 2005. The use of genetically modified *Saccharomyces cerevisiae* strains in the wine industry. Appl. Microbiol. Biotechnol. 68, 292–304.
Schuller, D., E. Valero, S. Dequin and M. Casal. 2004. Survey of molecular methods for typing of wine yeast strains. FEMS. Microbiol. Lett. 231, 19–26.
Schuller, D., L. Pereira, H. Alves, B. Cambon, S. Dequin and M. Casal. 2007. Genetic characterization of commercial *Saccharomyces cerevisiae* isolates recovered from vineyard environments. Yeast 24, 625–636.
Schulze, C., and R. Heidrich. 2001. Megabacteria-associated proventriculitis in poultry in the state of Brandenburg, Germany. Dtsch. Tierärztl. Wschr. 108, 264–266.
Schumacher, H.C.F. 1803. Enumeratio plantarum in partibus Sællandiae septentrionalis et orientalis crescentium 2. Fridericum Brummer, typis E.M. Cohen, 489pp.
Schumacher, T., and L. Ryvarden. 1981. *Dipodascus polyporicola* nov. sp., a parasitic Hemiascomycete on *Piptoporus soloniensis* (Fr.) Pil. Mycotaxon 12, 525–530.
Schuster, S.C. 2008. Next-generation sequencing transforms today's biology. Nat. Methods 5, 16–18.
Schutzbach, J., H. Ankelb and I. Brockhausen. 2007. Synthesis of cell envelope glycoproteins of *Cryptococcus laurentii*. Carbohydr. Res. 342, 881–893.
Schwan, R.F. 1998. Cocoa fermentations with a defined microbial cocktail inoculum. Appl. Environ. Microbiol. 64, 1477–1484.
Schwan, R.F., and A.E. Wheals. 2003. Mixed microbial fermentations of chocolate and coffee. In: T. Boekhout and V. Robert (Eds), Yeasts in Food, Beneficial and Detrimental Aspects. B. Behr's Verlag., Hamburg, pp. 429–449.
Schwan, R.F., and A.E. Wheals. 2004. The microbiology of cocoa fermentation and its role in chocolate quality. Crit. Rev. Food Sci. Nutr. 44, 205–221.
Schwan, R.F., A.T. Mendonça, J.J. da Silva Jr., V. Rodrigues and A.E. Wheals. 2001. Microbiology and physiology of cachaça (aguardente) fermentations. Antonie van Leeuwenhoek 79, 89–96.
Schwan, R.F., E.G. Almeida, M.A. Souza-Dias and L. Jespersen. 2007. Yeast diversity in rice-cassava fermentations produced by the indigenous Tapirapé people of Brazil. FEMS Yeast Res. 7, 966–972.
Schwarz, G. 1978. Estimating the dimension of a model. Ann. Stat. 6, 461–464.
Schweigkofler, W., K. Lopandic, O. Molnár and H. Prillinger. 2002. Analysis of phylogenetic relationships among Ascomycota with yeast phases using ribosomal DNA sequences and cell wall sugars. Org. Divers. Evol. 2, 117.
Schweizer, C. 1921. Études sur la fermentation des cerises. Levures du genre *Saccharomyces* isolées de macérations de cerises. Ann. Inst. Pasteur 35, 820–833.
Scorzetti, G., I. Petrescu, D. Yarrow and J.W. Fell. 2000. *Cryptococcus adeliensis* sp. nov., a xylanase producing basidiomycetous yeast from Antarctica. Antonie van Leeuwenhoek 77, 153–157.
Scorzetti, G., J.W. Fell, A. Fonseca and A. Statzell-Tallman. 2002. Systematics of basidiomycetous yeasts: a comparison of large sub-unit D1D2 and internal transcribed spacer rDNA regions. FEMS Yeast Res. 2, 495–517.
Scott, D.B., and J.P. van der Walt. 1970a. *Hansenula sydowiorum* sp. n. Antonie van Leeuwenhoek 36, 45–48.
Scott, D.B., and J.P. van der Walt. 1970b. Three new yeasts from South African insect sources. Antonie van Leeuwenhoek 36, 389–396.
Scott, D.B., and J.P. van der Walt. 1971a. *Hansenula dryadoides* sp. n., a new species from South African insect sources. Antonie van Leeuwenhoek 37, 171–175.
Scott, D.B., and J.P. van der Walt. 1971b. *Pichia cicatricosa* sp. n., a new auxiliary ambrosia fungus. Antonie van Leeuwenhoek 37, 177–183.
Scott, W.J. 1936. The growth of micro-organisms on ox muscle 1. The influence of water content of substrate on rate of growth at -1°C. Council Sci. Ind. Res. 9, 177–190.
Scrimshaw, N.S., and E.B. Murray. 1995. Nutritional value and safety of "single cell protein." In: G. Reed and T.W. Nagodawithana, Vol. 9. Enzymes, Biomass, Food and Feed. H.-J. Rehm and G. Reed (Eds), Biotechnology, 2nd, edn. VCH, Weinheim, pp. 221–237.
Scrivani, P. 1939. Ricerche sui microorganismi produttori della fioretta nel vino. Arch. Mikrobiol. 10, 446–472.
Scupham, A.J., L.L. Presley, B. Wei, E. Bent, N. Griffith, M. McPherson, F. Zhu, O. Oluwadara, N. Rao, J. Braun and J. Borneman. 2006. Abundant and diverse fungal microbiota in the murine intestine. Appl. Environ. Microbiol. 72, 793–801.
Scurlock, J.M.O., G.P. Asner, and S.T. Gower. 2001. Global Leaf Area Index Data from Field Measurements, 1932–2000. Data set. Available on-line http://www.daac.ornl.gov from the Oak Ridge National Laboratory Distributed Active Archive Center, Oak Ridge, Tennessee.
Sebolai, O.M., J.L. Kock, C.H. Pohl, P.J. Botes, C.J. Strauss, P.W. van Wyk and S. Nigam. 2005. The presence of 3-hydroxy oxylipins on the ascospore surfaces of some species representing *Saccharomycopsis* Schiönning. Can. J. Microbiol. 51, 605–612.
Sebti, A., T.E. Kiehn, D. Perlin, V. Chaturvedi, M. Wong, A. Doney, S. Park and K.A. Sepkowitz. 2001. *Candida dubliniensis* at a cancer center. Clin. Infect. Dis. 32, 1034–1038.
Seeliger, H.P.R. 1956. Use of a urease test for the screening and identification of cryptococci. J. Bacteriol. 72, 127–131.

Segal, E., and G.L. Baum. 1994. Pathogenic Yeasts and Yeast Infections. CRC Press, Boca Raton, FL.

Seibold, A., A. Fried, S. Kunz, E. Moltmann, E. Lange and W. Jelkmann. 2004. Yeasts as antagonists against fireblight. EPPO Bull. 34, 389–390.

Seidler, R.J., and M. Mandel. 1971. Quantitative aspects of deoxyribonucleic acid renaturation: base composition, state of chromosome replication, and polynucleotide homologies. J. Bacteriol. 106, 608–614.

Seifert, G.J. 2004. Nucleotide sugar interconversions and cell wall biosynthesis: how to bring the inside to the outside. Curr. Opin. Plant Biol. 7, 227–284.

Seifert, K., F. Oberwinkler and R.J. Bandoni. 1992. Notes on *Stilbum vulgare* and *Fibulostilbum phylacicola* gen. et sp. nov. (Atractiellales). Bol. Soc. Argent. Bot. 28, 213–217.

Seifert, R.P. 1981. Application of mycological data base principles and concepts of population and community ecology. In: D.T. Wicklow and G.C. Carroll (Eds), The Fungal Community, Its Organization and Role in the Ecosystem. Marcel Dekker, New York, pp. 11–23.

Seiler, H., and M. Busse. 1990. The yeasts of cheese brines. Int. J. Food Microbiol. 11, 289–303.

Semenova, S.A., and W.I. Golubev. 1986. Pedogamic conjugation in the yeast *Nadsonia commutata*. Mikrobiologiia 55, 765–767.

Semenova, S.A., and W.I. Golubev. 1988. Characteristics and localization of a pigment from *Nadsonia commutata* ascospores. Mikrobiologiia 57, 664–668.

Senczek, D., U. Siesenop and K.H. Böhm. 1999. Characterization of *Malassezia* species by means of phenotypic characteristics and detection of electrophoretic karyotypes by pulsed-field gel electrophoresis (PFGE). Mycoses 42, 409–414.

Senses-Ergul, S., R. Agoston, A. Belák and T. Deák. 2006. Characterization of some yeasts isolated from foods by traditional and molecular tests. Int. J. Food Microbiol. 108, 120–124.

Sentheshanmuganathan, S., and W.J. Nickerson. 1962. Nutritional control of cellular form in *Trigonopsis variabilis*. J. Gen. Microbiol. 27, 437–449.

Seo, H.-S., H-J. Um, J. Min, S.-K. Rhee, T.J. Cho, Y.-H. Kim and J. Lee. 2007. *Pseudozyma jejuensis* sp. nov., a novel cutinolytic yeast species that is able to degrade plastic waste. FEMS Yeast Res. 7, 1035–1045.

Serena, C., F.J. Pastor, M. Ortoneda, J. Capilla, N. Nolard and J. Guarro. 2004. *In vitro* antifungal susceptibilities of uncommon basidiomycetous yeasts. Antimicrob. Agents Chemother. 48, 2724–2726.

Serjeant, K., R. Tang, N. Anfang, J.R. Beggs and M.R. Goddard. 2008. Yeasts associated with the New Zealand *Nothofagus* honeydew system. N. Z. J. Ecol. 32, 209–213.

Sesma, B., and C. Ramírez. 1978. A new species of *Blastobotrys*: *Blastobotrys navarrensis* sp. nov. (Hyphomycetes). Mycopathologia 63, 41–45.

Sethuraman, N., and T.A. Stadheim. 2006. Challenges in therapeutic glycoprotein production. Curr. Opin. Biotechnol. 17, 341–346.

Setliff, E.C., W.L. MacDonald and R.F. Patton. 1972. Fine structure of the septal pore apparatus in *Polyporus tomentosus, Poria latemarginata*, and *Rhizoctonia solani*. Can. J. Bot. 50, 2559–2563.

Seymour, F.R., M.E. Slodki, R.D. Plattner and R.M. Stodola. 1976. Methylation and acetolysis of extracellular D-mannans from yeast. Carbohydr. Res. 48, 225–237.

Shadomy, H.J. 1970. Clamp connections in two strains of *Cryptococcus neoformans*. In: D.G. Ahearn (Ed.), Recent Trends in Yeast Research, Vol. I, Spectrum. Georgia State University, Atlanta, GA, pp. 67–72.

Shafiee, R., I. Nahvi and G. Emtiazi. 2005a. Trehalose production by a starch assimilating yeast *Cryptococcus aerius*. Biotechnology 4, 279–283.

Shafiee, R., I. Nahvi and G. Emtiazi. 2005b. Bioconversion of raw starch to SCP by coculture of *Cryptococcus aerius* and *Saccharomyces cerevisiae*. J. Biol. Sci. 5, 717–723.

Shankar, G., and P. Baskaran. 1992. Regulation of yeast-like endosymbiotes in the rice brown planthopper *Nilaparvata lugens* Stal; (O: Homoptera, F: Delphacidae). Symbiosis 14, 161–173.

Shann, C. 1987a. Presenza di nematodi in uve affette da marciume acido. L'Informatore Agrario 43, 137–138.

Shann, C. 1987b. Correlazioni tra sistemi ecologici nel marciume acido delle uve. Atti dell'Accademia Italiana della Vite e del Vino 39, 333–355.

Sharma, V., J. Shankar and V. Kotamarthi. 2006. Endogeneous endophthalmitis caused by *Sporobolomyces salmonicolor*. Eye 20, 945–946.

Shaw, C.E., and L. Kapica. 1972. Production of diagnostic pigment by phenoloxidase activity of *Cryptococcus neoformans*. Appl. Microbiol. 24, 824–830.

Shaw, C.R., and R. Prasad. 1970. Starch gel electrophoresis of enzymes – a compilation of recipes. Biochem. Genet. 4, 297–310.

Shaw, F.W. 1926. A new species of *Monilia* pathogenic for man. Science 64, 300.

Shaw, J.A., P.C. Mol, B. Bowers, S.J. Silverman, M.H. Valdivieso, A. Duran and E. Cabib. 1991. The function of chitin synthases 2 and 3 in the *Saccharomyces cerevisiae* cell cycle. J. Cell Biol. 114, 111–123.

Shearer, A.E.H., A.S. Mazzotta, R. Chuyate and D.E. Gombas. 2002. Heat resistance of juice spoilage microorganisms. J. Food Prot. 65, 1271–1275.

Shehata, A.M.T., E.M. Mrak and H.J. Phaff. 1955. Yeasts isolated from *Drosophila* and their suspected feeding places in Southern and Central California. Mycologia 47, 799–881.

Shehata, E.T.A.M. 1960. Yeasts isolated from sugar-cane and its juice during the production of Aguardente de Cana. Appl. Microbiol. 8, 73–75.

Shehata, E.T.A.M., and E.M. Mrak. 1952. Intestinal yeast floras of successive populations of *Drosophila*. Evolution 6, 325–332.

Sheldon, R.A. 2007. Enzyme immobilization: the quest for optimum performance. Adv. Synth. Catal. 349, 1289–1307.

Shen, D., J.H. Xu, P.F. Gong, H.Y. Wu and Y.Y. Liu. 2001. Isolation of an esterase-producing *Trichosporon brassicae* and its catalytic performance in kinetic resolution of ketoprofen. Can. J. Microbiol. 47, 1101–1106.

Shen, R., and M.-A. Lachance. 1993. Phylogenetic study of ribosomal DNA of cactophilic *Pichia* species by restriction mapping. Yeast 9, 315–330.

Shepherd, H.S., J.M. Ligon, P.L. Bolen and C.P. Kurtzman. 1987. Cryptic DNA plasmids of the heterothallic yeast *Saccharomycopsis crataegensis*. Curr. Genet. 12, 297–304.

Sherman, D., P. Durrens, F. Iragne, E. Beyne, M. Nikolski and J.L. Souciet. 2006. Génolevures complete genomes provide data and tools for comparative genomics of hemiascomycetous yeasts. Nucleic Acids Res. 34, D432–D435.

Sherman, F. 1998. Getting started with yeast. Methods Enzymol. 359, 3–41.

Shete, A.M., G. Wadhawa, I.M. Banat and B.A. Chopade. 2006. Mapping of patents on bioemulsifier and biosurfactant: a review. J. Sci. Ind. Res. 65, 91–115.

Shetty, P.H., B. Hald and L. Jespersen. 2007. Surface binding of aflatoxin B-1 by *Saccharomyces cerevisiae* strains with potential decontaminating abilities in indigenous fermented foods. Int. J. Food Microbiol. 113, 41–46.

Sheu, M.J., C.C. Wang, W.J. Shi and M.L. Chu. 1994. *Rhodotorula* septicemia: report of a case. J. Formos. Med. Assoc. 93, 645–647.

Shields, A.B., and L. Ajello. 1966. Medium for selective isolation of *Cryptococcus neoformans*. Science 151, 208.

Shifrine, M., and H.J. Phaff. 1956. The association of yeasts with certain bark beetles. Mycologia 48, 41–55.

Shifrine, M., and H. Phaff. 1958. On the isolation, ecology and taxonomy of *Saccharomycopsis guttulatus*. Antonie van Leeuwenhoek 24, 193–209.

Shifrine, M., and H. Phaff. 1959. Nutritional requirements of *Saccharomycopsis guttulatus* (Robin) Schiönning. Mycologia 51, 318–328.

Shifrine, M., H.J. Phaff and A.L. Demain. 1954. Determination of carbon assimilation patterns of yeasts by replica plating. J. Bacteriol. 68, 28–35.

Shihira, I., and R.W. Krauss. 1965. *Chlorella*, Physiology and Taxonomy of Forty-one Isolates. Port City Press, Baltimore, MD, 97pp.

Shimada, K., E. Kimura, Y. Yasui, H. Tanaka, S. Matsushita, H. Hagihara, M. Nagakura and M. Kawahisa. 1992. Styrene formation by the decomposition by *Pichia carsonii* of trans-cinnamic acid added to a ground fish product. Appl. Environ. Microbiol. 58, 1577–1582.

Shimotoyodome, A., H. Kobayashi, J. Nakamura, I. Tokimitsu, T. Hase, T. Inoue, T. Matsukubo and Y. Takaesu. 2006. Reduction of saliva-promoted adhesion of *Streptococcus mutans* MT8148 and dental biofilm development by tragacanth gum and yeast-derived phosphomannan. Biofouling 22, 261–268.

Shin, K.S., S.D. Hong and K.S. Bae. 1996. The significance of ITS-RFLPS and coenzyme-Q system in determining taxonomic relationships among *Candida* species. J. Gen. Appl. Microbiol. 42, 481–491.

Shin, K.-S., Y.K. Shin, J.-H. Yoon and Y.-H. Park. 2001. *Candida thermophila* sp. nov., a novel thermophilic yeast isolated from soil. Int. J. Syst. Evol. Microbiol. 51, 2167–2170.

Shin, K.-S., Y.-H. Park, D.-J. Park and C.-J. Kim. 2005. *Cryptococcus taeanensis* sp. nov., a new anamorphic basidiomycetous yeast isolated from a salt farm. Int. J. Syst. Evol. Microbiol. 55, 1365–1368.

Shin, K.-S., H.-M. Oh, Y.-H. Park, K.H. Lee, H. Poo, G.-S. Kwon and O.-Y. Kwon. 2006. *Cryptococcus mujuensis* sp. nov. and *Cryptococcus cuniculi* sp. nov., basidiomycetous yeasts isolated from wild rabbit faeces. Int. J. Syst. Evol. Microbiol. 56, 2241–2244.

Shinde, S.M., K.S. Vanarse and A.N. Pandit. 2004. Systemic humicolus cryptococcosis. Indian Pediatr. 41, 1162–1164.

Shintani, T., and D.J. Klionsky. 2004. Autophagy in health and disease: a double-edged sword. Science 306, 990–995.

Shiraishi, A., and H. Fujii. 1978. *Sporobolomyces* lytic enzyme produced by a bacterium no. 98. J. Agric. Chem. 12, 553–559.

Shivas, R.G., and J.F. Brown. 1984. Identification and enumeration of yeasts on *Banksia collina* and *Callistemon viminalis* leaves. Trans. Br. Mycol. Soc. 83, 687–689.

Shivas, R.G., and J.F. Brown. 1989. Yeasts associated with fluid in pitchers of *Nepenthes*. Mycol. Res. 93, 96–100.

Shivas, R.G., and L. Rodrigues de Miranda. 1983a. *Cryptococcus phylloplanus* and *Cryptococcus hinnuleus*, two new yeast species. Antonie van Leeuwenhoek 49, 153–158.

Shivas, R.G., and L. Rodrigues de Miranda. 1983b. Two new species of the genus *Sporobolomyces* and a new *Rhodotorula* species from leaf surfaces. Antonie van Leeuwenhoek 49, 159–166.

Shotts, E.J., T.F. Albert, R.E. Wooley and J. Brown. 1990. Microflora associated with the skin of the bowhead whale (*Balaena mysticetus*). J. Wildl. Dis. 26, 351–359.

Shubakov, A.A. 2000. Production of beta-xylosidase by the yeast *Cryptococcus podzolicus*. Bioorg. Khim. 26, 613–616. In Russian.

Shultz, L.D., P.A. Schweitzer, E.J. Hall, J.P. Sundberg, S. Taylor and P.D. Walzer. 1989. *Pneumocystis carinii* pneumonia in scid/scid mice. Curr. Top. Microbiol. Immunol. 152, 243–249.

Sia, R.A., K.B. Lengeler and J. Heitman. 2000. Diploid strains of the pathogenic basidiomycete *Cryptococcus neoformans* are thermally dimorphic. Fungal Genet. Biol. 29, 153–163.

Sibirny, A.A. 1996. *Pichia guilliermondii*. In: K. Wolf (Ed.), Nonconventional Yeasts in Biotechnology. A Handbook. Springer, Berlin, pp. 255–275.

Siciliano, M.J., and C.R. Shaw. 1976. In: I. Smith (Ed.), Chromatographic and Electrophoretic Techniques, 4th edn. Vol. 2. William Heinemann Medical Books, London, pp. 185–209.

Sidenberg, D.G., and M.A. Lachance. 1983. Speciation, species delineation, and electrophoretic isozyme patterns of the type strains of *Kluyveromyces* van der Walt emend. van der Walt. Int. J. Syst. Bacteriol. 33, 822–828.

Sidenberg, D.G., and M.A. Lachance. 1986. Electrophoretic isoenzyme variation in *Kluyveromyces* populations and revision of *Kluyveromyces marxianus* (Hansen) van der Walt. Int. J. Syst. Bacteriol. 36, 94–102.

Siepmann, R., and W. Höhnk. 1962. Über Hefen und einige Pilze (Fungi imp., Hyphales) aus dem Nordatlantik. Veröff. Inst. Meeresforsch. Bremerhaven 8, 79–97.

Sierra, G. 1957. A simple method for the detection of lipolytic activity of micro-organisms and some observations on the influence of the contact between cells and fatty substances. Antonie van Leeuwenhoek 23, 15–22.

Sierra, S., and J. Cifuentes. 1993. Contribución al studio taxonómico de los hongos Tremeloides (heterobasidiomycetes) de México. Rev. Mex. Mycol. 9, 119–137.

Sietmann, R., E. Hammer, J. Moody, C.E. Cerniglia and F. Schauer. 2000. Hydroxylation of biphenyl by the yeast *Trichosporon mucoides*. Arch. Microbiol. 174, 353–361.

Sigler, L., and P.E. Verweij. 2003. *Aspergillus, Fusarium*, and other opportunistic moniliaceous fungi. In: P.R. Murray and E.J. Baron (Eds), Manual of Clinical Microbiology, 8th edn. ASM Press, Washington, DC.

Silva, A.P., I.M. Miranda, C. Lisboa, C. Pina-Vaz and A.G. Rodrigues. 2009. Prevalence, distribution and antifungal susceptibility profile of *Candida parapsilosis*, *C. orthopsilosis* and *C. metapsilosis* in a tertiary care hospital. J. Clin. Microbiol. 2009, 47, 2392–2399.

Silva, C.F., and R.F. Schwan. 2000. Ë. Sousa Dias and A.E. Wheals. Microbial diversity during maturation and natural processing of coffee cherries of *Coffea arabica* in Brazil. Int. J. Food Microbiol. 60, 251–260.

Silva, P., H. Cardoso and H. Geros. 2004. Studies on the wine spoilage of *Brettanomyces*/*Dekkera* spp. Am. J. En. Viticult. 55, 65–71.

Silva-Graça, M., L. Neves and C. Lucas. 2003. Outlines for the definition of halotolerance/halophily in yeasts: *Candida versatilis* (halophila) CBS4019 as the archetype? FEMS Yeast Res. 3, 347–362.

Siminszky, B., F.T. Corbin, E.R. Ward, T.J. Fleischmann and R.E. Dewey. 1999. Expression of a soybean cytochrome P450 monooxygenase cDNA in yeast and tobacco enhances the metabolism of phenylurea herbicides. Proc. Natl. Acad. Sci. USA 96, 1750–1755.

Simione, F.R., and S.A. Meyer. 1978. Genetic relatedness between some physiologically similar *Candida* species with high GC contents. Abstr. Ann. Meet. Am. Soc. Microbiol. 81.

Simmons, M.P., K.M. Pickett and M. Miya. 2004. How meaningful are Bayesian support values? Mol. Biol. Evol. 21, 188–199.

Simmons, P.T., and C.J. Portier. 2002. Toxicogenomics: the new frontier in risk analysis. Carcinogenesis 23, 903–905.

Simmons, R.B., and D.G. Ahearn. 1985. Ascospore ornamentation in *Saccharomycodes ludwigii*. Mycologia 77, 660–662.

Simmons, R.B., and D.G. Ahearn. 1987. Cell wall ultrastructure and diazonium blue B reaction of *Sporopachydermia quercuum*, *Bullera tsugae*, and *Malassezia* spp. Mycologia 79, 38–43.

Simmons, R.B., and E. Guého. 1990. A new species of *Malassezia*. Mycol. Res. 94, 1146–1149.

Simoncini, N., D. Rotelli, R. Virgili and S. Quintavalla. 2007. Dynamics and characterization of yeasts during ripening of typical Italian dry-cured ham. Food Microbiol. 24, 577–584.

Sims, C.R., L. Ostrosky-Zeichner and J.H. Rex. 2005. Invasive candidiasis in immunocompromised hospitalized patients. Arch. Med. Res. 36, 660–671.

Sinclair, N.A., and S.L. Stokes. 1965. Obligately psychrophilic yeasts from the polar regions. Can. J. Microbiol. 11, 259–269.

Singh, G., and A.J.S. Klar. 2002. The 2.1-kb inverted repeat DNA sequences flank the mat2,3 silent region in two species of *Schizosaccharomyces* and are involved in epigenetic silencing in *Schizosaccharomyces pombe*. Genetics 162, 591–602.

Singh, G., and A.J.S. Klar. 2003. DNA sequence of the mat2,3 region of *Schizosaccharomyces kambucha* shares homology with the corresponding sequence from *Schizosaccharomyces pombe*. Yeast 20, 1273–1278.

Singh, R., and R.E. Kunkee. 1977. Multiplicity and control of alcohol dehydrogenase isozymes in various strains of wine yeasts. Arch. Microbiol. 114, 255–259.

Sinnott, J.T., J. Rodnite, P.J. Emmanuel and A. Campos. 1989. *Cryptococcus laurentii* infection complicating peritoneal dialysis. Pediatr. Infect. Dis. J. 8, 803–805.

Sipiczki, M. 1979. Interspecific protoplast fusion in fission yeasts. Curr. Microbiol. 3, 37–40.

Sipiczki, M. 2003. *Candida zemplinina* sp. nov., an osmotolerant and psychrotolerant yeast that ferments sweet botrytized wines. Int. J. Syst. Evol. Microbiol. 53, 2079–2083.

Sipiczki, M. 2006. *Metschnikowia* strains isolated from botrytized grapes antagonize fungal and bacterial growth by iron depletion. Appl. Environ. Microbiol. 72, 6716–6724.

Sipiczki, M., and E. Kajdacsi. 2009. *Jaminaea angkorensis* gen. nov., sp. nov. A novel anamorphic fungus containing an S943 nuclear small-subunit rRNA Group IB intron represenst a basal branch of Microstromatales. Int. J. Syst. Evol. Microbiol. 59, 914–920.

Sipiczki, M., J. Kucsera, S. Ulaszewski and J. Zsolt. 1982. Hybridization studies by crossing and protoplast fusion within the genus *Schizosaccharomyces* Lindner. J. Gen. Microbiol. 128, 1989–2000.

Siso, M.I.G. 1996. The biotechnological utilization of cheese whey: a review. Bioresour. Technol. 57, 1–11.

Sivakumaran, S., P. Bridge and P. Roberts. 2002. Genetic relatedness among *Filobasidiella* species. Mycopathologia 156, 157–162.

Sjamsuridzal, W., Y. Tajiri, H. Nishida, T. Thuan, H. Kawasaki, A. Hirata, A. Yokota and J. Sujiyama. 1997. Evolutionary relationships of members of the genera *Taphrina*, *Protomyces*, *Schizosaccharomyces*, and related taxa within the Archiascomycetes: integrated analysis of genotypic and phenotypic characters. Mycoscience 38, 267–280.

Sjamsuridzal, W., H. Nishida and A. Yokota. 2002. Phylogenetic position of *Mixia osmundae* inferred from 28S rDNA comparison. J. Gen. Appl. Microbiol. 48, 121–123.

Skinner, C.E. 1947a. The yeast-like fungi: *Candida* and *Brettanomyces*. Bacteriol. Rev. 11, 227–274.

Skinner, C.E. 1947b. Morphology and classification of the yeasts and yeast-like fungi. In: Henrici's Molds, Yeasts, and Actinomycetes, 2nd edn. Wiley, New York, pp. 264–304.

Skinner, C.E. 1950. Generic name for imperfect yeasts, *Cryptococcus* or *Torulopsis*? Am. Midl. Nat. 43, 242–250.

Skory, C.D., and S.N. Freer. 1995. Cloning and characterization of a gene encoding a cell-bound, extracellular beta-glucosidase in the yeast *Candida wickerhamii*. Appl. Environ. Microbiol. 61, 518–525.

Slaven, B.E., J. Meller, A. Porollo, T. Sesterhenn, A.G. Smulian and M.T. Cushion. 2006. Draft assembly and annotation of the *Pneumocystis carinii* genome. J. Eukaryot. Microbiol. 53 (Suppl. 1), S89–S91.

Sláviková, E., and R. Vadkertiová. 1995. Yeasts and yeastlike organisms isolated from fishpond waters. Acta Microbiol. Pol. 44, 181–189.

Sláviková, E., and R. Vadkertiová. 2000. The occurrence of yeasts in the forest soils. J. Basic Microbiol. 40, 207–212.

Slavikova, E., B. Kosikova and M. Mikulosova. 2002. Biotransformation of waste lignin products by the soil-inhabiting yeast *Trichosporon pullulans*. Can. J. Microbiol. 48, 200–203.

Sláviková, E., R. Vadkertiová and D. Vránová. 2007. Yeasts colonizing the leaf surfaces. J. Basic Microbiol. 47, 344–350.

Slininger, P.J., R.J. Bothast, J.E. VanCauwenberge and C.P. Kurtzman. 1982. Conversion of D-xylose to ethanol by the yeast *Pachysolen tannophilus*. Biotechnol. Bioeng. 24, 371–384.

Slininger, P.J., P.L. Bolen and C.P. Kurtzman. 1987. *Pachysolen tannophilus*: properties and process considerations for ethanol production from D-xylose. Enzyme Microb. Technol. 9, 5–15.

Slininger, P.J., L.E. Branstrator, R.J. Bothast, M.R. Okos and M.R. Ladisch. 1991. Growth, death, and oxygen uptake kinetics of *Pichia stipitis* on xylose. Biotech. Bioeng. 37, 973–980.

Slodki, M.E. 1962. Phosphate linkages in phosphomannans from yeast. Biochim. Biophys. Acta 57, 525–533.

Slodki, M.E. 1963. Structure of *Hansenula capsulata* NRRL Y1842 phosphomannan. Biochim. Biophys. Acta 69, 96–102.

Slodki, M.E. 1966. Hydrolysis products from an extracellular *Tremella* heteropolysaccharide. Can. J. Microbiol. 12, 495–499.

Slodki, M.E., L.J. Wickerham and R.J. Bandoni. 1966. Extracellular heteropolysaccharides from *Cryptococcus* and *Tremella*: a possible taxonomic relationship. Can. J. Microbiol. 12, 489–494.

Slodki, M.E., R.M. Ward, J.A. Boundy and M.C. Cadmus. 1972. Extracellular mannans and phosphomannans: structural and biosynthetic relationships. In: G. Terui (Ed.), Fermentation Technology Today, Proc. IV Int. Ferment. Symp., Soc. Ferment. Technol., Osaka, Japan, pp. 597–601.

Slooff, W.Ch. 1964. Mating types in *Pichia membranaefaciens*. Antonie van Leeuwenhoek 30, 129–131.

Slooff, W.Ch. 1970a. *Lipomyces* Lodder et Kreger-van Rij. In: J. Lodder (Ed.), The Yeasts, A Taxonomic Study, 2nd edn. North-Holland, Amsterdam, pp. 379–402.

Slooff, W.Ch. 1970b. *Schizosaccharomyces* Lindner. In: J. Lodder (Ed.), The Yeasts, A Taxonomic Study, 2nd edn. North-Holland, Amsterdam, pp. 733–755.

Slooff, W.Ch. 1970c. *Pityrosporum* Sabouraud. In: J. Lodder (Ed.), The Yeasts, A Taxonomic Study, 2nd edn. North-Holland, Amsterdam, pp. 1167–1186.

Slotema, W.F., G. Sandoval, D. Guieysse, A.J. Straathof and A. Marty. 2003. Economically pertinent continuous amide formation by direct lipase-catalyzed amidation with ammonia. Biotechnol. Bioeng. 82, 664–669.

Smit, E., C. Veenman and J. Baar. 2003. Molecular analysis of ectomycorrhizal basidiomycete communities in a *Pinus sylvestris* L. stand reveals long-term increased diversity after removal of litter and humus layers. FEMS Microbiol. Ecol. 45, 49–57.

Smit, J. 1934. Über die Ursachen des Aufblähens von Belebtschlamm. Arch. Mikrobiol. 5, 550–560.

Smit, J., and L. Meyers. 1928. *Oospora gigas* n. sp. Ned. Tijdschr. Hyg. Microbiol. Serol. 2, 85–92.

Smith, B.D., and K.G. Stott. 1964. The life history and behaviour of the willow weevil *Cryptorhynchus lapathi* L. Ann. Appl. Biol. 54, 141–151.

Smith, D., D. Metzgar, C. Wills and J. Fierer. 2002. Fatal *Saccharomyces cerevisiae* aortic graft infection. J. Clin. Microbiol. 40, 2691–2692.

Smith, D.L. 1996. Brewer's yeast as a cause of infection. Clin. Infect. Dis. 22, 201.

Smith, D.P., J.L.F. Kock, M.I. Motaung, P.W.J. van Wyk, P. Venter, D.J. Coetzee and S. Nigam. 2000a. Ascospore aggregation and oxylipin distribution in the yeast *Dipodascopsis tothii*. Antonie van Leeuwenhoek 77, 389–392.

Smith, D.P., J.L.F. Kock, P.W.J. van Wyk, P. Venter, D.J. Coetzee, E. van Heerden, D. Linke and S. Nigam. 2000b. The occurrence of 3-hydroxy oxylipins in the ascomycetous yeast family Lipomycetaceae. S. Afr. J. Sci. 96, 247–249.

Smith, M.Th. 1973. Centraalbureau voor Schimmelcultures, Baarn and Delft. Progress Report 1972. Verh. K. Ned. Akad. Wetensch., Afd. Natuurk. 61, 59–81.

Smith, M.Th. 1974. *Hanseniaspora occidentalis* sp. nov. Antonie van Leeuwenhoek 40, 441–444.

Smith, M.Th. 1984a. *Hanseniaspora* Zikes. In: N.J.W. Kreger-van Rij (Ed.), The Yeasts, A Taxonomic Study, 3rd edn. Elsevier, Amsterdam, pp. 154–164.

Smith, M.Th. 1984b. *Sarcinosporon* King et Jong. In: N.J.W. Kreger-van Rij (Ed.), The Yeasts, A Taxonomic Stusy, 3rd edn. Elsevier, Amsterdam, pp. 906–908.

Smith, M.Th. 1986. *Zygoascus hellenicus* gen. nov., sp. nov., the teleomorph of *Candida hellenica* (= *C. inositophila* = *C. steatolytica*). Antonie van Leeuwenhoek 52, 25–37.

Smith, M.Th. 1998a. *Babjevia* van der Walt & M.Th. Smith. In: C.P. Kurtzman and J.W. Fell (Eds), The Yeasts, A Taxonomic Study 4th edn. Elsevier, Amsterdam, pp. 141–142.

Smith, M.Th. 1998b. *Zygoascus* M.Th.Smith. In: C.P. Kurtzman and J.W. Fell (Eds), The Yeasts, A Taxonomic Study 4th edn. Elsevier, Amsterdam, pp. 422–423.

Smith, M.Th. 1998c. *Aciculoconidium* D.S. King & S.-C. Jong. In: C.P. Kurtzman and J.W. Fell (Eds), The Yeasts, A Taxonomic Study, 4th edn. Elsevier, Amsterdam, pp. 439–440.

Smith, M.Th. 1998d. *Arxula* van der Walt, M.Th. Smith & Y. Yamada. In: C.P. Kurtzman and J.W. Fell (Eds), The Yeasts, A Taxonomic Study, 4th edn. Elsevier, Amsterdam, pp. 441–442.

Smith, M.Th. 1998e. *Botryozyma* Shann & M.Th. Smith. In: C.P. Kurtzman and J.W. Fell (Eds), The Yeasts, A Taxonomic Study, 4th edn. Elsevier, Amsterdam, p. 449.

Smith, M.Th. 1998f. *Kloeckera* Janke. In: C.P. Kurtzman and J.W. Fell (Eds), The Yeasts, A Taxonomic Study, 4th edn. Elsevier, Amsterdam, pp. 580–581.

Smith, M.Th., and W.H. Batenburg-van der Vegte. 1984. Ascospore morphology and ultrastructure of species assigned to the genus *Lipomyces* Lodder et Kreger-van Rij. Int. J. Syst. Bacteriol. 34, 80–86.

Smith, M.Th., and W.H. Batenburg-van der Vegte. 1985. Ultrastructure of septa in *Blastobotrys* and *Sporothrix*. Antonie van Leeuwenhoek 51, 121–128.

Smith, M.Th., and W.H. Batenburg-van der Vegte. 1986a. *Pichia triangularis* sp. nov., the teleomorph of *Candida polymorpha* Ohara et Nonomura, nom. nud. Antonie van Leeuwenhoek 52, 437–443.

Smith, M.Th., and W.H. Batenburg-van der Vegte. 1986b. Additional information on the ultrastructure in the genus *Sporothrix*. J. Gen. Appl. Microbiol. 32, 549–552.

Smith, M.Th., and G.S. de Hoog. 1998a. *Stephanoascus* M.Th. Smith, van der Walt & E. Johannsen. In: C.P. Kurtzman and J.W. Fell (Eds), The Yeasts, A Taxonomic Study 4th edn. Elsevier, Amsterdam, pp. 400–403.

Smith, M.Th., and G.S. de Hoog. 1998b. *Dipodascopsis* Batra & P. Miller. In: C.P. Kurtzman and J.W. Fell (Eds), The Yeasts, A Taxonomic Study 4th edn. Elsevier, Amsterdam, pp. 178–180.

Smith, M.Th., and G.A. Poot. 1985. Conspecificity of *Hanseniaspora nodinigri* and *Hanseniaspora vineae*: comparison by

DNA reassociation. Antonie van Leeuwenhoek 51, 151–153.
Smith, M.Th., and G.A. Poot. 1998. *Dipodascus capitatus*, *Dipodascus spicifer* and *Geotrichum clavatum*: genomic characterization. Antonie van Leeuwenhoek 74, 229–235.
Smith, M.Th., and G.A. Poot. 2003. Genome comparison in the genus *Dipodascus* de Lagerheim. FEMS Yeast Res. 3, 301–311.
Smith, M.Th., and A.M. van Grinsven. 1984. *Dekkera anomala* sp. nov., the teleomorph of *Brettanomyces anomalus* recovered from spoiled soft drinks. Antonie van Leeuwenhoek 50, 143–148.
Smith, M.Th., J.P. van der Walt and E. Johannsen. 1976. The genus *Stephanoascus* gen. nov. (Ascoideaceae). Antonie van Leeuwenhoek 42, 119–127.
Smith, M.Th., F.P. Simione and S.A. Meyer. 1977. *Kloeckera apis* sp. nov.; the imperfect state of *Hanseniaspora guilliermondii* Pijper. Antonie van Leeuwenhoek 43, 219–223.
Smith, M.Th., W.H. Batenburg-van der Vegte and W.A. Scheffers. 1981. *Eeniella*, a new genus of the Torulopsidales. Int. J. Syst. Bacteriol. 31, 196–203.
Smith, M.Th., G.A. Poot and T. Kull. 1989a. Segregation of *Candida pseudolambica* sp. nov. from *Candida lambica* and closely related species by deoxyribonucleic acid relatedness. Stud. Mycol. 31, 171–176.
Smith, M.Th., J.P. van der Walt, Y. Yamada and W.H. Batenburg-van der Vegte. 1989b. *Zygozyma suomiensis,* sp. nov. (Lipomycetaceae), a new species from Finland. Antonie van Leeuwenhoek 56, 283–288.
Smith, M.Th., G.A. Poot and W.H. Batenburg-van der Vegte. 1990a. Genome comparison among species of the genus *Arthroascus* von Arx. Antonie van Leeuwenhoek 58, 249–253.
Smith, M.Th., M. Yamazaki and G.A. Poot. 1990b. *Dekkera*, *Brettanomyces* and *Eeniella*: electrophoretic comparison of enzymes and DNA–DNA homology. Yeast 6, 299–310.
Smith, M.Th., C. Shann, W.H. Batenburg-van der Vegte, R. Schmitt, E. Wehrli, H.J. Roeijmans and G.W. van Eijk. 1992. *Botryozyma nematodophila* gen. nov., spec. nov. (Candidaceae). Antonie van Leeuwenhoek 61, 277–284.
Smith, M.Th., G.A. Poot, W.H. Batenburg-van der Vegte and J.P. van der Walt. 1995a. Species delimitation in the genus *Lipomyces* by nuclear genome comparison. Antonie van Leeuwenhoek 68, 75–87.
Smith, M.Th., J.P. van der Walt and W.H. Batenburg-van der Vegte. 1995b. *Babjevia* gen. nov. – a new genus of the Lipomycetaceae. Antonie van Leeuwenhoek 67, 177–179.
Smith, M.Th., A.W.A.M. de Cock, G.A. Poot and H.Y. Steensma. 1995c. Genome comparisons in the yeast-like fungal genus *Galactomyces* Redhead et Malloch. Int. J. Syst. Bact. 45, 826–831.
Smith, M.Th., G.A. Poot and A.W.A.M. de Cock. 2000. Re-examination of some species of the genus *Geotrichum* Link:Fr. Antonie van Leeuwenhoek 77, 71–81.
Smith, M.Th., V. Robert, G.A. Poot, W. Epping and A.W.A.M. de Cock. 2005. Taxonomy and phylogeny of the ascomycetous yeast genus *Zygoascus*, with proposal of *Zygoascus meyerae* sp. nov. and related anamorphic varieties. Int. J. Syst. Evol. Microbiol. 55, 1353–1363.
Smith, R.A., M.J. Duncan and D.T. Moir. 1985. Heterologous protein secretion from yeast. Science 229, 1219–1224.
Smits, G.J., L.R. Schenkman, S. Brul, J.R. Pringle and F.M. Klis. 2006. Role of cell-cycle-regulated expression in the localized incorporation of cell-wall proteins in yeast. Mol. Biol. Cell 17, 3267–3280.
Smolinski, M.S., M.A. Hamburg and J. Lederberg. 2003. Microbial Threats to Health: Emergence, Detection, and Response. National Academies Press, Washington, DC.
Snel, B., P. Bork and M.A. Huynen. 1999. Genome phylogeny based on gene content. Nat. Genet. 21, 108–110.
Snel, B., M.A. Huynen and B.E. Dutilh. 2005. Genome trees and the nature of genome evolution. Annu. Rev. Microbiol. 59, 191–209.
Snell, T.W., S.E. Brogdon and M.B. Morgan. 2003. Gene expression profiling in ecotoxicology. Ecotoxicology 12, 475–483.
Snell, W.H., and E.A. Dick. 1957. A Glossary of Mycology. Harvard University Press, Cambridge, MA.
Snider, R., and C.L. Kramer. 1974a. Polyacrylamide gel electrophoresis and numerical taxonomy of *Taphrina caerulescens* and *T. deformans*. Mycologia 66, 750–753.
Sniegowski, P.D., P.G. Dombrowski and E. Fingerman. 2002. *Saccharomyces cerevisiae* and *Saccharomyces paradoxus* coexist in a natural woodland site in North America and display different levels of reproductive isolation from European conspecifics. FEMS Yeast Res. 1, 299–306.
Snowdon, E.M., M.C. Bowyer, P.R. Grbin and P.K. Bowyer. 2006. Mousy off-flavor: a review. J. Agric. Food Chem. 54, 6465–6474.
Soares, C.A., M. Maury, F.C. Pagnocca, F.V. Araujo, L.C. Mendonça-Hagler and A.N. Hagler. 1997. Ascomycetous yeasts from tropical intertidal dark mud of southeast Brazilian estuaries. J. Gen. Appl. Microbiol. 43, 265–272.
Soccol, C.R., L.P.S. Vandenberghe, C. Rodrigues and A. Pandey. 2006. New perspectives for citric acid production and application. Food Technol. Biotechnol. 44, 141–149.
Socias Amorós, A., C. Ramírez Gomez and R. Genestar Serra. 1954a. Una nueva especie de *Endomycopsis*: *Endomycopsis balearica* nov. sp. Aislada de concentrado de tanino de encina. Microbiol. Esp. 7, 107–110.
Socias Amorós, A., C. Ramírez Gomez and F. Peláez Campomanes. 1954b. Una nueva especie de *Debaryomyces*: el *Debaryomyces toletanus* nov. sp. Microbiol. Esp. 7, 111–114.
Sodoyer, R. 2004. Expression systems for the production of recombinant pharmaceuticals. BioDrugs 18, 51–62.
Sokal, R.R., and C.D. Michener. 1958. A statistical method for evaluating systematic relationships. Univ. Kansas Sci. Bull. 28, 1409–1438.
Solieri, L., S. Landi, L. de Vero and P. Giudici. 2006. Molecular assessment of indigenous yeast population from traditional balsamic vinegar. J. Appl. Microbiol. 101, 63–71.
Solieri, L., S. Cassanelli and P. Giudici. 2007. A new putative *Zygosaccharomyces* yeast species isolated from traditional balsamic vinegar. Yeast 24, 403–417.
Soll, D.R. 2000. The ins and outs of DNA fingerprinting the infectious fungi. Clin. Microbiol. Rev. 13, 332–370.
Soll, D.R. 2006. The mating-type locus and mating of *Candida albicans* and *Candida glabrata*. In: J. Heitman, S.G. Filler, J. E. Edwards, Jr. and A.P. Mitchell (Eds), Molecular Principles of Fungal Pathogenesis. ASM Press, Washington, DC, pp. 89–112.
Soltis, D.E., V.A. Albert, V. Savolainen, K. Hilu, Y.L. Qiu, M.W. Chase, J.S. Farris, S. Stefanovic, D.W. Rice, J.D. Palmer and P.S. Soltis. 2004. Genome-scale data, angiosperm

relationships, and "ending incongruence": a cautionary tale in phylogenetics. Trends Plant Sci. 9, 477–483.
Soltis, D.E., M.A. Gitzendanner and P.S. Soltis. 2007. A 567-taxon data set for angiosperms: the challenges posed by Bayesian analyses of large data sets. Int. J. Plant Sci. 168, 137–157.
Sonck, C.E. 1974. *Candida savonica* sp. nov. Antonie van Leeuwenhoek 40, 543–545.
Sonck, C.E., and D. Yarrow. 1969. Two new yeast species isolated in Finland. Antonie van Leeuwenhoek 35, 172–177.
Soneda, M. 1959. Studies on animal-dung inhabiting yeasts. Nagaoa, Mycol. J. Nagao Inst. 6, 1–24.
Soneda, M. 1960. On a new yeast genus *Wickerhamia*. Nagaoa, Mycol. J. Nagao Inst. 7, 9–13.
Soneda, M. 1962. An additional paper on animal-dung inhabiting yeasts and on the symbiosis with an amoeba. Trans. Mycol. Soc. Jpn 3, 36–42.
Soneda, M., and S. Uchida. 1971. A survey on the yeasts. Bull. Nat. Sci. Mus. Tokyo 14, 438–459.
Song, K.H., J.K. Lee, J.Y. Song, S.G. Hong, H. Baek, S.Y. Kim and H.H. Hyun. 2002. Production of mannitol by a novel strain of *Candida magnoliae*. HH–01. Biotech. Lett. 24, 9–12.
Soni, S.K., I.K. Sandhu, K.S. Bath, U.C. Banerjee and P.R. Patnaik. 1996. Extracellular amylase production by *Saccharomycopsis capsularis* and its evaluation for starch saccharification. Folia Microbiol. 41, 243–248.
Souciet, J.L., B. Dujon, C. Gaillardin, M. Johnston, P.V. Baret, P. Cliften, D.J. Sherman, J. Weissenbach, E. Westhof, P. Wincker, C. Jubin, J. Poulain, V. Barbe, B. Ségurens, F. Artiguenave, V. Anthouard, B. Vacherie, M.E. Val, R.S. Fulton, P. Minx, R. Wilson, P. Durrens, G. Jean, C. Marck, T. Martin, M. Nikolski, T. Rolland, M.L. Seret, S. Casarégola, L. Despons, C. Fairhead, G. Fischer, I. Lafontaine, V. Leh, M. Lemaire, J. de Montigny, C. Neuvéglise, A. Thierry, I. Blanc-Lenfle, C. Bleykasten, J. Diffels, E. Fritsch, L. Frangeul, A. Goëffon, N. Jauniaux, R. Kachouri-Lafond, C. Payen, S. Potier, L. Pribylova, C. Ozanne, G.F. Richard, C. Sacerdot, M.L. Straub and E. Talla. 2009. Comparative genomics of protoploid Saccharomycetaceae. Genome Res. 19, 1696–1709.
Sougioultzis, S., S. Simeonidis, K.R. Bhaskar, X.H. Chen, P.M. Anton, S. Keates, C. Pothoulakis and C.P. Kelly. 2006. *Saccharomyces boulardii* produces a soluble anti-inflammatory factor that inhibits NK-kappa B-mediated IL-8 gene expression. Biochem. Biophys. Res. Commun. 343, 69–76.
Soundararajan, S., G. Jedd, X. Li, M. Ramos-Pamploña, N.H. Chua and N.I. Naqvi. 2004. Woronin body function in *Magnaporthe grisea* is essential for efficient pathogenesis and for survival during nitrogen starvation stress. Plant Cell 16, 1564–1574.
Sousa, M.J., L. Miranda, M. Corte-Real and C. Leao. 1996. Transport of acetic acid in *Zygosaccharomyces bailii* – effects of ethanol and their implications on the resistance of the yeast to acidic environments. Appl. Environ. Microbiol. 62, 3152–3157.
Sousa, M.J., F. Rodrigues, M. Corte-Real and C. Leao. 1998. Mechanisms underlying the transport and intracellular metabolism of acetic acid in the presence of glucose in the yeast *Zygosaccharomyces bailii*. Microbiology 144, 665–670.
Sousa-Dias, S., T. Goncalves, J.S. Leyva, J.M. Peinado and M.C. Loureiro-Dias. 1996. Kinetics and regulation of fructose and glucose transport systems are responsible for fructophily in *Zygosaccharomyces bailii*. Microbiology 142, 1733–1738.
Spaaij, F., G. Weber, J.P. van der Walt and F. Oberwinkler. 1990. *Myxozyma udenii* sp. nov. (Candidaceae), a new yeast isolated from the rhizosphere of *Mangifera indica*. Syst. Appl. Microbiol. 13, 182–185.
Spaaij, F., G. Weber, H.J. Roeijmans, G.W. van Eijk and F. Oberwinkler. 1991. *Fellomyces horovitziae* sp. nov., a new basidiomycetous yeast species isolated from a *Xenasmatella* basidiocarp. Antonie van Leeuwenhoek 59, 293–298.
Spaaij, F., G. Weber and J.P. van der Walt. 1992a. *Myxozyma sirexii* sp. nov. (Candidaceae), a new yeast isolated from frass of the woodwasp *Sirex juvencus* L. Syst. Appl. Microbiol. 15, 427–431.
Spaaij, F., G. Weber, J.P. van der Walt and F. Oberwinkler. 1992b. *Myxozyma neotropica* sp. nov. (Candidaceae), a new yeast species from Costa Rica. Antonie van Leeuwenhoek 62, 261–265.
Spaaij, F., G. Weber, T. Aoki and J.P. van der Walt. 1993a. *Myxozyma nipponensis* sp. nov. (Candidaceae), a new species recovered from frass of *Ips typographus* f. *japonicus* Niijima. J. Gen. Appl. Microbiol. 39, 521–528.
Spaaij, F., G. Weber and M.Th. Smith. 1993b. *Myxozyma vanderwaltii* sp. nov. (Candidaceae), a new yeast species isolated from a flower of *Protea repens* (L.) L. Antonie van Leeuwenhoek 63, 17–21.
Spaaij, F., J. Wink, W. Stahl, J.P. van der Walt and G. Weber-Spaaij. 1998. *Myxozyma neglecta* sp. nov. (Candidaceae), a new yeast species from South Africa. Antonie van Leeuwenhoek 73, 143–146.
Spadaro, D., and M.L. Gullino. 2004. State of the art and future prospects of the biological control of postharvest fruit diseases. Int. J. Food Microbiol. 91, 185–194.
Spatafora, J.W., T.G. Mitchell and R. Vilgalys. 1995. Analysis of genes coding for small-subunit rRNA sequences in studying phylogenetics of dematiaceous fungal pathogens. J. Clin. Microbiol. 33, 1322–1326.
Speed, B., and D. Dunt. 1995. Clinical and host differences between infections with the two varieties of *Cryptococcus neoformans*. Clin. Infect. Dis. 2, 28–34.
Spellberg, B.J., S.G. Filler and J.E. Edwards Jr. 2006. Current treatment strategies for disseminated candidiasis. Clin. Infect. Dis. 42, 244–251.
Spencer, D.M., J.F.T. Spencer, L. Defigueroa and H. Heluane. 1992. Yeasts associated with rotting citrus fruits in Tucuman, Argentina. Mycol. Res. 96, 891–892.
Spencer, D.M., J.F.T. Spencer, L.I. de Figueroa, O. Garro and E. Fengler. 1996. Yeasts associated with pods and exudates of algarrobo trees (*Prosopis* spp.) and species of columnar cacti in northwest Argentina. Appl. Microbiol. Biotechnol. 44, 736–739.
Spencer, J.F.T., and P.A.J. Gorin. 1968. Mannose-containing polysaccharides of the apiculate yeasts *Nadsonia*, *Hanseniaspora*, *Kloeckera* and *Saccharomycodes*, and their use as an aid in classification. J. Bacteriol. 96, 180–183.
Spencer, J.F.T., H.J. Phaff and N.R. Gardner. 1964. *Metschnikowia kamienskii*, sp. n., a yeast associated with brine shrimp. J. Bacteriol. 88, 758–762.
Spencer, J.F.T., P.A.J. Gorin and A.P. Tulloch. 1970. *Torulopsis bombicola* sp. n. Antonie van Leeuwenhoek 36, 129–133.

Spencer, J.F.T., D.M. Spencer, C. Bizeau, A. Vaughan-Martini and A. Martini. 1985. The use of mitochondrial mutants in hybridization of industrial yeast strains. V. Relative parental contributions to the genomes of interspecific and intergeneric yeast hybrids obtained by protoplast fusion, as determined by DNA reassociation. Curr. Genet. 9, 623–625.

Spencer, J.F.T., A.L. Ragout de Spencer and C. Laluce. 2002. Non-conventional yeasts. Appl. Microbiol. Biotechnol. 58, 147–156.

Spencer-Martins, I. 1982. Extracellular isoamylase produced by the yeast *Lipomyces kononenkoae*. Appl. Environ. Microbiol. 44, 1253–1257.

Spencer-Martins, I. 1983. Bioconversion de amido per la levedura *Lipomyces kononenkoae*. PhD Thesis, New University of Lisbon, Caparica.

Spencer-Martins, I., and N. van Uden. 1982. The temperature profile of growth, death and yield of the starch-converting yeast *Lipomyces kononenkoae*. Z. Allg. Mikrobiol. 22, 503–505.

Špírek, M., J. Yang, C. Groth, R.F. Petersen, R.B. Langkjær, E.S. Naumova, P. Sulo, G.I. Naumov and J. Piškur. 2003. High rate evolution of *Saccharomyces* sensu lato chromosomes. FEMS Yeast Res. 3, 363–373.

Spiropoulos, A.J., J. Tanaka, I. Flerianos and L. Bisson. 2000. Characterization of hydrogen sulfide in commercial and natural wine isolate of *Saccharomyces*. Am. J. Enol. Viticult. 51, 233–248.

Spok, A. 2006. Safety regulations of food enzymes. Food Technol. Biotechnol. 44, 197–209.

Sreekrishna, K., and K.E. Kropp. 1996. *Pichia pastoris*. In: K. Wolf (Ed.), Nonconventional Yeasts in Biotechnology. A Handbook. Springer, Berlin, pp. 203–253.

Srikantha, T., S.A. Lachke and D.R. Soll. 2003. Three mating type-like loci in *Candida glabrata*. Eukaryot. Cell 2, 328–340.

Stadelmann, F. 1975. A new species of the genus *Bullera* Derx. Antonie van Leeuwenhoek 41, 575–582.

Stadler, B., and T. Müller. 1996. Aphid honeydew and its effect on the phyllosphere microflora of *Picea abies* (L.) Karst. Oecologia 108, 771–776.

Stahl, D.A., and J.M. Tiedje. 2002. Microbial ecology and genomics: a crossroads of opportunity. A report from the American Academy of Microbiology. ASM, Washington, DC, 32pp.

Stahl, U., and K. Esser. 1976. Genetics of fruit body production in higher Basidiomycetes. 1. Monokaryotic fruiting, its correlation with dikaryotic fruiting in *Polyporus ciliatus*. Mol. Gen. Genet. 148, 183–197.

Staib, F. 1962. *Cryptococcus neoformans* und *Guizotia abyssinica* (syn. *G. oleifera* D.C.) (Farbereaktion für C. *neoformans*). Z. Hyg. 148, 466–475.

Staib, F. 1963. Zur Kreatinin-Kreatin Assimilation in der Hefepilzdiagnostik. Zentralbl. Bakteriol. Parasitenkd., Abt. I, Orig. 191, 429–432.

Staib, F. 1971. Plants as a substratum for growth of *Cryptococcus neoformans*. Zbl. Bakt. Hyg. I. Abt. Orig. A 218, 486–495.

Staib, F. 1999. The green colour effect (GCE) of the killer strain *Cryptococcus laurentii* CBS 139 on Staib agar. Mycoses 42, 103–106.

Staib, F., M. Seibold, E. Antweiler and B. Frölich. 1989. Staib agar supplemented with a triple antibiotic combination for the detection of *Cryptococcus neoformans* in clinical specimens. Mycoses 32, 448–452.

Staib, P., and J. Morschhauser. 1999. Chlamydospore formation on Staib agar as a species-specific characteristic of *Candida dubliniensis*. Mycoses 42, 521–524.

Staib, P., and J. Morschhauser. 2007. Chlamydospore formation in *Candida albicans* and *Candida dubliniensis* – an enigmatic developmental programme. Mycoses 50, 1–12.

Stamatakis, A. 2006. RAxML-VI-HPC: maximum likelihood-based phylogenetic analyses with thousands of taxa and mixed models. Bioinformatics 22, 2688–2690.

Stamatakis, A., P. Hoover and J. Rougemont. 2008. A rapid bootstrap algorithm for RAxML webservers. Syst. Biol. 57, 758–771.

Stansfield, I. and M.J.R. Stark (Eds). 2007. Yeast Gene Analysis. Methods in Microbiology, Vol. 36. 2nd edn. Elsevier, Amsterdam, pp. 1–700.

Stark, D., T. Munch, B. Sonnleitner, I.W. Marison and U. von Stockar. 2002. Extractive bioconversion of 2-phenylethanol from L-phenylalanine by *Saccharomyces cerevisiae*. Biotechnol. Prog. 18, 514–523.

Stark, M.J.R., A. Boyd, A.J. Mileham and M.A. Romanos. 1990. The plasmid encoded killer system of *Kluyveromyces lactis*: a review. Yeast 6, 1–29.

Starmer, W.T. 1981. The evolutionary ecology of yeasts found in the decaying stems of cacti. In: G.G. Stewart and I. Russell (Eds), Current Developments in Yeast Research. Pergamon Press, Toronto, pp. 493–498.

Starmer, W.T. 1982. Associations and interactions among yeasts, *Drosophila* and their habitats. In: J.S.F. Barker and W.T. Starmer (Eds), Ecological Genetics and Evolution: The Cactus–Yeast–*Drosophila* model system. Academic Press, Sydney, pp. 159–174.

Starmer, W.T., and V. Aberdeen. 1990. The nutritional importance of pure and mixed cultures of yeasts in the development of *Drosophila mulleri* larvae in *Opuntia* tissues and its relationship to host plant shifts. In: J.S.F. Barker, W.T. Starmer and R.J. MacIntyre (Eds), Ecological and Evolutionary Genetics of *Drosophila*. Plenum Publishing Co., New York, pp. 145–160.

Starmer, W.T., and J.S.F. Barker. 1986. Ecological genetics of the Adh-1 locus of *Drosophila buzzatii*. Biol. J. Linn. Soc. 28, 373–385.

Starmer, W.T., and J.C. Fogleman. 1986. Coadaptation of *Drosophila* and yeasts in their natural habitat. J. Chem. Ecol. 12, 1035–1053.

Starmer, W.T., and H.J. Phaff. 1983. Analysis of the community structure of yeasts associated with the decaying stems of cactus. II. *Opuntia* species. Microb. Ecol. 9, 247–259.

Starmer, W.T., H.J. Phaff, M. Miranda and M.W. Miller. 1978a. *Pichia cactophila*, a new species of yeast found in decaying tissue of cacti. Int. J. Syst. Bacteriol. 28, 318–325.

Starmer, W.T., H.J. Phaff, M. Miranda and M.W. Miller. 1978b. *Pichia amethionina*, a new heterothallic yeast associated with the decaying stems of cereoid cacti. Int. J. Syst. Bacteriol. 28, 433–441.

Starmer, W.T., H.J. Phaff, M. Miranda, M.W. Miller and J.S.F. Barker. 1979. *Pichia opuntiae*, a new heterothallic species of yeast in the decaying cladodes of *Opuntia inermis* and

in the necrotic tissue of cereoid cacti. Int. J. Syst. Bacteriol. 29, 159–167.
Starmer, W.T., H.W. Kircher and H.J. Phaff. 1980a. Genetics and speciation of host plant specific yeasts. Evolution 34, 137–146.
Starmer, W.T., H.J. Phaff, M. Miranda, M.W. Miller and W.B. Heed. 1982. The yeast flora associated with the decaying stems of columnar cacti and *Drosophila* in North America. Evol. Biol. 14, 269–295.
Starmer, W.T., H.J. Phaff, J. Tredick, M. Miranda and V. Aberdeen. 1984. *Pichia antillensis*, a new species of yeast associated with necrotic stems of cactus in the Lesser Antilles. Int. J. Syst. Bacteriol. 34, 350–354.
Starmer, W.T., J.S.F. Barker, H.J. Phaff and J.C. Fogleman. 1986. The adaptations of *Drosophila* and yeasts: their interactions with the volatile, 2-propanol, in the cactus–microorganism–*Drosophila* model system. Aust. J. Biol. Sci. 39, 69–77.
Starmer, W.T., M.-A. Lachance and H.J. Phaff. 1987a. A comparison of yeast communities found in necrotic tissue of cladodes and fruits of *Opuntia stricta* on islands in the Caribbean Sea and where introduced into Australia. Microb. Ecol. 14, 179–192.
Starmer, W.T., P.F. Ganter, V. Aberdeen, M.A. Lachance and H.J. Phaff. 1987b. The ecological role of killer yeasts in natural communities of yeasts. Can. J. Microbiol. 33, 783–796.
Starmer, W.T., H.J. Phaff, J.M. Bowles and M.A. Lachance. 1988a. Yeasts vectored by insects feeding on decaying saguaro cactus. Southwest. Nat. 33, 362–363.
Starmer, W.T., F. Peris and A. Fontdevila. 1988b. The transmission of yeasts by *Drosophila buzzatii* during courtship and mating. Anim. Behav. 36, l69l–l695.
Starmer, W.T., V. Aberdeen and M.A. Lachance. 1988c. The yeast community associated with *Opuntia stricta* (Haworth) in Florida, with regard to the moth *Cactoblastis cactorum* (Berg.). Fla. Sci. 51, 7–11.
Starmer, W.T., M.A. Lachance, H.J. Phaff and W.B. Heed. 1990. The biogeography of yeasts associated with decaying cactus tissue in North America, the Caribbean, and Northern Venezuela. Evol. Biol. 24, 253–296.
Starmer, W.T., J.C. Fogleman and M.A. Lachance. 1991. The yeast community of cacti. In: J.H. Andrews and S.S. Hirano (Eds), Microbial Ecology of Leaves. Springer-Verlag, New York, pp. 158–178.
Starmer, W.T., P.F. Ganter and V. Aberdeen. 1992. Geographic distribution and genetics of killer phenotypes for the yeast *Pichia kluyveri* across the United States. Appl. Environ. Microbiol. 58, 990–997.
Starmer, W.T., H.J. Phaff, P.F. Ganter and M.A. Lachance. 2001. *Candida orba* sp. nov., a new cactus-specific yeast species from Queensland, Australia. Int. J. Syst. Evol. Microbiol. 51, 699–705.
Starmer, W.T., R.A. Schmedicke and M.A. Lachance. 2003. The origin of the cactus-yeast community. FEMS Yeast Res. 3, 441–448.
Starmer, W.T., J.W. Fell, C.M. Catranis, V. Aberdeen, L. Ma, S. Zhou and S.O. Rogers. 2005a. Yeasts in the genus *Rhodotorula* recovered from the Greenland ice sheet. In: S.O. Rogers and J.D. Castello (Eds), Life in Ancient Ice. Princeton University Press, Princeton, NJ, pp. 181–195.
Starmer, W.T., M.A. Lachance and V. Aberdeen. 2005b. The biogeographic diversity of cactophilic yeasts. In: C. Rosa and G. Peter (Eds), Biodiversity and Ecophysiology of Yeasts. Springer-Verlag, Berlin.
Statzell-Tallman, A. 1998. *Sterigmatosporidium* Kraepelin and Schulze. In: C.P. Kurtzman and J.W. Fell (Eds), The Yeasts, A Taxonomic Study, 4th edn. Elsevier, Amsterdam, pp. 700–702.
Statzell-Tallman, A.C., and J.W. Fell. 1998a. *Sympodiomyces* Fell & Statzell. In: C.P. Kurtzman and J.W. Fell (Eds), The Yeasts, A Taxonomic Study, 4th edn. Elsevier, Amsterdam, pp. 603–604.
Statzell-Tallman, A., and J.W. Fell. 1998b. *Sporidiobolus* Nyland. In: C.P. Kurtzman and J.W. Fell (Eds), The Yeasts, A Taxonomic Study, 4th edn. Elsevier, Amsterdam, pp. 693–699.
Statzell-Tallman, A., C. Belloch and J.W. Fell. 2008. *Kwoniella mangroviensis* gen. nov., sp. nov. (Tremellales, Basidiomycota), a teleomorphic yeast from mangrove habitats in the Florida Everglades and Bahamas. FEMS Yeast Res. 8, 103–113.
Statzell-Tallman, A., G. Scorzetti and J.W. Fell. 2010. Three species of yeasts: *Candida spencermartinsiae, Candida taylori* and *Pseudozyma abaconensis* spp. nov. from mangrove and coral reef ecosystems. Int. J. Syst. Evol. Microbiol. 60, 1978–1984.
Stautz, W. 1931. Beiträge zur Schleimflussfrage. Phytopathol. Z. 3, 163–229.
Steel, M. 1994. Recovering a tree from the Markov leaf colourations it generates under a Markov model. Appl. Math. Lett. 7, 19–23.
Steels, H. 2005. The "forensic" ecology of soft drinks spoilage yeasts. PhD Thesis, University of Nottingham.
Steels, H., S.A. James, I.N. Roberts and M. Stratford. 1999a. *Zygosaccharomyces lentus*: a significant new osmophillic, preservative-resistant spoilage yeast, capable of growth at low temperature. J. Appl. Microbiol. 87, 520–527.
Steels, H., C.J. Bond, M.D. Collins, I.N. Roberts, M. Stratford and S.A. James. 1999b. *Zygosaccharomyces lentus* sp. nov., a new member of the yeast genus *Zygosaccharomyces* Barker. Int. J. Syst. Bacteriol. 49, 319–327.
Steels, H., M. Stratford, S.A. James, I.N. Roberts and R.R. Davenport. 2000a. Taxonomy, type strains and representative strains of *Zygosaccharomyces* spoilage yeasts evaluated by cluster analysis of preservative resistance. In: J.P. van Dijken and W.A. Scheffers (Eds), Abstracts 10th Int. Symp. Yeasts. Delft University Press, pp. 189–190.
Steels, H., S.A. James, I.N. Roberts and M. Stratford. 2000b. Sorbic acid resistance: the inoculum effect. Yeast 16, 1173–1183.
Steels, H., S.A. James, C.J. Bond, I.N. Roberts and M. Stratford. 2002. *Zygosaccharomyces kombuchaensis*: the physiology of a new species related to the spoilage yeasts *Zygosaccharomyces lentus* and *Zygosaccharomyces bailii*. FEMS Yeast Res. 2, 113–121.
Steenbergen, J.N., H.A. Shuman and A. Casadevall. 2001. *Cryptococcus neoformans* interactions with amoebae suggest an explanation for its virulence and intracellular pathogenic strategy in macrophages. Proc. Natl. Acad. Sci. USA 98, 15245–15250.
Steenbergen, J.N., J.D. Nosanchuk, S.D. Malliaris and A. Casadevall. 2003. *Cryptococcus neoformans* virulence is enhanced after growth in the genetically malleable host *Dictyostelium discoideum*. Infect. Immun. 71, 4862–4872.

Stefanovic, S., D.W. Rice and J.D. Palmer. 2004. Long branch attraction, taxon sampling, and the earliest angiosperms: *Amborella* or monocots? BMC Evol. Biol. 4, 35.

Steger, C.L.C., and M.G. Lambrechts. 2000. The selection of yeast strains for the production of premium quality South African brandy base products. J. Ind. Microbiol. Biotechnol. 24, 431–440.

Steiman, R., P. Guiraud, L. Sage and F. Seigle-Murandi. 1997. Soil mycoflora from Dead Sea oases of Ein Gedi and Einot Zuquim (Israel). Antonie van Leeuwenhoek 72, 261–270.

Steinberg, G. 2000. The cellular roles of molecular motors in fungi. Trends Microbiol. 8, 162–168.

Steiner, J.M. 1924. Étude sur les levures actives des vins valaisins. Thesis, Genève.

Steinhaus, P., and P. Schieberle. 2007. Characterization of the key aroma compounds in soy sauce using approaches of molecular sensory science. J. Agric. Food Chem. 55, 6262–6269.

Steinkraus, K.H. (Ed.) 2004. Industrialization of Indigenous Fermented Foods, 2nd edn. Marcel Dekker, New York.

Steinlauf, R., T. Peery, Y. Koltin and J. Bruenn. 1988. The *Ustilago maydis* virus-encoded toxin, effect of KP6 on cells and spheroplasts. Exp. Mycol. 12, 264–274.

Steinmetz, L.M., C. Scharfe, A.M. Deutschbauer, D. Mokranjac, Z.S. Herman, T. Jones, A.M. Chu, G. Giavever, H. Prokisch, P.J. Oefner and R.W. Davis. 2002. Systematic screen for human disease genes in yeast. Nat. Genet. 31, 400–404.

Steinwascher, K. 1979. Host–parasite interaction as a potential population-regulating mechanism. Ecology 60, 884–890.

Stelling-Dekker, N. 1931. *Saccharomycopsis* Schiönning. Die sporogenen Hefen, vol. Tweede Sectie. Verh. K. Ned. Akad. Wetensch., Afd. Natuurk., Sect. II, Amsterdam, pp. 392–393.

Stender, H., C. Kurtzman, J.J. Hyldig-Nielsen, D. Sørensen, A. Broomer, K. Oliveira, H. Perry-O'Keefe, A. Sage, B. Young and J. Coull. 2001. Identification of *Dekkera bruxellensis* (*Brettanomyces*) from wine by fluorescence *in situ* hybridization using peptide nucleic acid probes. Appl. Environ. Microbiol. 67, 938–941.

Stenderup, A. 1986. Ecology of yeast and epidemiology of yeast infections. Acta Derm. Venereol. Suppl. (Stockh.) 121, 27–37.

Stenderup, A., and A.L. Bak. 1968. Deoxyribonucleic acid base composition of some species within the genus *Candida*. J. Gen. Microbiol. 52, 231–236.

Stenderup, A., and J.B. Thomsen. 1964. Identification of *Candida albicans*. Acta Pathol. Microbiol. Scand. 62, 303–304.

Stenderup, A., S.A. Meyer, A.L. Bak and C. Christiansen. 1972. Taxonomy of *Candida* and *Torulopsis*. In: G. Terui (Ed.), Fermentation Technology Today, Proc. IV Int. Ferment. Symp., Soc. Ferment. Technol., Osaka, Japan, pp. 793–795.

Stepanova, V.P., S.G. Davydenko, V.N. Donich, S.S. Smolina, O. N. Kurennaia and B.F. Iarovoi. 2001. Lysine overproduction mutations in the yeast *Saccharomyces cerevisiae* and its transfection into industrial yeast strains. Genetika 37, 570–573.

Stephanopoulos, G. 2007. Challenges in engineering microbes for biofuels production. Science 315, 801–804.

Stewart, J.D. 2006. Genomes as resources for biocatalysis. Adv. Appl. Microbiol. 59, 31–52.

Stewart-Tull, D.E.S., W.R. Timperley and C.H.W. Horne. 1966. Some immunological observations on the cell walls of yeasts. Sabouraudia 5, 104–109.

Steyn, A.-J., and I.S. Pretorius. 1995. Characterization of a novel alpha-amylase from *Lipomyces kononenkoae* and expression of its gene (LKA1) in *Saccharomyces cerevisiae*. Curr. Genet. 28, 526–533.

Steyn, A.-J., J. Marmur and I.S. Pretorius. 1996. Cloning, mapping and characterization of a genomic copy of the *Lipomyces kononenkoae* alpha-amylase-encoding gene (LKA1). Yeast 12, 925–937.

Stoddard, J.L., and E.C. Cutler. 1916. *Torula* infection in man. Stud. Rock. Inst. Med. Res. 25, 1–98.

Stodola, F.H., and L.J. Wickerham. 1960. Formation of extracellular sphingolipids by microorganisms. II. Structural studies on tetraacetyl-phytosphingosine from the yeast *Hansenula ciferrii*. J. Biol. Chem. 235, 2584–2585.

Stodola, F.H., M.H. Deinema and J.F.T. Spencer. 1967. Extracellular lipids. Bact. Rev. 31, 194–213.

Stolk, A.C., and J.C. Dakin. 1966. *Moniliella*, a new genus of Moniliales. Antonie van Leeuwenhoek 32, 399–409.

Stollarova, V. 1982. The presence of yeasts and yeast-like microorganisms on cherry fruits *Cerasus avium* (L.) Moench. Biol. (Bratislava) 37, 1115–1120.

Stone, J.K., J.D. Polishook and J.F. White. 2004. Endolithic fungi. In: G.M. Mueller, G.F. Bills and M.S. Fostser (Eds), Biodiversity of Fungi. Inventory and Monitoring Methods. Elsevier, Amsterdam, pp. 241–270.

Storck, R. 1966. Nucleotide composition of nucleic acids of fungi. II. Deoxyribonucleic acids. J. Bacteriol. 91, 227–230.

Storck, R., C.J. Alexopoulos and H.J. Phaff. 1969. Nucleotide composition of deoxyribonucleic acid of some species of *Cryptococcus*, *Rhodotorula* and *Sporobolomyces*. J. Bacteriol. 98, 1069–1072.

Stout, D.L., and C.R. Shaw. 1973. Comparative enzyme patterns in *Thamnidium elegans* and *T. anomalum*. Mycologia 65, 803–808.

Stout, D.L., and C.R. Shaw. 1974. Genetic distance among certain species of *Mucor*. Mycologia 66, 969–977.

Straathof, A.J.J., and P. Adlercreutz. 2000. Applied Biocatalysis, 2nd edn. Harwood Scientific Publishers, Amsterdam.

Straathof, A.J.J., S. Panke and A. Schmid. 2002. The production of fine chemicals by biotransformations. Curr. Opin. Biotechnol. 13, 548–556.

Strachan, A.A., R.J. Yu and F. Blank. 1971. Pigment production of *Cryptococcus neoformans* grown with extracts of *Guizotia abyssinica*. Appl. Microbiol. 22, 478–479.

Stratford, M. 2006. Food and beverage spoilage yeasts. In: A. Querol and G.H. Fleet (Eds), Yeasts in Food and Beverages. Springer-Verlag, Berlin, pp. 335–380.

Stratford, M., and S.A. James. 2003. Non-alcoholic beverages and yeasts. In: T. Boekhout and V. Robert (Eds), Yeasts in Food. Beneficial and Detrimental Aspects. Behr's Verlag, Hamburg, pp. 309–345.

Stratford, M., and B.M. Pearson. 1992. Lectin-mediated flocculation of the yeast *Saccharomycodes ludwigii* NCYC 734. Lett. Appl. Microbiol. 14, 214–216.

Stratford, M., P. Morgan and A.H. Rose. 1987. Sulphur dioxide resistance in *Saccharomyces cerevisiae* and *Saccharomycodes ludwigii*. J, Gen. Microbiol. 133, 2173–2179.

Stratford, M., P.D. Hofman and M. Cole. 2000. Fruit juices, fruit drinks and soft drinks. In: B.M. Lund, A.C. Baird-Parker and G.W. Gould (Eds), The Microbiological Quality

and Safety of Food. Aspen Publishers, Gaithersburg, MD, pp. 836–869.

Stratford, M., C.J. Bond, S.A. James, I.N. Roberts and H. Steels. 2002. *Candida davenportii* sp. nov., a potential soft-drinks spoilage yeast isolated from a wasp. Int. J. Syst. Evol. Microbiol. 52, 1369–1375.

Strauss, M.C.A., N.P. Jolly, M.G. Lambrechts and P. van Resemburg. 2001. Screening for the production of extracellular hydrolytic enzymes by non-*Saccharomyces* wine yeasts. J. Appl. Microbiol. 91, 182–190.

Streiblová, E. 1963. On the question of the taxonomy of *Endomycopsis javanensis* (Klöcker) Dekker. Folia Microbiol. (Prague) 8, 170–175.

Streiblová, E. 1971. Cell division in yeasts. In: A. Pérez-Miravette and D. Pelàez (Eds), Recent Advances in Microbiology, Proc. 10th Int. Congress on Microbiology, Mexico City, pp. 131–140.

Strimmer, K., and A. von Haeseler. 1996. Quartet puzzling: a quartet maximum likelihood method for reconstructing tree topologies. Mol. Biol. Evol. 13, 964–969.

Stringer, J.R., and M.T. Cushion. 1998. The genome of *Pneumocystis carinii*. FEMS Immunol. Med. Microbiol. 22, 15–26.

Stringer, J.R., and S.P. Keely. 2001. Genetics of surface antigen expression in *Pneumocystis carinii*. Infect. Immun. 69, 627–639.

Stringer, J.R., S.L. Stringer, J. Zhang, R. Baughman, A.G. Smulian and M.T. Cushion. 1993. Molecular genetic distinction of *Pneumocystis carinii* from rats and humans. J. Eukaryot. Microbiol. 40, 733–741.

Stringer, J.R., A.E. Wakefield, M.T. Cushion and E. Dei-Cas. 1997. *Pneumocystis* taxonomy and nomenclature: an update. J. Eukaryot. Microbiol. 44, 5S–6S.

Stringer, J.R., M.T. Cushion and A.E. Wakefield. 2001. New nomenclature for the genus *Pneumocystis*. J. Eukaryot. Microbiol (Suppl.) 184S–189S.

Stringer, S.L., J.R. Stringer, M.A. Blase, P.D. Walzer and M.T. Cushion. 1989. *Pneumocystis carinii*: sequence from ribosomal RNA implies a close relationship with fungi. Exp. Parasitol. 68, 450–461.

Studier, J.A., and K.J. Keppler. 1988. A note on the neighbor-joining algorithm of Saitou and Nei. Mol. Biol. Evol. 5, 729–731.

Stumm, C., J.M.H. Hermans, E.J. Middelbeek, A.F. Croes and G. J.M.L. de Vries. 1977. Killer-sensitive relationships in yeasts from natural habitats. Antonie van Leeuwenhoek 43, 125–128.

Stündl, U.M., D. Patzak and F. Schauer. 2000. Purification of a soluble cytochrome P450 from *Trichosporon montevideense*. J. Basic Microbiol. 40, 289–292.

Sturm, J. 1829. Deutschlands Flora in Abbildungen nach der Natur, Abt. 3, Vol. 8. Nürnberg.

Su, C.-S. 1990. Genetic and biochemical characterization of some physiologically similar *Candida* species. Dissertation, Georgia State University, Atlanta, GA.

Su, C.-S., and S.A. Meyer. 1991. Characterization of mitochondrial DNA in various *Candida* species: isolation, restriction endonuclease analysis, size, and base composition. Int. J. Syst. Bacteriol. 41, 6–14.

Suárez, R., J.A. Suárez-Lepe, A. Morata and F. Calderón. 2007. The production of ethylphenols in wine by yeasts of the genera *Brettanomyces* and *Dekkera*: a review. Food Chem. 102, 10–21.

Suárez Valles, B., R. Pando Bedriñana, A. Gonzáles García and A. Querol Simón. 2007. A molecular genetic study of natural strains of *Saccharomyces* isolated from Asturian cider fermentations. J. Appl. Microbiol. 103, 778–786.

Suezawa, Y., and M. Suzuki. 2007. Bioconversion of ferulic acid to 4-vinylguaiacol and 4-ethylguaicol and of 4-vinylguaiacol to 4-ethyl guaiacol by halotolerant yeasts belonging to the genus *Candida*. Biosci. Biotechnol. Biochem. 71, 1058–1062.

Sugar, D., J.M. Benbow, K.A. Powers and S.R. Basile. 2003. Effects of sequential calcium chloride, ziram, and yeast orchard sprays on postharvest decay of pear. Plant Dis. 87, 1260–1262.

Sugawara, T., S. Takahashi, M. Osumi and N. Ohno. 2004. Refinement of the structures of cell-wall glucans of *Schizosaccharomyces pombe* by chemical modification and NMR spectroscopy. Carbohydr. Res. 339, 2255–2265.

Sughihara, T.F., L. Kline and M.W. Miller. 1971. Microorganisms of the San Francisco sour dough bread process. I. Yeasts responsible for the leavening action. Appl. Microbiol. 3, 456–458.

Sugita, T., and T. Nakase. 1998a. *Trichosporon japonicum* sp. nov. isolated from the air. Int. J. Syst. Bacteriol. 48, 1425–1429.

Sugita, T., and T. Nakase. 1998b. Molecular phylogenetic study of the basidiomycetous anamorphic yeast genus *Trichosporon* and related taxa based on small subunit ribosomal DNA sequences. Mycoscience 39, 7–13.

Sugita, T., and T. Nakase. 1999. Non-universal usage of the leucine CUG codon and the molecular phylogeny of the genus *Candida*. Syst. Appl. Microbiol. 22, 79–86.

Sugita, T., A. Nishikawa and T. Shinoda. 1992. DNA relatedness among three varieties of *Cryptococcus albidus*. J. Gen. Appl. Microbiol. 38, 83–86.

Sugita, T., A. Nishikawa and T. Shinoda. 1994. Reclassification of *Trichosporon cutaneum* by DNA relatedness by the spectrophotometric method and the chemiluminometric method. J. Gen. Appl. Microbiol. 40, 397–408.

Sugita, T., A. Nishikawa, T. Shinoda, K. Yoshida and M. Ando. 1995. A new species, *Trichosporon domesticum*, isolated from the house of a summer-type hypersensitivity pneumonitis patient in Japan. J. Gen. Appl. Microbiol. 41, 429–436.

Sugita, T., A. Nishikawa, T. Shinoda and T. Kusunoki. 1996. Taxonomic studies on clinical isolates from superficial Trichosporonosis patients by DNA relatedness. Jpn. J. Med. Mycol. 37, 107–110.

Sugita, T., M. Takashima, M. Hamamoto, P. Budhaka and T. Nakase. 1997. *Bensingtonia sakaguchii* sp. nov. isolated from a leaf of *Bischofia javanica* in the Ogasawara Islands. J. Gen. Appl. Microbiol. 43, 231–235.

Sugita, T., A. Nishikawa, R. Ikeda, T. Shinoda, H. Sakashita, Y. Sakai and Y. Yoshizawa. 1998. First report of *Trichosporon ovoides* isolated from the home of a summer-type hypersensitivity pneumonitis patient. Microbiol. Immunol. 42, 475–478.

Sugita, T., K. Kagaya, M. Takashima, M. Suzuki, Y. Fukazawa and T. Nakase. 1999a. A clinical isolate of *Candida palmioleophila* formerly identified as *Torulopsis candida*. Nippon Ishinkin Gakkai Zasshi 40, 21–25.

Sugita, T., C.F. Cañete-Gibas, M. Takashima and T. Nakase. 1999b. Three new species of *Bullera* isolated from leaves in the Ogasawara Islands. Mycoscience 40, 491–501.

Sugita, T., A. Nishikawa, R. Ikeda and T. Shinoda. 1999c. Identification of medically relevant *Trichosporon* species based on sequences of internal transcribed spacer regions and construction of a database for *Trichosporon* identification. J. Clin. Microbiol. 37, 1985–1993.

Sugita, T., M. Takashima, R. Ikeda, T. Nakase and T. Shinoda. 2000a. Intraspecies diversity of *Cryptococcus laurentii* as revealed by sequences of internal transcribed spacer regions and 28S rRNA gene and taxonomic position of *C. laurentii* clinical isolates. J. Clin. Microbiol. 38, 1468–1471.

Sugita, T., M. Takashima, R. Ikeda, T. Nakase and T. Shinoda. 2000b. Phylogenetic and taxonomic heterogeneity of *Cryptococcus humicolus* by analysis of the sequences of the internal transcribed spacer regions and 18S rDNA, and the phylogenetic relationships of *C. humicolus*, *C. curvatus*, and the genus *Trichosporon*. Microbiol. Immunol. 44, 455–461.

Sugita, T., A. Nishikawa, T. Ichikawa, R. Ikeda and T. Shinoda. 2000c. Isolation of *Trichosporon asahii* from environmental materials. Med. Mycol. 38, 27–30.

Sugita, T., R. Ikeda and T. Shinoda. 2001a. Diversity among strains of *Cryptococcus neoformans* var. *gattii* as revealed by sequence analysis of multiple genes and chemotype analysis of capsular polysaccharide. Microbiol. Immunol. 45, 757–768.

Sugita, T., M. Takashima, R. Ikeda, T. Nakase and T. Shinoda. 2001b. Intraspecies diversity of *Cryptococcus albidus* isolated from human as revealed by sequences of internal transcribed spacer regions. Microbiol. Immunol. 45, 291–297.

Sugita, T., T. Ichikawa, M. Matsukura, M. Sueda, M. Takashima, R. Ikeda, A. Nishikawa and T. Shinoda. 2001c. Genetic diversity and biochemical characteristics of *Trichosporon asahii* isolated from clinical specimens, houses of patients with summer-type-hypersensitivity pneumonitis, and environmental materials. J. Clin. Microbiol. 39, 2405–2411.

Sugita, T., M. Takashima, T. Nakase, T. Ichikawa, R. Ikeda and T. Shinoda. 2001d. Two new yeasts, *Trichosporon debeurmannianum* sp. nov. and *Trichosporon dermatis* sp. nov., transferred from the *Cryptococcus humicola* complex. Int. J. Syst. Evol. Microbiol. 51, 1221–1228.

Sugita, T., H. Suto, T. Unno, R. Tsuboi, H. Ogawa, T. Shinoda and A. Nishikawa. 2001e. Molecular analysis of *Malassezia* microflora on the skin of atopic dermatitis patients and healthy subjects. J. Clin. Microbiol. 39, 3486–3490.

Sugita, T., M. Takashima, T. Nakase, T. Ichikawa, T. Shinoda and A. Nishikawa. 2002a. A basidiomycetous anamorphic yeast, *Trichosporon terricola* sp. nov., isolated from soil. J. Gen. Appl. Microbiol. 48, 293–297.

Sugita, T., M. Nakajima, R. Ikeda, T. Matsushima and T. Shinoda. 2002b. Sequence analysis of the ribosomal DNA intergenic spacer 1 regions of *Trichosporon* species. J. Clin. Microbiol. 40, 1826–1830.

Sugita, T., M. Takashima, T. Shinoda, H. Suto, T. Unno, R. Tsuboi, H. Ogawa and A. Nishikawa. 2002c. New yeast species, *Malassezia dermatis*, isolated from patients with atopic dermatitis. J. Clin. Microbiol. 40, 1363–1367.

Sugita, T., M. Saito, T. Ito, Y. Kato, R. Tsuboi, S. Takeuchi and A. Nishikawa. 2003a. The basidiomycetous yeasts *Cryptococcus diffluens* and *C. liquefaciens* colonize the skin of patients with atopic dermatitis. Microbiol. Immunol. 47, 945–950.

Sugita, T., M. Takashima, N. Poonwan, N. Mekha, K. Malaithao, B. Thungmuthasawat, S. Prasarn, P. Luangsook and T. Kudo. 2003b. The first isolation of ustilaginomycetous anamorphic yeasts, *Pseudozyma* species, from patients' blood and a description of two new species: *P. parantarctica* and *P. thailandica*. Microbiol. Immunol. 47, 183–190.

Sugita, T., M. Kodam, M. Saito, T. Ito, Y. Kato, R. Tsuboi and A. Nishikawa. 2003c. Sequence diversity of the intergenic spacer region of the rRNA gene of *Malassezia globosa* colonizing the skin of patients with atopic dermatitis and healthy individuals. J. Clin. Microbiol. 41, 3022–3027.

Sugita, T., M. Takashima, M. Kodama, R. Tsuboi and A. Nishikawa. 2003d. Description of a new species, *Malassezia japonica*, and its detection in patients with atopic dermatitis and healthy subjects. J. Clin. Microbiol. 41, 4695–4699.

Sugita, T., M. Tajima, M. Takashima, M. Amaya, M. Saito, R. Tsuboi and A. Nishikawa. 2004a. A new yeast, *Malassezia yamatoensis*, isolated from a patient with seborrheic dermatitis, and its distribution in patients and healthy subjects. Microbiol. Immunol. 48, 579–583.

Sugita, T., M. Tajima, M. Amaya, R. Tsuboi and A. Nishikawa. 2004b. Genotype analysis of *Malassezia restricta* as the major cutaneous flora in patients with atopic dermatitis and healthy subjects. Microbiol. Immunol. 48, 755–759.

Sugita, T., R. Ikeda and A. Nishikawa. 2004c. Analysis of *Trichosporon* isolates obtained from the houses of patients with summer-type hypersensitivity pneumonitis. J. Clin. Microbiol. 42, 5467–5471.

Sugita, T., K. Kikuchi, K. Makimura, K. Urata, T. Someya, K. Kamei, M. Niimi and Y. Uehara. 2005. *Trichosporon* species isolated from guano samples obtained from bat-inhabited caves in Japan. Appl. Environ. Microbiol. 71, 7626–7629.

Sugita, T., M. Tajima, H. Tsubuku, R. Tsuboi and A. Nishikawa. 2006a. Quantitative analysis of cutaneous *Malassezia* in atopic dermatitis patients using real-time PCR. Microbiol. Immunol. 50, 549–552.

Sugita, T., M. Takashima, N. Poonwan and N. Mekha. 2006b. *Candida pseudohaemulonii* sp. nov., an amphotericin B- and azole-resistant yeast species, isolated from the blood of a patient from Thailand. Microbiol. Immunol. 50, 469–473.

Sugita, T., M. Takashima, A. Sano, K. Nishimura, T. Kinebuchi, S. Yamaguchi and H. Osanai. 2007. *Cryptococcus arboriformis* sp. nov., a novel anamorphic basidiomycetous yeast species isolated from a patient's urine. Microbiol. Immunol. 51, 543–545.

Sugiyama, J. 1998. Relatedness, phylogeny, and evolution of the fungi. Mycoscience 39, 487–511.

Sugiyama, J., and S. Goto. 1967. Coprophilous fungi from Karakorum I. J. Jpn. Bot. 42, 75–84.

Sugiyama, J., and S. Goto. 1969. Mycoflora in core samples from stratigraphic drillings in middle Japan IV. The yeast genera *Candida* Berkhout, *Trichosporon* Behrend, and *Rhodotorula* Harrison em. Lodder from core samples. J. Fac. Sci. Tokyo Univ., Sect. III, Bot. 10, 97–116.

Sugiyama, J., and K. Katumoto. 2008a. Identity of the plasmodial slide mold *Phytoceratiomyxa osmundae* and the lectotypification for *Taphrina osmundae*, the basionym of *Mixia osmundae*. Mycoscience 49, 192–198.

Sugiyama, J., and K. Katumoto. 2008b. Proposal to conserve the name *Mixia* (Basidiomycota) against *Phytoceratiomyxa* (Myxomycetes). Taxon 57, 991–992.

Sugiyama, J., and S.-O. Suh. 1993. Phylogenetic analysis of basidiomycetous yeasts by means of 18S ribosomal RNA sequences: relationship of *Erythrobasidium hasegawianum* and other basidiomycetous yeast taxa. Antonie van Leeuwenhoek 63, 201–209.

Sugiyama, J., and K. Yamatoya. 1990. Electrophoretic comparison of enzymes as a chemotaxonomic aid among *Aspergillus* taxa: (1) *Aspergillus* sects. Ornati and Cremei. In: R.A. Samson and J.I. Pitt (Eds), Modern Concepts in *Penicillium* and *Aspergillus* Classification. Plenum Press, New York, pp. 385–393.

Sugiyama, J., M. Fukagawa, S.-W. Chiu and K. Komagata. 1985. Cellular carbohydrate composition, DNA base composition, ubiquinone systems and diazonium blue B color test in the genera *Rhodosporidium*, *Leucosporidium*, *Rhodotorula* and related basidiomycetous yeasts. J. Gen. Appl. Microbiol. 31, 519–550.

Sugiyama, J., K. Tokuoka, S.-O. Suh, A. Hirata and K. Komagata. 1991. *Sympodiomycopsis*: a new yeast-like anamorph genus with basidiomycetous nature from orchid nectar. Antonie van Leeuwenhoek 59, 95–108.

Sugiyama, J., H. Nishida and S.-O. Suh. 1993. The paradigm of fungal diagnoses and descriptions in the era of molecular systematics: *Saitoella complicata* as an example. In: D.R. Reynolds and J.W. Taylor (Eds), The Fungal Holomorph: Mitotic, Meiotic and Pleomorphic Speciation in Fungal Systematics. CAB International, Wallingford, pp. 261–269.

Sugiyama, J., K. Hosaka and S.O. Suh. 2006. Early diverging Ascomycota: phylogenetic divergence and related evolutionary enigmas. Mycologia 98, 996–1005.

Sugiyama, K., H. Mukae, H. Ishii, M. Ide, H. Ishimoto, T. Kakugawa, K. Hisatomi, S. Nakayama, R. Shirai, Y. Miyazaki and S. Kohno. 2005. Familial summer-type hypersensitivity pneumonitis – case report and review of literature. Nihon Kokyuki Gakkai Zasshi 43, 683–688. In Japanese.

Suh, S.-O., and M. Blackwell. 2004. Three new beetle-associated yeast species in the *Pichia guilliermondii* clade. FEMS Yeast Res. 5, 87–95.

Suh, S.O., and M. Blackwell. 2005. Four new yeasts in the *Candida mesenterica* clade associated with basidiocarp-feeding beetles. Mycologia 97, 167–177.

Suh, S., and M. Blackwell. 2006. Three new asexual arthroconidial yeasts, *Geotrichum carabidarum* sp. nov., *Geotrichum histeridarum* sp. nov., and *Geotrichum cucujoidarum* sp. nov., isolated from the gut of insects. Mycol. Res. 110, 220–228.

Suh, S.-O., and T. Nakase. 1995. Phylogenetic analysis of the ballistosporous anamorphic genera *Udeniomyces* and *Bullera*, and related basidiomycetous yeasts, based on 18S rDNA sequences. Microbiology 141, 901–906.

Suh, S.-O., and J. Sugiyama. 1993. Phylogeny among the basidiomycetous yeasts inferred from small subunit ribosomal DNA sequence. J. Gen. Microbiol. 139, 1595–1598.

Suh, S.-O., and J. Sugiyama. 1994. Phylogenetic placement of the basidiomycetous yeasts *Kondoa malvinella* and *Rhodosporidium dacryoidum*, and the anamorphic yeast *Sympodiomycopsis paphiopedili* by means of 18S gene sequence analysis. Mycoscience 35, 367–375.

Suh, S.-O., A. Hirata, J. Sugiyama and K. Komagata. 1993a. Septal ultrastructure of basidiomycetous yeasts and their taxonomic implications with observations on the ultrastructure for *Erythrobasidium hasegawianum* and *Sympodiomycopsis paphiopedili*. Mycologia 85, 30–37.

Suh, S.-O., T. Kuroiwa and J. Sugiyama. 1993b. Quantitative differences of nuclear DNA content and their taxonomic implications in *Leucosporidium scottii*, *Rhodosporidium toruloides*, and related basidiomycetous yeasts. J. Gen. Appl. Microbiol. 39, 295–302.

Suh, S.-O., C.P. Kurtzman and M. Blackwell. 2001a. The status of *Endomyces scopularum*, a filamentous fungus and two yeasts. Mycologia 83, 317–322.

Suh, S.-O., H. Noda and M. Blackwell. 2001b. Insect symbiosis: derivation of yeast-like endosymbionts within an entompathogenic filamentous lineage. Mol. Biol. Evol. 18, 995–1000.

Suh, S.-O., C.J. Marshall, J.V. McHugh and M. Blackwell. 2003. Wood ingestion by passalid beetles in the presence of xylose-fermenting gut yeasts. Mol. Ecol. 12, 3137–3145.

Suh, S.O., C.M. Gibson and M. Blackwell. 2004a. *Metschnikowia chrysoperlae* sp. nov., *Candida picachoensis* sp. nov. and *Candida pimensis* sp. nov., isolated from the green lacewings *Chrysoperla comanche* and *Chrysoperla carnea* (Neuroptera: Chrysopidae). Int. J. Syst. Evol. Microbiol. 54, 1883–1890.

Suh, S.-O., J.V. McHugh and M. Blackwell. 2004b. Expansion of the *Candida tanzawaensis* yeast clade: 16 novel *Candida* species from basidiocarp-feeding beetles. Int. J. Syst. Evol. Microbiol. 54, 2409–2429.

Suh, S.-O., J.V. McHugh, D.D. Pollock and M. Blackwell. 2005a. The beetle gut: a hyperdiverse source of novel yeasts. Mycol. Res. 109, 261–265.

Suh, S.-O., N.H. Nguyen and M. Blackwell. 2005b. Nine new *Candida* species near *C. membranifaciens* isolated from insects. Mycol. Res. 109, 1045–1056.

Suh, S.-O., N.H. Nguyen and M. Blackwell. 2006a. A yeast clade near *Candida kruisii* uncovered: nine novel *Candida* species associated with basidioma-feeding beetles. Mycol. Res. 110, 1379–1394.

Suh, S.-O., M. Blackwell, C.P. Kurtzman and M.-A. Lachance. 2006b. Phylogenetics of Saccharomycetales, the ascomycete yeasts. Mycologia 98, 1006–1017.

Suh, S.-O., N.H. Nguyen and M. Blackwell. 2008. Yeasts isolated from plant-associated beetles and other insects: seven novel *Candida* species near *Candida albicans*. FEMS Yeast Res. 8, 88–102.

Sukhotina, N.N., E.S. Naumova and G.I. Naumov. 2006. Molecular polymorphism of the yeast *Kluyveromyces dobzhanskii*: geographic populations. Doklady Biochem. Biophys. 409, 236–240.

Sukroongreung, S., and L. Rodrigues de Miranda. 1973. A new aspect of the life cycle of *Candida tropicalis*. Antonie van Leeuwenhoek 39, 65–80.

Sukroongreung, S., K. Kitiniyom, C. Nilakul and S. Tantimavanich. 1998. Pathogenicity of basidiospores of *Filobasidiella neoformans* var. *neoformans*. Med. Mycol. 36, 419–424.

Sul, D., and E.S. Kaneshiro. 2001. *Pneumocystis carinii* f. sp. *carinii* synthesizes de novo four homologs of ubiquinone. J. Eukaryot. Microbiol. 48, 182–187.

Sullivan, D., and D. Coleman. 1998. *Candida dubliniensis*: characteristics and identification. J. Clin. Microbiol. 36, 329–334.

Sullivan, D.J., T.J. Westerneng, K.A. Haynes, D.E. Bennett and D.C. Coleman. 1995. *Candida dubliniensis* sp. nov.: phenotypic and molecular characterization of a novel species associated with oral candidosis in HIV-infected individuals. Microbiology 141, 1507–1521.

Sullivan, D.J., G.P. Moran, E. Pinjon, A. Al-Mosaid, C. Stokes, C. Vaughan and D.C. Coleman. 2004. Comparison of the epidemiology, drug resistance mechanisms, and virulence of *Candida dubliniensis* and *Candida albicans*. FEMS Yeast Res. 4, 369–376.

Sullivan, D.J., G.P. Moran and D.C. Coleman. 2005. *Candida dubliniensis*: ten years on. FEMS Microbiol. Lett. 253, 9–17.

Sullivan, J., and D.L. Swofford. 1997. Are guinea pigs rodents? The importance of adequate models in molecular phylogenetics. J. Mamm. Evol. 4, 77–86.

Sulo, P., M. Laurenčík, S. Poláková, G. Minárik and E. Sláviková. 2009. *Geotrichum bryndzae* sp. nov. species related to the genus *Galactomyces*. Int. J. Syst Evol. Microbiol. 59, 2370–2374.

Suminoe, K., and H. Miwa. 1930. *Saccharomyces eryobotryae* sp. n. Suminoe et Miwa. J. Agric. Chem. Soc. Jpn 6, 721–728. In Japanese.

Summerbell, R.C. 1983. The heterobasidiomycetous yeast genus *Leucosporidium* in an area of temperate climate. Can. J. Bot. 61, 1401–1410.

Sumpradit, T., S. Limtong, W. Yongmanitchai, H. Kawasaki and T. Seki. 2005. *Tetrapisispora namnaonensis* sp. nov., a novel ascomycetous yeast species isolated from forest soil of Nam Nao National Park, Thailand. Int. J. Syst. Evol. Microbiol. 55, 1735–1738.

Sumstine, D.R. 1913. Studies in North American Hyphomycetes – II. The tribe Oosporeae. Mycologia 5, 45–61.

Sunnerhagen, P., and J. Piškur (Eds). 2006. Comparative Genomics Using Fungi as Models. Topics in Current Genetics, Springer, Berlin.

Surawicz, C.M., G.W. Elmer, P. Speelman, L.V. McFarland, J. Chinn and G. van Beele. 1989. Prevention of antibiotic-associated diarrhea by *Saccharomyces boulardii*: a prospective study. Gastroenterology 96, 981–988.

Suriyawattanakul, L., W. Surareungchai, P. Sritongkam, M. Tanticharoen and K. Kirtikara. 2002. The use of co-immobilization of *Trichosporon cutaneum* and *Bacillus licheniformis* for a BOD sensor. Appl. Microbiol. Biotechnol. 59, 40–44.

Surmont, I., A. Gavilenes, J. Vandepitte and E. Eggermont. 1989. *Malassezia furfur* fungaemia in infants receiving intravenous lipid emulsions. A rarity or just underestimated? Eur J. Pediatr. 148, 435–438.

Survase, S.A., I.B. Bajaj and R.S. Singhai. 2006. Biotechnological production of vitamins. Food Technol. Biotechnol. 44, 381–396.

Suter, B.D., Auerbach and I. Stagljar. 2006a. Yeast-based functional genomics and proteomics technologies: the first 15 years and beyond. Biotechniques 40, 625–644.

Suzuki, C., and S. Nikkuni. 1989. Purification and properties of the killer toxin produced by a halotolerant yeast, *Pichia farinosa*. Agric. Biol. Chem. 53, 2599–2604.

Suzuki, C., and S. Nikkuni. 1994. The primary and subunit structure of a novel type killer toxin produced by a halotolerant yeast, *Pichia farinosa*. J. Biol. Chem. 269, 3041–3046.

Suzuki, C., K. Yamada, N. Okada and S. Nikkuni. 1989. Isolation and characterization of halotolerant killer yeasts from fermented foods. Agric. Biol. Chem. 53, 2593–2597.

Suzuki, C., Y. Ando and S. Machida. 2001. Interaction of SMKT, a killer toxin produced by *Pichia farinosa*, with the yeast cell membranes. Yeast 18, 1471–1478.

Suzuki, M., and T. Nakase. 1986. Heterogeneity of ubiquinone systems in the genus *Sporothrix*. J. Gen. Appl. Microbiol. 32, 165–168.

Suzuki, M., and T. Nakase. 1988a. The distribution of xylose in the cells of ballistosporogenous yeasts: application of high performance liquid chromatography without derivatization to the analysis of xylose in whole cell hydrolysates. J. Gen. Appl. Microbiol. 34, 95–103.

Suzuki, M., and T. Nakase. 1988b. Validity of *Candida natalensis* van der Walt et Tscheuschner. Yeast 5, S361–S365.

Suzuki, M., and T. Nakase. 1993. A taxonomic study of *Candida glaebosa* and phenotypically related species *Candida saitoana*, with a description of a new species *Candida* pseudoglaebosa. Bull. Jpn. Fed. Cult. Coll. 9, 120–134.

Suzuki, M., and T. Nakase. 1998. Cellular neutral sugar compositions and ubiquinone systems of the genus *Candida*. Microbiol. Cult. Coll. 14, 49–62.

Suzuki, M., and T. Nakase. 1999. A phylogenetic study of ubiquinone Q8 species of the genera *Candida*, *Pichia*, and *Citeromyces* based on 18S ribosomal DNA sequence divergence. J. Gen. Appl. Microbiol. 45, 239–246.

Suzuki, M., and T. Nakase. 2002. A phylogenetic study of ubiquinone-7 species of the genus *Candida* based on 18S ribosomal DNA sequence divergence. J. Gen. Appl. Microbiol. 48, 55–65.

Suzuki, M., T. Nakase and Y. Fukazawa. 1991. *Candida fragi*, a new species of anamorphic yeast isolated from fermenting strawberry. J. Gen. Appl. Microbiol. 37, 423–429.

Suzuki, M., T. Nakase, H. Mori, H. Toriumi and C.P. Kurtzman. 1992. Chemotaxonomic study on halophilic/halotolerant yeasts in the matured soy sauce mashes. Bull. Jpn. Fed. Cult. Coll. 8, 18–27.

Suzuki, M., T. Nakase and K. Komagata. 1994. *Candida stellimalicola*, a new species of anamorphic yeast isolated from star apple in Thailand. J. Gen. Appl. Microbiol. 40, 115–121.

Suzuki, M., S.-O. Suh, T. Sugita and T. Nakase. 1999. A phylogenetic study on galactose-containing *Candida* species based on 18S ribosomal DNA sequences. J. Gen. Appl. Microbiol. 45, 229–238.

Suzuki, T., Y. Sumino, S. Akiyama and H. Fukada. 1973. Method of producing citric acid. US Patent 3733253.

Suzuki, T., T. Yamaguchi and M. Ishida. 1998. Immobilization of *Prototheca zopfii* in calcium-alginate beads for the degradation of hydrocarbons. Proc. Biochem. 33, 541–546.

Suzuki, Y., and K. Uchida. 1992b. Formation of beta-galactosyl compounds of pyridoxine in growing culture of *Sporobolomyces singularis*. Biochim. Biophys. Acta 1116, 67–71.

Suzuki, Y., and K. Uchida. 1994b. Formation of beta-galactosyl compounds of arabinosylcytosine in growing culture of

Sporobolomyces singularis. Biosci. Biotechnol. Biochem. 58, 639–643.

Suzuki, Y., G.V. Glazko and M. Nei. 2002. Overcredibility of molecular phylogenies obtained by Bayesian phylogenetics. Proc. Natl. Acad. Sci. USA 99, 16138–16143.

Suzzi, G., M. Schirone, M. Martuscelli, M. Gatti, M.E. Fornasari and E. Neviani. 2003. Yeasts associated with Manteca. FEMS Yeast Res. 3, 159–166.

Swann, E.C., and J.W. Taylor. 1993. Higher taxa of basidiomycetes: an 18S rRNA gene perspective. Mycologia 85, 923–936.

Swann, E.C., and J.W. Taylor. 1995a. Toward a phylogenetic systematics of the Basidiomycota: integrating yeasts and filamentous Basidiomycetes using 18S rRNA gene sequences. Stud. Mycol. 38, 147–161.

Swann, E.C., and J.W. Taylor. 1995b. Phylogenetic perspectives on basidiomycete systematics: evidence from the 18S rRNA gene. Can. J. Bot. 73 (Suppl. 1), S862–S868.

Swann, E.C., E.M. Frieders and DJ. McLaughlin. 2001. Urediniomycetes. In: D.J. McLaughlin, E.G. McLaughlin and P.A. Lemke (Eds), Systematics and Evolution. The Mycota XII Part B. Springer Verlag, Berlin, pp. 37–56.

Sweigers, J.H., E.J. Bartowsky, P.A. Henschke and I.S. Pretorius. 2005. Yeast and bacterial modulation of wine aroma and flavor. Aust. J. Grape Wine Res. 11, 139–173.

Swift, J.A., and S.F. Dunbar. 1965. Ultrastructure of *Pityrosporum ovale* and *Pityrosporum canis*. Nature 206, 1174–1175.

Swoboda-Kopec, E., A. Rokosz, A. Sawicka-Grzelak, M. Wroblewska, E. Krawczyk, E. Stelmach and M. Luczak. 2001. Etiologic agents of fungemia in hospitalized patients. Med. Dosw. Mikrobiol. 53, 291–295.

Swofford, D.L., G.J. Olsen, P.J. Waddell and D.M. Hillis. 1996. Phylogenetic Inference. In: D.M. Hillis, C. Moritz and B.K. Mable (Eds), Molecular Systematics. Sinauer Associates, Sunderland, MA, pp. 407–514.

Sydow, H. 1912. *Guilliermondia*, un nouveau genre de la famille des Saccharomycètes à copulation hétérogamique. Ann. Mycol. 10, 347–348.

Sydow, H., and P. Sydow. 1918. Mykologische Mitteilungen. Ann. Mycol. 16, 240–248.

Sydow, H., and P. Sydow. 1919. Mykologische Mitteilungen. Ann. Mycol. 17, 33–47.

Syrop, M., and A. Beckett. 1975. Leaf curl disease of almond caused by *Taphrina deformans*. III. Ultrastructural cytology of the pathogen. Can. J. Bot. 54, 293–305.

Szcebara, F.M., C. Chandelier, C. Villeret, A. Masurel, S. Bourot, C. Dupor, S. Blanchard, A. Groisillier, E. Testet, P. Costaglioli, G. Cauet, E. Degryse, D. Balbuena, J. Winer, T. Achstetter, R. Spagnoli, D. Pompon and B. Dumas. 2003. Total synthesis of hydrocortisone from a simple carbon source in yeast. Nat. Biotechnol. 21, 143–148.

Szép, E., and E.K. Novák. 1963. A new yeast species: *Candida requinyii* n. sp. Acta Bot. Acad. Sci. Hung 9, 447–453.

Sztejnberg, A., Z. Paz, T. Boekhout, A. Gafni and U. Gerson. 2004. A new fungus with dual biocontrol capabilities: reducing the numbers of phytophagous mites and powdery mildew disease damage. Crop Sci. 23, 1125–1129.

Sztejnberg, A., U. Gerson and A. Gafni. 2005. Species of fungi and their use in pest and disease control. Patent pending PCT/IL 03/00059.

Taj-Aldeen, S.J., S.H. Doiphode and X.Y. Han. 2006. *Kodamaea* (*Pichia*) *ohmeri* fungaemia in a premature neonate. J. Med. Microbiol. 55, 237–239.

Taj-Aldeen, S.J., N. Al-Ansari., S. El Shafei, J.F. Meis, I. Curfs-Breuker, B. Theelen and T. Boekhout. 2009. Molecular identification and susceptibility of *Trichosporon* species isolated from clinical specimens in Qatar: isolation of *Trichosporron dohaense* Taj-Aldeen, Meis & Boekhout sp. nov. J. Clin. Microbiol. 47, 1791–1799.

Takada, H., T. Yagi and J.-I. Hiraoka. 1965. Elektronenoptiche Untersuchungen an *Endomycopsis fibuliger* auf festen Nährböden. Protoplasma 59, 494–505.

Takagi, H., F. Matsui, A. Kawaguchi, H. Wu, H. Shimoi and Y. Kubo. 2007. Construction and analysis of self-cloning sake yeasts that accumulate proline. J. Biosci. Bioeng. 103, 377–380.

Takahashi, S., T. Takahashi, Y. Kera, R. Matsunaga, H. Shibuya and R.H. Yamada. 2004. Cloning and expression in *Escherichia coli* of the D-aspartate oxidase gene from the yeast *Cryptococcus humicola* and characterization of the recombinant enzyme. J. Biochem. (Tokyo) 135, 533–540.

Takahashi, S., T. Kakuichi, K. Fujii, Y. Kera and R.H. Yamada. 2005. Physiological role of D-aspartate oxidase in the assimilation and detoxification of D-aspartate in the yeast *Cryptococcus humicola*. Yeast 22, 1203–1212.

Takahashi, S., Y. Yeo, B.T. Greenhagen, T. McMullin, L. Song, J. Maurina-Brunker, R. Rosson, J.P. Noel and J. Chappell. 2007. Metabolic engineering of sequiterpene metabolism in yeast. Biotechnol. Bioeng. 97, 170–181.

Takahashi, T. 1911. Rep. Governm. Inst. Brewing Japan 43, 417.

Takahashi, T., and M. Yukawa. 1915. On the budding fungi of "Shoyu-Moromi" and "Shoyu-Koji". J. Coll. Agric. Imp. Univ. Tokyo 5, 227–261. In Japanese.

Takahata, Y., T. Sugita, M. Hiruma and M. Muto. 2007. Quantitative analysis of *Malassezia* in the scale of patients with psoriasis using a real-time polymerase chain reaction assay. Br. J. Dermatol. 157, 670–673.

Takano, I., and Y. Oshima. 1967. An allele specific and a complementary determinant controlling homothallism in *Saccharomyces oviformis*. Genetics 57, 875–885.

Takano, I., and Y. Oshima. 1970. Mutational nature of an allele-specific conversion of the mating type by the homothallic gene HOα *Saccharomyces*. Genetics 65, 421–427.

Takashima, M., and T. Nakase. 1997. A phylogenetic analysis of three group I introns found in the nuclear small subunit ribosomal RNA gene of the ballistoconidiogenous anamorphic yeast-like fungus *Tilletiopsis flava*. Genes Genet. Syst. 72, 205–214.

Takashima, M., and T. Nakase. 1998. *Bullera penniseticola* sp. nov. and *Kockovaella sacchari* sp. nov., two new yeast species isolated from plants in Thailand. Int. J. Syst. Bacteriol. 48, 1025–1030.

Takashima, M., and T. Nakase. 1999. Molecular phylogeny of the genus *Cryptococcus* and related species based on the sequences of SSU rDNA and internal transcribed spacer regions. Microbiol. Cult. Coll. 15, 35–47.

Takashima, M., and T. Nakase. 2000. Four new species of the genus *Sporobolomyces* isolated from leaves in Thailand. Mycoscience 41, 357–369.

Takashima, M., and T. Nakase. 2001. *Tilletiopsis derxii*, *Tilletiopsis oryzicola* and *Tilletiopsis penniseti*, three new

species of the ustilagionomycetous anamorphic genus *Tilletiopsis* isolated from leaves in Thailand. Antonie van Leeuwenhoek 80, 43–56.

Takashima, M., S.-O. Suh and T. Nakase. 1995a. Phylogenetic relationships among species of the genus *Bensingtonia* and related taxa based on small subunit ribosomal DNA sequences. J. Gen. Appl. Microbiol. 41, 131–141.

Takashima, M., S.-O. Suh and T. Nakase. 1995b. *Bensingtonia musae* sp. nov. isolated from a dead leaf of *Musa paradisiaca* and its phylogenetic relationship among basidiomycetous yeasts. J. Gen. Appl. Microbiol. 41, 143–151.

Takashima, M., M. Hamamoto and T. Nakase. 2000. Taxonomic significance of fucose in the class Urediniomycetes: distribution of fucose in cell wall and phylogeny of urediniomycetous yeasts. Syst. Appl. Microbiol. 23, 63–70.

Takashima, M., T. Deak and T. Nakase. 2001a. Emendation of *Dioszegia* with redescription of *Dioszegia hungarica* and two new combinations, *Dioszegia aurantiaca* and *Dioszegia crocea*. J. Gen. Appl. Microbiol. 47, 75–84.

Takashima, M., T. Sugita, T. Shinoda and T. Nakase. 2001b. Reclassification of the *Cryptococcus humicola* complex. Int. J. Syst. Evol. Microbiol. 51, 2199–2210.

Takashima, M., T. Sugita, T. Shinoda and T. Nakase. 2003. Three new combinations from the *Cryptococcus laurentii* complex: *Cryptococcus aureus*, *Cryptococcus carnescens* and *Cryptococcus peneaus*. Int. J. Syst. Evol. Microbiol. 53, 1187–1194.

Takashima, M., T. Sugita, Y. Toriumi and T. Nakase. 2009. *Cryptococcus tepidarius* sp. nov., a thermotolerant yeast species isolated from a stream from a hot-spring area in Japan. Int. J. Syst. Evol. Microbiol. 59, 181–185.

Takasuka, T., T. Komiyama, Y. Furuichi and T. Watanabe. 1995. Cell wall synthesis specific cytocidal effect of *Hansenula mrakii* toxin-1 on *Saccharomyces cerevisiae*. Cell Mol. Biol. Res. 41, 575–581.

Takeda, I., Iguchi, K., Tsuzuki, K. and Nakano, T. 1972. Method for the cultivation of yeasts in a nutritive medium containing a nonionic surface active agent. US Patent 3,658,647.

Takeo, K., and E. Nakai. 1986. Mode of cell growth of *Malassezia* (*Pityrosporum*) as revealed by using plasma membrane configurations as natural markers. Can. J. Microbiol. 32, 389–394.

Takeo, K., K. Nishimura and M. Miyaji. 1986. Resistance of the neck plasma membrane between the mother and the bud of *Saccharomyces cerevisiae* and *Candida albicans* to amphoterin B-induced deformation. FEMS Microbiol. Lett. 48, 321–324.

Takeuchi, A., A. Shimizu-Ibuka, Y. Nishiyama, K. Mura, S. Okada, C. Tokue and S. Arai. 2006. Purification and characterization of an α-amylase of *Pichia burtonii* isolated from the traditional starter "murcha" in Nepal. Biosci. Biotechnol. Biochem. 70, 3019–3024.

Takishita, K., M. Tsuchiya, J.D. Reimer and T. Maruyama. 2006. Molecular evidence demonstrating the basidiomycetous fungus *Cryptococcus curvatus* is the dominant microbial eukaryote in sediment at the Kuroshima Knoll methane seep. Extremophiles 10, 165–169.

Talavera, G., and J. Castresana. 2007. Improvement of phylogenies after removing divergent and ambiguously aligned blocks from protein sequence alignments. Syst. Biol. 56, 564–577.

Talbot, P.H.B. 1968. Fossilized pre-Patouillardian taxonomy. Taxon 17, 620–628.

Talens, L.T., M.W. Miller and M. Miranda. 1973. Electron micrograph study of the asci and ascospores of *Metschnikowia* Kamienski. J. Bacteriol. 115, 316–322.

Talhari, S., and R. Pradinaud. 2005. Lobomycosis. In: W.G. Merz and R.J. Hay (Eds), Medical Mycology, 10th edn. Hodder Arnold, London, pp. 430–435.

Talice, R.V., and J.E. Mackinnon. 1934. Determinación de algunas cepas argentinas de hongos levuriformes. Bol. Inst. Clin. Quirúrgica 8, 160–167.

Tamaoka, J., Y. Katayama-Fujimura and H. Karaishi. 1993. Analysis of bacterial menaquinone mixtures by high performance liquid chromatography. J. Appl. Bacteriol. 54, 31–36.

Tamaoka, M., and K. Komagata. 1984. Determinatiion of DNA base composition by reversed phase high-performance liquid chromatography. FEMS Microbiol. Lett. 25, 125–128.

Tamura, K., and M. Nei. 1993. Estimation of the number of nucleotide substitution in the control region of mitochondrial DNA in humans and chimpanzees. Mol. Biol. Evol. 10, 512–526.

Tamura, T., K. Ueda, T. Furuta, Y. Goto and K. Fujiwara. 1978. Electron microscopy of spontaneous pneumocystosis in a nude mouse. Jpn. J. Exp. Med. 48, 363–368.

Tanaka, A., and M. Ueda. 1993. Assimilation of alkanes by yeasts – functions and biogenesis of peroxisomes. Mycol. Res. 97, 10–44.

Tanaka, E., K. Shimizu, Y. Imanoshi, F. Yasuda and C. Tanaka. 2008. Isolation of basidiomycetous anamorph yeast-like fungus *Meira argovae* found on Japanese bamboo. Mycoscience 49, 329–333.

Tanaka, J., S. Oda and H. Ohta. 2001. Synthesis of (S)-ibuprofen via enantioselective degradation of racemic ibuprofen with an isolated yeast, *Trichosporon cutaneum* KPY 30802, in an interface bioreactor. J. Biosci. Bioeng. 91, 314–315.

Tanaka, R., K. Nishimura, Y. Imanishi, I. Takahashi, Y. Hata and M. Miyaji. 2003. Analysis of serotype AD strains from F1 progenies between urease-positive- and negative-strains. Jpn. J. Med. Mycol. 44, 293–297.

Tanaka, R., K. Nishimura, K. Kamei and S.Y. Murayama. 2001. Assimilation test of *Malassezia furfur* isolated from the environment. Nippon Ishinkin Gakkai Zasshi 42, 123–126.

Tanaka-Tsuo, F., S. Mizukami-Murata, Y. Murata, T. Nakamura, A. Ando, H. Takagi and J. Shima. 2007. Functional genomics of commercial baker's yeasts that have different abilities for sugar utilization and high-sucrose tolerance under different sugar conditions. Yeast 24, 901–911.

Tang, S.J., K.H. Sun, G.H. Sun, T.Y. Chang, W.L. Wu and G.C. Lee. 2003. A transformation system for the nonuniversal CUGSer codon usage species *Candida rugosa*. J. Microbiol. Methods 52, 231–238.

Tanghe, A., P. van Kijck and J.M. Thevelein. 2003. Determinants of freeze tolerance in microorganisms, physiological importance, and biotechnological applications. Adv. Appl. Microbiol. 53, 129–176.

Tanghe, A., B. Prior and J.M. Thevelein. 2006. Yeast responses to stresses. In: C.A. Rosa and G. Peter (Eds), Biodiversity and Ecophysiology of Yeasts. Springer-Verlag, Berlin, pp. 175–196.

Taniguchi, Y. 1926. Experimentelle Studie über "erosio interdigitalis blastomycetica", besonders über diejenigen bei den

Papierarbeitern in der Provinz Gifu ("Sadare"-Krankheit). Jpn. J. Med. Sci., Trans. XIII. Dermatol. Urol 1, 75–94.

Tanner, F.W. Jr., L.J. Wickerham and J.M. van Lanen. 1948. Biological process for the production of riboflavin. US Patent 2,445,128.

Tarazooie, B., P. Kordbacheh, F. Zaini, K. Zomorodian, F. Saadat, H. Zeraati, Z. Hallaji and S. Rezaie. 2004. Study of the distribution of *Malassezia* species in patients with pityriasis versicolor and healthy individuals in Tehran, Iran. BMC Dermatol. 4, 5.

Tartar, A., D.G. Boucias, J.J. Becnel and B.J. Adams. 2003. Comparison of plastid 16S rRNA (rrn16) genes from *Helicosporidium* spp.: evidence supporting the reclassification of *Helicosporidia* as green algae (Chlorophyta). Int. J. Syst. Evol. Microbiol. 53, 1719–1723.

Tatsumi, C., and H. Katagiri. 1950. Studies on the utilization of pentose by microbiological method. On pentose-assimilable yeasts. Bull. Inst. Chem. Res. Kyoto Univ. 22, 53–61.

Tavanti, A., A.D. Davidson, N.A.R. Gow, M.C.J. Maiden and F.C. Odds. 2005a. *Candida orthopsilosis* and *Candida metapsilosis* spp. nov. to replace *Candida parapsilosis* Groups II and III. J. Clin. Microbiol. 43, 284–292.

Tavanti, A., A.D. Davidson, E.M. Johnson, M.C. Maiden, D.J. Shaw, N.A. Gow and F.C. Odds. 2005b. Multilocus sequence typing for differentiation of strains of *Candida tropicalis*. J. Clin. Microbiol. 43, 5593–5600.

Tavares, S., J. Inácio, Á. Fonseca and C. Oliveira. 2004. Direct detection of *Taphrina deformans* on peach trees using molecular methods. Eur. J. Plant Pathol. 110, 973–982.

Taylor, D.J., and W.H. Piel. 2004. An assessment of accuracy, error, and conflict with support values from genome-scale phylogenetic data. Mol. Biol. Evol. 21, 1534–1537.

Taylor, J., and D.O. Birdwell. 2000. A scanning electron microscopy study of the infection of water oak (*Quercus nigra*) by *Taphrina caerulescens*. Mycologia 92, 309–311.

Taylor, J.W., and K. Wells. 1979. A light and electron microscopic study of mitosis in *Bullera alba* and the histochemistry of some cytoplasmic substances. Protoplasma 98, 31–62.

Taylor, J.W., D.M. Geiser, A. Burt and V. Koufopanou. 1999. The evolutionary biology and population genetics underlying fungal strain typing. Clin. Microbiol. Rev. 12, 126–146.

Taylor, J.W., D.J. Jacobson, S. Kroken, T. Kasuga, D.M. Geiser, D.S. Hibbett and M.C. Fisher. 2000. Phylogenetic species recognition and species concepts in fungi. Fungal Genet. Biol. 31, 21–32.

Taylor, J.W., J. Spatafora, K. O'Donnell, F. Lutzoni, T. James, D.S. Hibbett, D. Geiser, T.D. Bruns and M. Blackwell. 2004. The Fungi. In: J. Cracraft and M.J. Donoghue (Eds), Assembling the Tree of Life. Oxford University Press, Oxford, pp. 171–194.

Taylor, N.W. 1965. Purification of sexual agglutination factor from the yeast *Hansenula wingei* by chromatography and gradient sedimentation. Arch. Biochem. Biophys. 111, 181–186.

Taylor, N.W., and W.L. Orton. 1968. Sexual agglutination in yeast. VII. Significance of the 1.7S component from reduced 5 agglutinin. Arch. Biochem. Biophys. 126, 912–921.

Taysi, I., and N. van Uden. 1964. Occurrence and population densities of yeast species in an estuarine–marine area. Limnol. Oceanogr. 9, 42–45.

Techapun, C., N. Poosaran, M. Watanabe and K. Sasaki. 2003. Thermostable and alkaline-tolerant microbial cellulose-free xylanases produced from agricultural wastes and the properties required for use in pulp bleaching bioprocesses: a review. Process. Biochem. 38, 1327–1340.

Teisseire, P.J. 1994. Chemistry of Fragrant Substances. VCH Publishers, New York.

Teixeira, A.C.P., M.M. Marini, J.R. Nicoli, Y. Antonini, R.P. Martins, M.A. Lachance and C.A. Rosa. 2003. *Starmerella meliponinorum*, a novel ascomycetous yeast species associated with stingless bees. Int. J. Syst. Evol. Microbiol. 53, 339–343.

Teixeira, R.M., D. Cavalheiro, J.L. Ninow and A. Furigo. 2002. Optimization of acetoin production by *Hanseniaspora guilliermondii* using experimental design. Braz. J. Chem. Eng. 19, 181–186.

Teixidó, N., I. Viñas, J. Usall and N. Magan. 1998a. Control of blue mold of apples by preharvest application of *Candida sake* grown in media with different water activity. Phytopathology 88, 960–964.

Teixidó, N., I. Viñas, J. Usall, V. Sanchis and N. Magan. 1998b. Ecophysiological responses of the biocontrol yeast *Candida sake* to water, temperature and pH stress. J. Appl. Microbiol. 84, 192–200.

Teixidó, N., J. Usall and I. Viñas. 1999. Efficacy of preharvest and postharvest *Candida sake* biocontrol treatments to prevent blue mould on apples during cold storage. Int. J. Food Microbiol. 50, 203–210.

Telzak, E.E., R.J. Cote, J.W. Gold, S.W. Campbell and D. Armstrong. 1990. Extrapulmonary *Pneumocystis carinii* infections. Rev. Infect. Dis. 12, 380–386.

Templeton, A.R. 1983. Systematics of basidiomycetes based on 5S rRNA sequences and other data. Nature (London) 303, 731.

Tengku Zainal Mulok, T.E. 1988. Nuclear DNA base composition and base sequence complementarity of recently described *Candida* species and strains of selected species. Thesis, Georgia State University, Atlanta, GA.

Tenney, K., I. Hunt, J. Sweigard, J.I. Pounder, C. McClain, E.J. Bowman and B.J. Bowman. 2000. Hex-1, a gene unique to filamentous fungi, encodes the major protein of the Woronin body and functions as a plug for septal pores. Fungal Genet. Biol. 31, 205–217.

Teo, L.H., and Y.K. Tay. 2006. *Ustilago* species infection in humans. Br. J. Dermatol. 155, 1096–1097.

Teoh, A.L., G. Heard and J. Cox. 2004. Yeast ecology of kombucha fermentation. Int. J. Food Microbiol. 95, 119–126.

Terentiev, Y., U. Breuer, W. Bable and G. Kunze. 2004a. Non-conventional yeasts as producers of polyhydroxyalkanoates – genetic engineering of *Arxula adeninivorans*. Appl. Microbiol. Biotechnol. 64, 376–381.

Terentiev, Y., A.H. Pico, E. Boër, T. Wartmann, J. Klabunde, U. Breuer, W. Babel, M. Suckow, G. Gellissen and G. Kunze. 2004b. A wide-range integrative yeast expression vector system based on *Arxula adeninivorans*-derived elements. J. Ind. Microbiol. Biotechnol. 31, 223–228.

Teunnison, D.J. 1954. Yeasts from freshly combined rough rice stored in a sealed bin. Appl. Microbiol. 2, 215–220.

Teunisson, D.J., H.H. Hall and L.J. Wickerham. 1960. *Hansenula angusta*, an excellent species for demonstration of the

coexistence of haploid and diploid cells in a homothallic yeast. Mycologia 52, 184–188.
Texeira, M.C., P. Duque and I. Sá-Correia. 2007. Environmental genomics: mechanistic insights into toxicity of and resistance to the herbicide 2,4-D. Trends Biotechnol. 25, 363–370.
Thanh, V.N. 2006. *Lipomyces orientalis* sp. nov., a yeast species isolated from soil in Vietnam. Int. J. Syst. Evol. Microbiol. 56, 2009–2013.
Thanh, V.N., M.S. van Dyk and M.J. Wingfield. 2002. *Debaryomyces mycophilus* sp. nov., a siderophore-dependent yeast isolated from woodlice. FEMS Yeast Res. 2, 415–427.
Thanh, V.N., D.A. Hai and M.-A. Lachance. 2003. *Issatchenkia hanoiensis*, a new yeast species isolated from frass of the litchi fruit borer *Conopomorpha cramerella* Snellen. FEMS Yeast Res. 4, 113–117.
Thanh, V.N., M.S. Smit, N. Moleleki and J.W. Fell. 2004. *Rhodotorula cycloclastica* sp. nov., *Rhodotorula retinophila* sp. nov. and *Rhodotorula terpenoidalis* sp. nov., three limonene-utilizing yeasts isolated from soil. FEMS Yeast Res. 4, 857–863.
Thanh, V.N., D.A. Hai and M.-A. Lachance. 2006. *Cryptococcus bestiolae* and *Cryptococcus dejecticola*, two new yeast species isolated from frass of the litchi fruit borer *Conopomorpha sinensis* Bradley. FEMS Yeast Res. 6, 298–304.
Thaysen, A.C., and M. Morris. 1943. Preparation of a giant strain of *Torulopsis utilis*. Nature 152, 526–528.
Theelen, B., M. Silvestri, E. Guého, A. van Belkum and T. Boekhout. 2001. Identification and typing of *Malassezia* yeasts using amplified length polymorphim (AFLP™), random amplified polymorphic DNA (RAPD) and denaturing gradient gel electrophoresis (DGGE). FEMS Yeast Res. 1, 79–86.
Theisen, S., E. Molkenau and M.J. Schmitt. 2000. Wicaltin, a new protein toxin secreted by the yeast *Williopsis californica* and its broad-spectrum antimycotic potential. J. Microbiol. Biotechnol. 10, 547–550.
Thérizol-Ferly, M., M. Kombila, M. Gomez de Diaz, T.H. Duong and D. Richard-Lenoble. 1994. White piedra and *Trichosporon* species in equatorial Africa. I. History and clinical aspects: an analysis of 449 superficial inguinal specimens. Mycoses 37, 249–253.
Thielke, C. 1972. Die dolipore der Basidiomyceten. Arch. Mikrobiol. 82, 31–37.
Thiéry, J.P. 1967. Mise én evidence des polysaccharides sur coupes fines en microscopie électronique. J. Microscopie 6, 987–1018.
Thim, L., M.T. Hansen, K. Norris, I. Hoegh, E. Boel, J. Forstrom, G. Ammerer and N.P. Fiil. 1986. Secretion and processing of insulin precursors in yeast. Proc. Natl. Acad. Sci. USA 83, 6766–6770.
Thomas, C.F. Jr., and A.H. Limper. 2007. Current insights into the biology and pathogenesis of *Pneumocystis* pneumonia. Nat. Rev. Microbiol. 5, 298–308.
Thomas, D.S., and R.R. Davenport. 1985. *Zygosaccharomyces bailii* – a profile of characteristics and spoilage activities. Food Microbiol. 2, 157–169.
Thomas, S. 1993. Yeasts as spoilage organisms in beverages. In: A.H. Rose and J.S. Harrison (Eds), The Yeasts, 2nd edn, Vol. 5. Academic Press, London, pp. 517–561.
Thomas-Hall, S. 2004. Phylogenetic studies of fungi. Part A Physiological and biochemical analysis of novel species from Antarctica. PhD Thesis, University of New England, Australia, pp. 1–178.
Thomas-Hall S.R., Turchetti B., Buzzini P., Branda E., Boekhout T., Theelen B., and Watson K. 2010. Cold-adapted yeasts from Antarctica and the Italian Alps-description of three novel species: Mrakia robertii sp. nov., Mrakia blollopis sp. nov. and Mrakiella niccombsii sp. nov. Extremophiles14:47–59.
Thomas-Hall, S., and K. Watson. 2002. *Cryptococcus nyarrowii* sp. nov., a basidiomycetous yeast from Antarctica. Int. J. Syst. Evol. Microbiol. 2, 1023–1038.
Thomas-Hall, S., K. Watson and G. Scorzetti. 2002. *Cryptococcus statzelliae* sp. nov. and three novel strains of *Cryptococcus victoriae*, yeasts isolated from Antarctic soils. Int. J. Syst. Evol. Microbiol. 52, 2303–2308.
Thomas-Hall, S.R., B. Turchetti, P. Buzzini, E. Branda, T. Boekhout, B. Theelen and K. Watson. 2010. Cold adapted yeasts from Antarctica and the Italian Alps. Description of three novel species: *Mrakia robertii* sp. nov., *Mrakia blollopis* sp. nov. and *Mrakiella niccombsii* sp. nov. Extremophiles 14, 47–59.
Thompson, J.D., T.J. Gibson, F. Plewniak, F. Jeanmougin and D.G. Higgins. 1997. The ClustalX windows interface: flexible strategies for multiple sequence alignment aided by quality analysis tools. Nucleic Acids Res. 24, 4876–4882.
Thompson, J.R., C.M. Douglas, W. Li, C.K. Jue, B. Pramanik, X. Yuan, T.H. Rude, D.L. Toffaletti, J.R. Perfect and M. Kurtz. 1999. A glucan synthase FKS1 homolog in *Cryptococcus neoformans* is single copy and encodes an essential function. J. Bacteriol. 181, 444–453.
Thorne, J.L., H. Kishino and J. Felsenstein. 1991. An evolutionary model for maximum likelihood alignment of DNA sequences. Evolution 33, 114–124.
Threlfall, R.T., and J.R. Morris. 2002. Using dimethyldicarbonate to minimize sulfur dioxide or prevention of fermentation from excessive yeast contamination in juice and semi-sweet wine. J. Food Sci. 67, 2758–2762.
Tian, S., G. Qin and Y. Xu. 2004. Survival of antagonistic yeasts under field conditions and their biocontrol ability against postharvest diseases of sweet cherry. Postharvest Biol. Technol. 33, 327–331.
Tian, S., G. Qin and Y. Xu. 2005. Synergistic effects of combining biocontrol agents with silicon against postharvest diseases of jujube fruit. J. Food Prot. 68, 544–550.
Tian, S.P., H.J. Yao, X. Deng, B. Xu, G.Z. Quin and Z.L. Chan. 2007. Characterization and expression of β-1,3-glucanase genes in jujube fruit induced by the microbial biocontrol agent *Cryptococcus laurentii*. Phytopathology 97, 260–268.
Tietjen, W.J., L.R. Ayyagari and G.W. Uetz. 1987. Symbiosis between social spiders and yeast: the role in prey attraction. Psyche 94, 151–157.
Tietz, H.J., M. Hopp, A. Schmalreck, W. Sterry and V. Czaika. 2001. *Candida africana* sp. nov., a new human pathogen or a variant of *Candida albicans*? Mycoses 44, 437–445.
Tilbury, R.H. 1980. Xerotolerant yeasts at high sugar concentrations. In: G.W. Gould and J.E.L. Corry (Eds), Microbial Growth and Survival in Extremes of Environment. Academic Press, New York, pp. 103–128.
Timke, M., N.Q. Wang-Lieu, K. Altendorf and A. Lipski. 2008. Identity, beer spoiling and biofilm forming potential of

yeasts from beer bottling plant associated biofilms. Antonie van Leeuwenhoek 93, 151–161.

Tintelnot, K., and H. Losert. 2005. Isolation of *Cryptococcus adeliensis* from clinical samples and the environment in Germany. J. Clin. Microbiol. 43, 1007.

Tipper, D.J., and K.A. Bostian. 1984. Double-stranded ribonucleic acid killer systems in yeasts. Microbiol. Rev. 48, 125–156.

Todd, R.L., and W.W. Herrmann. 1936. The life cycle of the organism causing yeast meningitis. J. Bacteriol. 32, 89–97.

Toffaletti, D.L., T.H. Rude, S.A. Johnston, D.T. Durack and J.R. Perfect. 1993. Gene transfer in *Cryptococcus neoformans* by use of ballistic delivery of DNA. J. Bacteriol. 175, 1405–1411.

Toh-e, A., H. Araki, I. Utatsu and Y. Oshima. 1984. Plasmids resembling 2-micrometers DNA in the osmotolerant yeasts *Saccharomyces bailii* and *Saccharomyces bisporus*. J. Gen. Microbiol. 130, 2527–2534.

Toh-e, A., S. Yasunaga, H. Nisogi, K. Tanaka, T. Oguchi and Y. Matsui. 1993. Three yeast genes, PIR1, PIR2 and PIR3, containing internal tandem repeats, are related to each other, and PIR1 and PIR2 are required for tolerance to heat shock. Yeast 9, 481–494.

Toivola, A., D. Yarrow, E. van den Bosch, J.P. van Dijken and W.A. Scheffers. 1984. Alcoholic fermentation of D-xylose by yeasts. Appl. Environ. Microbiol. 47, 1221–1223.

Tokimatsu, I., and J. Kadota. 2006. Emerging deep-seated fungal infection, *Trichosporon*osis. Kansenshogaku Zasshi 80, 196–202. In Japanese.

Tokimatsu, I., R. Karashima, E. Yamagata, Y. Yamakami, H. Nagai, J. Kadota and M. Nasu. 2003. Pathogenesis of *Trichosporon asahii* and strategies for infectious control of disseminated trichosporonosis. Jpn. J. Med. Mycol. 44, 181–186.

Tokuoka, K. 1993. Sugar and salt-tolerant yeasts. J. Appl. Bacteriol. 74, 101–110.

Tokuoka, K., T. Ishitani, S. Goto and K. Komagata. 1987. Four new yeast species belonging to the genus *Candida*. J. Gen. Appl. Microbiol. 33, 1–10.

Tomaska, L., J. Nosek, A.M. Makhov, A. Pastorakova and J.D. Griffith. 2000. Extragenomic double-stranded DNA circles in yeast with linear mitochondrial genomes: potential involvement in telomere maintenance. Nucleic Acids Res. 28, 4479–4487.

Tomaszewski, E.K., K.S. Logan, K.F. Snowden, C.P. Kurtzman and D.N. Phalen. 2003. Phylogenetic analysis identifies the "megabacterium" of birds as a novel anamorphic ascomycetous yeast, *Macrorhabdus ornithogaster* gen. nov., sp. nov. Int. J. Syst. Evol. Microbiol. 53, 1201–1205.

Tominaga, T., Y. Okuzawa, S. Kato and M. Suzuki. 2003. The first isolation of two types of trifluoroleucine resistant mutants of *Saccharomyces servazzii*. Biotechnol. Lett. 25, 1735–1738.

Tong, S.L., and H.Z. Miao. 1999. A new species of marine yeast *Kluyveromyces penaeid* isolated from the heart of penaeid shrimp *Penaeus chinensis*. J. Mar. Biol. Assoc. UK 79, 559–561.

Toriumi, Y., T. Sugita, M. Nakajima, T. Matsushima and T. Shinoda. 2002. Antifungal pharmacodynamic characteristics of amphotericin B against *Trichosporon asahii*, using time-kill methodology. Microbiol. Immunol. 46, 89–93.

Torkelsen, A.-E. 1968. The genus *Tremella* in Norway. Nytt Mag. Bot. 15L, 225–239.

Tornai-Lehoczki, J.,G., Péter and D. Dlauchy. 2003. CHROMagar *Candida* medium as a practical tool for the differentiation and presumptive identification of yeast species isolated from salads. Int. J. Food Microbiol. 86, 189–200.

Toro, M.E., and F. Vazquez. 2002. Fermentation behaviour of controlled mixed and sequential cultures of *Candida cantarellii* and *Saccharomyces cerevisiae* wine yeasts. World J. Microbiol. Biotechnol. 18, 347–354.

Torto, B., D.G. Boucias, R.T. Arbogast, J.H. Tumlinson and P.E.A. Teal. 2007. Multitrophic interaction facilitates parasite–host relationship between an invasive beetle and the honey bee. Proc. Natl. Acad. Sci. USA 104, 8374–8378.

Tortorano, A.M., M.A. Viviani, A.L. Rigoni, M. Coliati, A. Roverselli and A. Pagano. 1997. Prevalence of serotype D in *Cryptococcus neoformans* isolates from HIV positive and HIV negative patients in Italy. Mycoses 40, 297–302.

Tosi, S., S. Onofri, M. Brusoni, L. Zucconi and H. Vishniac. 2005. Response of Antarctic soil fungal assemblages to experimental warming and reduction of UV radiation. Polar Biol. 28, 470–482.

Tournu, H., J. Serneels and P. van Dijck. 2005. Fungal pathogens research: novel and improved approaches for the discovery of antifungal drug targets. Curr. Drug Targ. 6, 909–922.

Toyomasu, T., and A. Zennyozi. 1981. On the application of isozyme electrophoresis to identification of strains in *Lentinus edodes* (shiitake). Mushroom Science XI, Proc. 11th Int. Scientific Cong. on Cultivation of Edible Fungi, Australia, pp. 675–684.

Tracey, M.L., K. Nelson, D. Hedgecock, R.A. Schleser and M.L. Pressick. 1975. Biochemical genetics of lobsters (*Homarus*): genetic variation and structure of American lobster populations. J. Fish. Res. Board Can. 33, 1108–1119.

Traquair, J.A., L.A. Shaw and W.R. Jarvis. 1988a. *Stephanoascus farinosus*, teleomorph of *Sporothrix fungorum*. Mycologia 80, 244–246.

Traquair, J.A., L.A. Shaw and W.R. Jarvis. 1988b. New species of *Stephanoascus* with *Sporothrix* anamorphs. Can. J. Bot. 66, 926–933.

Travassos, L.R. 1986. *Sporothrix schenckii*. In: P.J. Szaniszlo and J.L. Harris (Eds), Fungal Dimorphism. With Emphasis on Fungi Pathogenic for Humans. Plenum Press, New York, pp. 121–163.

Trilles, L., M. Lazera, B. Wanke, B. Theelen and T. Boekhout. 2003. Genetic characterization of environmental isolates of the *Cryptococcus neoformans* species complex from Brazil. Med. Mycol. 41, 383–390.

Trinci, A.P.J., and A.J. Collinge. 1974. Occlusion of the septal pores of damaged hyphae of *Neurospora crassa* by hexagonal crystals. Protoplasma 80, 57–67.

Trinci, A.P.J., and K. Gull. 1973. *Protomyces inundatus*, a yeast which is sensitive to griseofulvin. Arch. Mikrobiol. 94, 359–364.

Trindade, R.C., M.A. Resende, C.M. Silva and C.A. Rosa. 2002. Yeasts associated with fresh and frozen pulps of Brazilian tropical fruits. Syst. Appl. Microbiol. 25, 294–300.

Trindade, R.C., M.A. Resende, R.S. Pimenta, M.A. Lachance and C.A. Rosa. 2004. *Candida sergipensis*, a new asexual yeast

species isolated from frozen pulps of tropical fruits. Antonie van Leeuwenhoek 86, 27–32.
Tripathi, A.K., R.K.S. Chauhan, A.M. Bartaria and S. Chauhan. 2003. Quantitative and qualitative loss in coriander due to *Protomyces macrosporus*. Indian Phytopathol. 56, 451–452.
Trivedi, N.B. 1986. Baker's yeast. Crit. Rev. Biotechnol. 4, 75–110.
Trotsenko, Yu.A., S.V. Bykovskaya, N.N. Kirikova and I.P. Bab'eva. 1974. *Candida methylica* sp. n.: a new methanol-utilizing yeast species. Mikol. Fitopatol. 8, 323–326. In Russian.
Tsai, C.T., and C.-T. Huang. 2008. Overexpression of the *Neocallimastix frontalis* xylanase gene in the methylotrophic yeasts *Pichia pastoris* and *Pichia methanolica*. Enzyme Microb. Technol. 42, 459–465.
Tschalenko, D.K. 1941. Die Ursachen für die Verringerung des Säuregehaltes bei der Gärung von Fruchtweinen. Arb. Zentr. Wiss. Önolog. Labor, Moscow-Leningrad, 1 (cited by Kudryavtsev 1960).
Tscharke, R.L., M. Lazera, Y.C. Chang, B.L. Wickes and K.J. Kwon-Chung. 2003. Haploid fruiting in *Cryptococcus neoformans* is not mating type α-specific. Fungal Genet. Biol. 39, 230–237.
Tsong, A.E., B.B. Tuch, H. Li and A.D. Johnson. 2006. Evolution of alternative transcriptional circuits with identical logic. Nature 443, 415–420.
Tsuchiya, T., and M. Imai, 1968. Serological relationships among various yeast species of *Hansenula*, *Kloeckera* and *Hanseniaspora*. In: Taxonomy of Microorganisms, Proc. 10th I.A.M. Symposium on Microbiology, October 1968, pp. 147–158.
Tsuchiya, T., S. Kawakita, M. Imai and K. Miyagawa. 1966. Serological classification of the genera *Kloeckera* and *Hanseniaspora*. Jpn J. Exp. Med. 36, 555–562.
Tsuchiya, T., Y. Fukazawa, T. Shinoda and M. Imai. 1967. Perfect form of *Candida krusei*. Jpn. J. Exp. Med. 37, 285–290.
Tsuchiya, T., Y. Fukazawa and K. Suzuki. 1969. Serological classification of the genus *Sporobolomyces*. Jpn. J. Exp. Med. 39, 101–107.
Tsuchiya, T., Y. Fukazawa, M. Taguchi, T. Nakase and T. Shinoda. 1974. Serologic aspects on yeast classification. Mycopathol. Mycol. Appl. 53, 77–91.
Tsugawa, R., T. Nakase, T. Kobayashi, K. Yamashita and S. Okumura. 1969. Fermentation of n-paraffins by yeast. Part III. α-Ketoglutarate productivity of various yeasts. Agric. Biol. Chem. (Tokyo) 33, 929–938.
Tsui, C.K.M., H.-M. Daniel, V. Robert and W. Meyer. 2008. Re-examining the phylogeny of clinically relevant *Candida* species and allied genera based on multigene analyses. FEMS Yeast Res. 8, 651–659.
Tsuneda, A. 1987. Developmental plasticity in conidiogenesis of *Dipodascus aggregatus*. Trans. Mycol. Soc. Jpn 28, 303–312.
Tsuneda, A. 1989. Sporogenesis and septum schizolysis in *Dipodascus aggregatus*. Can. J. Bot. 67, 2150–2153.
Tsuneda, A., and R.S. Currah. 2006. Toward a deeper understanding of the nature of pleiomorphism in conidial fungi. Rep. Tottori Mycol. Inst. 44, 152.
Tsuyoshi, N., R. Fudou, S. Yamanaka, M. Kozaki, N. Tamang, S. Thapa and J.P. Tamang. 2005. Identification of yeast strains isolated from marcha in Sikkim, a microbial starter for amylolytic fermentation. Int. J. Food Microbiol. 99, 135–146.
Tubaki, K. 1952. Studies on the Sporobolomycetaceae in Japan: I. On *Tilletiopsis*. Nagaoa 1, 26–31.
Tubaki, K. 1953. Studies on the Sporobolomycetaceae in Japan: III. On *Sporobolomyces* and *Bullera*. Nagaoa 3, 12–21.
Tubaki, K. 1957. Biological and cultural studies of three species of *Protomyces*. Mycologia 49, 44–54.
Tubaki, K. 1958. Studies on the Japanese Hyphomycetes (IV) Miscellaneous group. Bot. Mag. Tokyo 71, 131–137.
Tubaki, K., and M. Soneda. 1959. Cultural and taxonomic studies on *Prototheca*. Nagaoa (Mycol. J. Nagao Inst. Tokyo) 6, 25–34.
Tuch, B.B., D.J. Galgoczy, A.D. Hernday, H. Li and A.D. Johnson. 2008. The evolution of combinatorial gene regulation in fungi. PLoS Biol. 6, e38.
Tudor, E.A., and R.G. Board. 1993. Food spoilage yeasts. In: A. H. Rose and J.S. Harrison (Eds), The Yeasts, 2nd edn. Vol. 5. Academic Press, London, pp. 435–516.
Tulasne, L.R., and C. Tulasne. 1865. Selecta Fungorum Carpologia. Vol. 3. Paris, pp. 61–62.
Tulasne, L.R. 1866. Super Friesano Taphrinarum genere, et Acyptolospore Mazeriana, accedente Ustilaginis marinae. Ann. d. Sci. Nat. (Bot.) V, 5, 122–136.
Turakainen, H., M. Hankaanpää, M. Korhola and S. Aho. 1994. Characterization of MEL genes in the genus *Zygosaccharomyces*. Yeast 10, 733–745.
Turchetti, B., P. Buzzini, M. Goretti, E. Branda, G. Diolaiuti, C. D'Agata, C. Smiraglia and A. Vaughan-Martini. 2008. Psychrophilic yeasts in glacial environments of Alpine glaciers. FEMS Microbiol. Ecol. 63, 73–83.
Turk, M., Z. Abramovic, A. Plemenitas and N. Gunde-Cimerman. 2007. Salt stress and plasma-membrane fluidity in selected extremophilic yeasts and yeast-like fungi. FEMS Yeast Res. 7, 550–557.
Turkiewicz, M., M. Pazgier, H. Kalinowska and S. Bielecki. 2003. A cold-adapted extracellular serine proteinase of the yeast *Leucosporidium antarcticum*. Extremophiles 7, 435–442.
Turner, S.H., R. Cherniak, E. Reiss and K.J. Kwon-Chung. 1992. Structural variability in the glucuronoxylomannan of *Cryptococcus neoformans* serotype A isolates determined by ^{13}C NMR spectroscopy. Carbohydr. Res. 233, 205–218.
Tuynenburg-Muys, G., and R. Willemse. 1965. The detection and enumeration of lipolytic microorganisms by means of a modified Eykman-plate method. Antonie van Leeuwenhoek 31, 103–112.
Uchida, K., and Y. Suzuki. 2003. Formation of 3′-O-beta-galactosyl compounds of 5-bromouridine by *Sporobolomyces singularis*. Biosci. Biotechnol. Biochem. 67, 643–645.
Ueda, M., and A. Tanaka. 2000. Cell surface engineering of yeast, construction of arming yeast with biocatalyst. J. Biosci. Bioeng. 90, 125–136.
Ueda-Nishimura, K., and K. Mikata. 1999. A new yeast genus, *Tetrapisispora* gen. nov.: *Tetrapisispora iriomotensis* sp. nov., *Tetrapisispora nanseiensis* sp. nov. and *Tetrapisispora arboricola* sp. nov., from the Nansei Islands, and reclassification of *Kluyveromyces phaffii* (van der Walt) van der Walt as *Tetrapisispora phaffii* comb. nov. Int. J. Syst. Bacteriol. 49, 1915–1924.

Ueda-Nishimura, K., and Mikata, K. 2000. Two distinct 18S rRNA secondary structures in *Dipodascus* (Hemiascomycetes). Microbiology 146, 1045–1051.

Ueda-Nishimura, K., and K. Mikata. 2001. Reexamination of *Dipodascus* and *Geotrichum* strains by DNA–DNA hybridization. IFO Res. Commun. 20, 92–96.

Ueda-Nishimura, K., and K. Mikata. 2001b. Reclassification of *Pichia scaptomyzae* and *Pichia galeiformis*. Antonie van Leeuwenhoek 79, 371–375.

Ueda-Nishimura, K., and K. Mikata. 2002a. Species distinction of the ascomycetous heterothallic yeast-like fungus *Stephanoascus ciferrii* complex: description of *Candida allociferrii* sp. nov. and reinstatement of *Candida mucifera* Kockova-Kratochvilova et Slavikova. Int. J. Syst. Evol. Microbiol. 52, 463–471.

Ueno, R., N. Urano, M. Suzuki and S. Kimura. 2002. Isolation characterization, and fermentative pattern of a novel thermotolerant *Prototheca zopfii* var. *hydrocarbonea* strain producing ethanol and CO_2 from glucose at 40°C. Arch. Microbiol. 177, 244–250.

Ueno, R., N. Urano and M. Suzuki. 2003. Phylogeny of the non-photosynthetic green micro-algal genus *Prototheca* (Trebouxiophyceae, Chlorophyta) and related taxa inferred from SSU and LSU ribosomal DNA partial sequence data. FEMS Microbiol. Lett. 223, 275–280.

Ueno, R., N. Hanagata, N. Urano and M. Suzuki. 2005. Molecular phylogeny and phenotypic variation in heterotrophic green algal genus *Prototheca* (Trebouxiophyceae, Chlorophyta). J. Phycol. 41, 1268–1280.

Uijthof, J.M. 1996. Relationships within the black yeast genus *Exophiala* based on ITS1 sequences. Mycol. Res. 100, 1265–1272.

Ukai, S., K. Hirose, T. Kiho and T. Irikura. 1972. Antitumor activity on sarcoma 180 of the polysaccharides from *Tremella fuciformis* Berk. Chem. Pharm. Bull. 20, 2293–2294.

Ulber, R., and K. Soyez. 2004. From wine to penicillin – 5000 years of biotechnology. Chemie Unser. Zeit 38, 172–180.

Ulitsky, I., D. Burstein, T. Tuller and B. Chor. 2006. The average common substring approach to phylogenomic reconstruction. J. Comput. Biol. 13, 336–350.

Ulloa, M., and T. Herrera. 1973. Descripcíon de una variedad de *Kloeckera* corticis aislada del pulque. Bol. Soc. Mex. 7, 27–32.

Ulloa, M., and T. Herrera. 1978. *Torulopsis taboadae*, una nueva especie de levadura aislada del colonche de Zacatecas. Mexico. Bol. Soc. Mex. Micol. 12, 5–12.

Ullrich, R., and M. Hofrichter. 2007. Enzymatic hydroxylation of aromatic compounds. Cell. Mol. Life Sci. 64, 271–293.

Unger, F. 1833. Die Exantheme der Pflanzen. Wien, 422pp.

Upton, A., J.A. Fraser, S.E. Kidd, C. Bretz, K.H. Bartlett, J. Heitman and K.A. Marr. 2007. First contemporary case of human infection with *Cryptococcus gattii* in Puget Sound: evidence for spread of the Vancouver Island outbreak. J. Clin. Microbiol. 45, 3086–3088.

Urakami, T. 1975. Process for cultivating ethanol-assimilating yeasts. US Patent 3929578.

Urakami, T., and R. Michimi. 1977. Process for producing yeast cells. US Patent 4 033 821.

Urlacher, V.B., and S. Eiben. 2006. Cytochrome P450 monooxygenases: perspectives for synthetic applications. Trends Biotechnol. 24, 324–330.

Urquehart, E.J., and Z.K. Punja. 2002. Hydrolytic enzymes and antifungal compounds produced by *Tilletiopsis* species, phyllosphere yeasts that are antagonists of powdery mildew fungi. Can. J. Microbiol. 48, 219–229.

Urquhart, E.J., J.G. Menzies and Z.K. Punja. 1994. Growth and biological control activity in *Tilletiopsis* species against powdery mildew (*Sphaerotheca fuliginea*) on greenhouse cucumber. Phytopathology 84, 341–351.

U.S. Food and Drug Administration, Center for Food Safety and Applied Nutrition, Office of Food Additives Safety: September 2001. 2001. Agency Response Letter: GRAS Notice No. GRN 000076.

Usall, J., N. Teixidó, E. Fons and I. Viñas. 2000. Biological control of blue mould on apple by a strain of *Candida sake* under several controlled atmosphere conditions. Int. J. Food Microbiol. 58, 83–92.

Uthurry, C.A., J.A. Suarez Lepe, J. Lombardero and J.R. Garcia del Hierro. 2006. Ethyl carbamate production by selected yeasts and lactic acid bacteria in red wine. Food Chem. 94, 262–270.

Utkhede, R.S., and C.A. Koch. 2004. Evaluation of biological and chemical treatments for control of gummy stem blight on cucumber plants grown hydroponically in greenhouses. BioControl 49, 109–117.

Utkhede, R.S., and S. Mathur. 2002. Biological control of stem canker of greenhouse tomatoes caused by *Botrytis cinerea*. Can. J. Microbiol. 48, 550–554.

Utkhede, R.S., and S. Mathur. 2006. Preventive and curative biological treatments for control of *Botrytis cinerea* stem canker of greenhouse tomatoes. BioControl 51, 363–373.

Utkhede, R., C. Bogdanoff and J. McNevin. 2001. Effects of biological and chemical treatments on *Botrytis* stem canker and fruit yield of tomato under greenhouse conditions. Can. J. Plant Pathol. 23, 253–259.

Vacek, D.C. 1982. Interactions between microorganisms and cactophilic *Drosophila* in Australia. In: J.S.F. Barker and W. T. Starmer (Eds), Ecological Genetics and Evolution: The Cactus–*Drosophila* Model System. Academic Press, Sydney, pp. 175–190.

Vacek, D.C., W.T. Starmer and W.B. Heed. 1979. Relevance of the ecology of citrus yeasts to the diet of *Drosophila*. Microb. Ecol. 5, 43–49.

Vacek, D.C., P.D. East, J.S.F. Barker and M.H. Soliman. 1985. Feeding and oviposition preferences of *Drosophila buzzatii* for microbial species isolated from its natural environment. Biol. J. Linn. Soc. (London) 24, 175–187.

Vagnoli, P., A. Musmanno, S. Cresti, T. di Maggio and G. Coratza. 1993. Occurrence of killer yeasts in spontaneous wine fermentations from the Tuscany region of Italy. Appl. Environ. Microbiol. 59, 4037–4043.

Vaishnav, V.V., B.E. Bacon, M. O'Neill and R. Cherniak. 1998. Structural characterization of the galactoxylomannan of *Cryptococcus neoformans* Cap67. Carbohydr. Res. 306, 315–330.

Vakhlu, J., and A. Kour. 2006. Yeast lipases: enzyme purification, biochemical properties and gene cloning. Electron. J. Biotechnol. 9, 69–85.

Valadon, L.R.G. 1966. Carotenoids of fungi. Adv. Frontiers Plant. Sci. 15, 183–206.

Valadon, L.R.G., J.G. Manners and A. Myers. 1962. Studies on the life-history and taxonomic position of *Protomyces inundatus* Dangeard. Trans. Br. Mycol. Soc. 45, 573–586.

Valério, E., M. Gadanho and J.P. Sampaio. 2002. *Sporobolomyces odoratus* sp. nov., a new species in the *Sporidiobolus ruineniae* clade. FEMS Yeast Res. 2, 9–16.

Valério, E., M. Gadanho and J.P. Sampaio. 2008a. A reappraisal of the *Sporobolomyces roseus* species complex and description of *Sporidiobolus metaroseus* sp. nov. Int. J. Syst. Evol. Microbiol. 58, 736–741.

Valério, E., M. Gadanho and J.P. Sampaio. 2008b. *Sporidiobolus johnsonii* and *Sporidiobolus salmonicolor* revisited. Mycol. Prog. 7, 125–131.

Valles, B.S., R.P. Bedrinana, N.F. Tascon, A.Q. Simon and R.R. Madrera. 2007. Yeast species associated with the spontaneous fermentation of cider. Food Microbiol. 24, 25–31.

Vallini, G., S. Frassinetti and G. Scorzetti. 1997. *Candida aquaetextoris* sp. nov., a new species of yeast occurring in sludge from a textile industry wastewater treatment plant in Tuscany, Italy. Int. J. Syst. Bacteriol. 47, 336–340.

Valverde, M.E., O. Paredes-Lopez, J.K. Pataky and F. Guevara-Lara. 1995. Huitlacoche (*Ustilago maydis*) as a food source – biology, composition, and production. Crit. Rev. Food Sci. Nutr. 35, 191–229.

Valverde, R.A., and G.E. Templeton. 1984. Leaf gall of *Torilis japonica* caused by *Protomyces macrosporus* in Arkansas. Plant Dis. 68, 716–717.

van Abbe, N.J. 1964. The investigation of dandruff. J. Soc. Cosmetic Chem. 52, 173–188.

van Asbeck, E., K.V. Clemons, M. Martinez, A.J. Tong and D.A. Stevens. 2008. Significant differences in drug susceptibility among species in the *Candida parapsilosis* group. Diagn. Microbiol. Infect. Dis. 62, 106–109.

van Beilen, J.B., and Z. Li. 2002. Enzyme technology: an overview. Curr. Opin. Biotechnol. 13, 338–344.

van Belkum, A., T. Boekhout and R. Bosboom. 1994. Monitoring spread of *Malassezia* infections in a neonatal intensive care unit by PCR-mediated genetic typing. J. Clin. Microbiol. 32, 2528–2532.

van Beyma, F.H. 1933. On some moulds of the genus *Monilia* isolated from tobacco. Zentralbl. Bakteriol. Parasitenkd. Abt. 2, 88, 124–131.

van de Peer, Y., L. Hendriks, A. Goris, J.-M. Neefs, M. Vancanneyt, K. Kersters, J.-F. Berny, G.L. Hennebert and R. de Wachter. 1992. Evolution of basidiomycetous yeasts as deduced from small ribosomal subunit RNA sequences. Syst. Appl. Microbiol. 15, 250–258.

van den Brink, H.J.M., R.F.M. van Gorcom, A.C.M.J.J. van den Hondel and P.J. Punt. 1998. Cyrochrome P450 enzyme systems in fungi. Fungal Genet. Biol. 23, 1–17.

van der Burg, A.C. 1974. The occurrence of *Sporobolomyces roseus*, a red yeast, on leaves of *Phragmites australis*. PhD Thesis, Free University Amsterdam.

van der Klei, I.J., and M. Veenhuis. 2006. Yeast and filamentous fungi as model organisms in microbody research. Biochim. Biophys. Acta 1763, 1364–1373.

van der Klei, I.J., and M. Veenhuis. 2007. Protein targeting to yeast peroxisomes. In: M. van der Giezen (Ed.), Protein Targeting Protocols. Humana Press, Totowa, NJ.

van der Klei, I.J., H. Yurimoto, Y. Sakai and M. Veenhuis. 2006. The significance of peroxisomes in methanol metabolism in methylotrophic yeast. Biochim. Biophys. Acta 1763, 1453–1462.

van der Kühle, A., and L. Jespersen. 1998. Detection and identification of wild yeasts in lager breweries. Int. J. Food Microbiol. 43, 205–213.

van der Kühle, A., and L. Jespersen. 2003. The taxonomic position of *Saccharomyces boulardii* as evaluated by sequence analysis of the D1/D2 domain of 26S rDNA, the ITS1-5.8S rDNA-ITS2 region and the mitochondrial cytochrome-c oxidase II gene. Syst. Appl. Microbiol. 26, 564–571.

van der Sluis, C., C.J. Stoffelen, S.J. Castelein, G.H. Engbers, E. G. ter Schure, J. Tramper and R.H. Wijffels. 2001. Immobilized salt-tolerant yeasts: application of a new polyethylene-oxide support in a continuous stirred-tank reactor for flavour production. J. Biotechnol. 88, 129–139.

van der Valk, P., and R. Marchant. 1978. Hyphal ultrastructure in fruit-body primordia of the basidiomycetes *Schizophylum commune* and *Coprinus cinereus*. Protoplasma 95, 57–72.

van der Valk, P., R. Marchant and J.G.H. Wessels. 1977. Ultrastructural localization of polysaccharides in the wall and septum of the basidiomycete *Schizophyllum commune*. Exp. Mycol. 1, 69–82.

van der Vossen, J.M.B.M., H. Rahaoui, M.W.C.M. de Nus and B.J. Hartog. 2003. PCR methods for tracing and detection of yeasts in the food chain. In: T. Boekhout and V. Robert (Eds), Yeasts in Food: Beneficial and Detrimental Aspects. Behrs-Verlag, Hamburg, pp. 123–138.

van der Walt, J.P. 1956a. *Kluyveromyces* – a new yeast genus of the Endomycetales. Antonie van Leeuwenhoek 22, 265–272.

van der Walt, J.P. 1956b. The yeast *Kluyveromyces africanus* nov. spec. and its phylogenetic significance. Antonie van Leeuwenhoek 22, 321–326.

van der Walt, J.P. 1956c. *Saccharomyces transvaalensis* nov. spec., a new yeast from soil. Antonie van Leeuwenhoek 22, 190–192.

van der Walt, J.P. 1957. Three new sporogenous yeasts from soil. Antonie van Leeuwenhoek 23, 23–29.

van der Walt, J.P. 1959a. *Pichia robertsii* nov. spec., a new haploid homothallic yeast. Antonie van Leeuwenhoek 25, 337–343.

van der Walt, J.P. 1959b. *Endomycopsis wickerhamii* nov. spec., a new heterothallic yeast. Antonie van Leeuwenhoek 25, 344–348.

van der Walt, J.P. 1959c. *Endomyces reessii* nov. sp. Antonie van Leeuwenhoek 25, 458–464.

van der Walt, J.P. 1961. *Brettanomyces custersianus* nov. spec. Antonie van Leeuwenhoek 27, 332–336.

van der Walt, J.P. 1962. *Schwanniomyces persoonii* nov. spec. Antonie van Leeuwenhoek 28, 81–84.

van der Walt, J.P. 1963. *Fabospora phaffii* sp. n. Antonie van Leeuwenhoek 29, 319–322.

van der Walt, J.P. 1964. *Dekkera*, a new yeast genus of the Saccharomycetaceae. Antonie van Leeuwenhoek 30, 273–280.

van der Walt, J.P. 1965a. *Saccharomyces vafer* and *S. inconspicuus* spp. n. Antonie van Leeuwenhoek 31, 187–192.

van der Walt, J.P. 1965b. *Saccharomyces inusitatus* sp. n. Antonie van Leeuwenhoek 31, 277–281.

van der Walt, J.P. 1965c. The emendation of the genus *Kluyveromyces* van der Walt. Antonie van Leeuwenhoek 31, 341–348.

van der Walt, J.P. 1966a. *Lodderomyces*, a new genus of the Saccharomycetaceae. Antonie van Leeuwenhoek 32, 1–5.
van der Walt, J.P. 1966b. *Pichia acaciae* sp. n. Antonie van Leeuwenhoek 32, 159–161.
van der Walt, J.P. 1967a. *Wingea*, a new yeast genus of the Saccharomycetaceae. Antonie van Leeuwenhoek 33, 97–99.
van der Walt, J.P. 1967b. Sexually active strains of *Candida albicans* and *Cryptococcus albidus*. Antonie van Leeuwenhoek 33, 246–256.
van der Walt, J.P. 1970a. Criteria and methods used in classification. In: J. Lodder (Ed.), The Yeasts, A Taxonomic Study, 2nd edn. North-Holland, Amsterdam, pp. 34–113.
van der Walt, J.P. 1970a. The genus *Syringospora* Quinquaud emend. Mycopathol. Mycol. Appl. 40, 231–243.
van der Walt, J.P. 1970c. *Kluyveromyces* (van der Walt) emend. van der Walt. In: J. Lodder (Ed.), The Yeasts, A Taxonomic Study, 2nd edn. North-Holland, Amsterdam, pp. 316–378.
van der Walt, J.P. 1970d. *Saccharomyces* (Meyen) emend. Reess. In: J. Lodder (Ed.), The Yeasts, A Taxonomic Study, 2nd edn. North-Holland, Amsterdam, pp. 555–718.
van der Walt, J.P. 1970e. *Brettanomyces* Kufferath et van Laer. In: J. Lodder (Ed.), The Yeasts, A Taxonomic Study, 2nd edn. North-Holland, Amsterdam, pp. 863–892.
van der Walt, J.P. 1970f. The perfect and imperfect states of *Sporobolomyces salmonicolor*. Antonie van Leeuwenhoek 36, 49–55.
van der Walt, J.P. 1971. New combinations in the genera *Brettanomyces*, *Kluyveromyces*, *Lodderomyces* and *Wingea*. Bothalia 10, 417–418.
van der Walt, J.P. 1972. The yeast genus *Ambrosiozyma* gen. nov. (Ascomycetes). Mycopathol. Mycol. Appl. 46, 305–316.
van der Walt, J.P. 1973. *Aessosporon dendrophilum* sp. nov., the perfect state of *Bullera* dendrophila. Antonie van Leeuwenhoek 39, 455–460.
van der Walt, J.P. 1978. The genus *Pachytichospora* gen. nov. (Saccharomycetaceae). Bothalia 12, 563–564.
van der Walt, J.P. 1982a. *Pichia meyerae*, a new, sexually agglutinating, heterothallic, diploid yeast species. Antonie van Leeuwenhoek 48, 383–388.
van der Walt, J.P. 1982b. *Hansenula euphorbiaphila* sp. nov., a new, diploid heterothallic yeast species. Antonie van Leeuwenhoek 48, 465–470.
van der Walt, J.P. 1984a. *Dekkera* van der Walt. In: N.J.W. Kreger-van Rij (Ed.), The Yeasts, A Taxonomic Study, 3rd edn. Elsevier, Amsterdam, pp. 146–150.
van der Walt, J.P. 1984b. *Lodderomyces* van der Walt. In: N.J.W. Kreger-van Rij (Ed.), The Yeasts, A Taxonomic Study, 3rd edn. Elsevier, Amsterdam, pp. 263–265.
van der Walt, J.P. 1984c. *Brettanomyces* Kufferath et van Laer. In: N.J.W. Kreger-van Rij (Ed.), The Yeasts, A Taxonomic Study, 3rd edn. Elsevier, Amsterdam, pp. 562–576.
van der Walt, J.P. 1987. The yeasts – a conspectus. In: G.S. de Hoog, M.Th. Smith and A.C.M. Weijman (Eds), The Expanding Realm of Yeast-like Fungi. Elsevier, Amsterdam, pp. 19–32. (Stud. Mycol. 30, 19–31).
van der Walt, J.P. 1992. The Lipomycetaceae, a model family for phylogenetic studies. Antonie van Leeuwenhoek 62, 247–250.
van der Walt, J.P., and P.B. Baker. 1978. *Candida fermenticarens* – a new yeast from *arboricole* lichen. Bothalia 12, 561–562.
van der Walt, J.P., and J. de Leeuw. 1970. Ploidy differences in *Cryptococcus albidus*. Mycopathologia 42, 17–24.
van der Walt, J.P., and V.K. Hopsu-Havu. 1976. A colour reaction for the differentiation of ascomycetous and hemibasidiomycetous yeasts. Antonie van Leeuwenhoek 42, 157–163.
van der Walt, J.P., and E. Johannsen. 1973. The perfect state of *Torulopsis magnoliae*. Antonie van Leeuwenhoek 39, 635–647.
van der Walt, J.P., and E. Johannsen. 1974. Ascospores in *Torulopsis dattila* (Kluyver) Lodder. Antonie van Leeuwenhoek 40, 275–279.
van der Walt, J.P., and E. Johannsen. 1975a. The genus *Torulaspora* Lindner. CSIR Res. Rep. 325, 1–23.
van der Walt, J.P., and E. Johannsen. 1975b. *Hansenula lynferdii* sp. nov. Antonie van Leeuwenhoek 41, 13–16.
van der Walt, J.P., and E. Johannsen. 1975c. *Pichia philogaea* sp. nov. Antonie van Leeuwenhoek 41, 173–177.
van der Walt, J.P., and E. Johannsen. 1975d. *Trichosporon terrestre* sp. nov. Antonie van Leeuwenhoek 41, 361–365.
van der Walt, J.P., and E. Johannsen. 1978. The genus *Debaryozyma* van der Walt et Johannsen, nom. nov. Persoonia 10, 146–148.
van der Walt, J.P., and E. Johannsen. 1980. *Debaryozyma yamadae* spec. nov. (Saccharomycetaceae). J. Gen. Appl. Microbiol. 26, 217–222.
van der Walt, J.P., and E. Johannsen. 1984. *Kluyveromyces* van der Walt emend. van der Walt. In: N.J.W. Kreger-van Rij (Ed.), The Yeasts, A Taxonomic Study, 3rd edn. Elsevier, Amsterdam, pp. 224–251.
van der Walt, J.P., and N.V.D.W. Liebenberg. 1973a. The yeast genus *Wickerhamiella* gen. nov. (Ascomycetes). Antonie van Leeuwenhoek 39, 121–128.
van der Walt, J.P., and N.V.D.W. Liebenberg. 1973b. Agglutinative mating types of *Saccharomyces transvaalensis*. Antonie van Leeuwenhoek 39, 629–633.
van der Walt, J.P., and T. Nakase. 1973. *Candida homilentoma*, a new yeast from South African insect sources. Antonie van Leeuwenhoek 39, 449–453.
van der Walt, J.P., and E.E. Nel. 1963. *Saccharomyces vanudenii* nov. spec. Mycopathol. Mycol. Appl. 20, 71–74.
van der Walt, J.P., and E.E. Nel. 1968. *Candida edax* sp. n. Antonie van Leeuwenhoek 34, 106–108.
van der Walt, J.P., and A. Opperman. 1983. *Pichia euphorbiae* sp. nov., a new haploid heterothallic yeast species. Antonie van Leeuwenhoek 49, 51–59.
van der Walt, J.P., and M.J. Pitout. 1969. Ploidy differences in *Sporobolomyces salmonicolor* and *Candida albicans*. Antonie van Leeuwenhoek 35, 227–231.
van der Walt, J.P., and D.B. Scott. 1970. *Bullera dendrophila* sp. n. Antonie van Leeuwenhoek 36, 383–387.
van der Walt, J.P., and D.B. Scott. 1971a. *Pichia ambrosiae* sp. n., a new auxiliary ambrosia fungus. Antonie van Leeuwenhoek 37, 15–20.
van der Walt, J.P., and D.B. Scott. 1971b. *Saccharomycopsis synnaedendra*, a new yeast from South African insect sources. Mycopathol. Mycol. Appl. 44, 101–106.
van der Walt, J.P., and D.B. Scott. 1971c. *Pichia xylopsoci*, a new yeast from South African insect sources. Mycopathol. Mycol. Appl. 44, 321–324.
van der Walt, J.P., and D.B. Scott. 1971d. The yeast genus *Saccharomycopsis* Schiönning. Mycopathol. Mycol. Appl. 2604 43, 279–288.
van der Walt, J.P., and I.T. Tscheuschner. 1956a. *Pichia vanriji* n. sp. isolated from soil. J. Gen. Microbiol. 15, 459–461.

van der Walt, J.P., and I.T. Tscheuschner. 1956b. *Saccharomyces delphensis* nov. spec., a new yeast from South African dried figs. Antonie van Leeuwenhoek 22, 162–166.
van der Walt, J.P., and I.T. Tscheuschner. 1956c. *Saccharomyces pretoriensis* n. sp. from South African soil. J. Gen. Microbiol. 14, 485–486.
van der Walt, J.P., and I.T. Tscheuschner. 1956d. *Saccharomyces capensis* nov. spec., a new yeast from South African grape must. Antonie van Leeuwenhoek 22, 257–260.
van der Walt, J.P., and I.T. Tscheuschner. 1957a. Three new yeasts. Antonie van Leeuwenhoek 23, 184–190.
van der Walt, J.P., and I.T. Tscheuschner. 1957b. *Hanseniaspora vineae* sp. nov. Trans. Br. Mycol. Soc. 40, 211–212.
van der Walt, J.P., and W.C. van der Klift. 1972. *Pichia melissophila* sp. n., a new osmotolerant yeast from apiarian sources. Antonie van Leeuwenhoek 38, 361–364.
van der Walt, J.P., and A.E. van Kerken. 1959. The wine yeasts of the Cape. Part II. The occurrence of *Brettanomyces intermedius* and *Brettanomyces schanderlii* in South African table wines. Antonie van Leeuwenhoek 25, 145–151.
van der Walt, J.P., and A.E. van Kerken. 1960. *Torulopsis domercqii* nov. spec. Antonie van Leeuwenhoek 26, 314–316.
van der Walt, J.P., and A.E. van Kerken. 1961a. The wine yeasts of the Cape. Part V. Studies on the occurrence of *Brettanomyces intermedius* and *Brettanomyces schanderlii*. Antonie van Leeuwenhoek 27, 81–90.
van der Walt, J.P., and A.E. van Kerken. 1961b. Three new anascosporogenous yeasts. Antonie van Leeuwenhoek 27, 206–212.
van der Walt, J.P., and A.E. van Kerken. 1961c. *Candida ingens* nov. spec. Antonie van Leeuwenhoek 27, 284–286.
van der Walt, J.P., and J.A. von Arx. 1980. The yeast genus *Yarrowia* gen. nov. Antonie van Leeuwenhoek 46, 517–521.
van der Walt, J.P., and J.A. von Arx. 1985. The septal ultrastructure of *Hormoascus ambrosiae* and the emendation of the genus *Hormoascus*. Syst. Appl. Microbiol. 6, 90–92.
van der Walt, J.P., and D. Yarrow. 1984a. Methods for the isolation, maintenance, classification and identification of yeasts. In: N.J.W. Kreger-van Rij (Ed.), The Yeasts, A Taxonomic Study, 3rd edn. Elsevier, Amsterdam, pp. 45–104.
van der Walt, J.P., and D. Yarrow. 1984b. The genus *Arxiozyma* gen. nov. (Saccharomycetaceae). S. Afr. J. Bot. 3, 340–342.
van der Walt, J.P., E.E. Nel and A.E. van Kerken. 1966. *Kluyveromyces wikenii* and *Kluyveromyces cicerisporus* spp. n. Antonie van Leeuwenhoek 32, 393–398.
van der Walt, J.P., D.B. Scott and W.C. van der Klift. 1971a. Four new, related *Candida* species from South African insect sources. Antonie van Leeuwenhoek 37, 449–460.
van der Walt, J.P., D.B. Scott and W.C. van der Klift. 1971b. Five new *Torulopsis* species from South African insect sources. Antonie van Leeuwenhoek 37, 461–471.
van der Walt, J.P., D.B. Scott and W.C. van der Klift. 1972. Six new *Candida* species from South African insect sources. Mycopathol. Mycol. Appl. 47, 221–236.
van der Walt, J.P., E. Johannsen and T. Nakase. 1973. *Candida naeodendra*, a new species of the *Candida diddensii* group. Antonie van Leeuwenhoek 39, 491–495.
van der Walt, J.P., M.B. Taylor and N.V.D.W. Liebenberg. 1977. Ploidy, ascus formation and recombination in *Torulaspora* (*Debaryomyces*) *hansenii*. Antonie van Leeuwenhoek 43, 205–218.
van der Walt, J.P., E. Johannsen and D. Yarrow. 1978. *Torulopsis geochares* and *Torulopsis azyma*, two new haploid species of ascomycetous affinity. Antonie van Leeuwenhoek 44, 97–104.
van der Walt, J.P., A.C.M. Weijman and J.A. von Arx. 1981. The anamorphic yeast genus *Myxozyma* gen. nov. Sydowia. Ann. Mycol. Ser. II, 34, 191–198.
van der Walt, J.P., D. Yarrow, A. Opperman and L. Halland. 1982. *Pichia kodamae* sp. nov., a new homothallic yeast species. J. Gen. Appl. Microbiol. 28, 155–160.
van der Walt, J.P., N.P. Ferreira and P.D.G. Richards. 1986a. New basidiomycetous yeasts from South Africa I: *Sporobolomyces kluyverinielii*. Antonie van Leeuwenhoek 52, 431–436.
van der Walt, J.P., E. Johannsen, A. Opperman and L. Halland. 1986b. *Kluyveromyces yarrowii* sp. nov., a haploid, heterothallic, arboreal species. Syst. Appl. Microbiol. 8, 208–212.
van der Walt, J.P., N.P. Ferreira and R.L. Steyn. 1987a. *Candida lyxosophila* sp. nov., a new D-xylose fermenting yeast from southern Africa. Antonie van Leeuwenhoek 53, 93–97.
van der Walt, J.P., J.A. von Arx, N.P. Ferreira and P.D.G. Richards. 1987b. *Zygozyma* gen. nov., a new genus of the Lipomycetaceae. Syst. Appl. Microbiol. 9, 115–120.
van der Walt, J.P., Y. Yamada, T. Nakase and P.D.G. Richards. 1987c. *Myxozyma geophila* and *Myxozyma lipomycoides* spp. nov., two new anamorphic, lipomycetaceous yeasts from southern Africa. Syst. Appl. Microbiol. 9, 121–124.
van der Walt, J.P., Y. Yamada, N.P. Ferreira and P.D.G. Richards. 1987d. New basidiomycetous yeast from southern Africa, II. *Sterigmatomyces wingfieldii* sp. n. Antonie van Leeuwenhoek 53, 137–142.
van der Walt, J.P., Y. Yamada, N.P. Ferreira and P.D.G. Richards. 1988. New basidiomycetous yeasts from South Africa III. *Sporobolomyces phyllomatis* sp. nov. (Sporobolomycetaceae). Antonie van Leeuwenhoek 54, 201–206.
van der Walt, J.P., Y. Yamada, N.P. Ferreira and P.D.G. Richards. 1989a. New basidiomycetous yeasts from South Africa IV. *Sporobolomyces phyllades* sp. nov., characterized by the coenzyme Q9 system (Sporobolomycetaceae). Antonie van Leeuwenhoek 55, 189–195.
van der Walt, J.P., M.Th. Smith and Y. Yamada. 1989b. *Debaryomyces udenii*, sp. nov. (Saccharomycetaceae), a new species from soil. Antonie van Leeuwenhoek 56, 233–239.
van der Walt, J.P., M.Th. Smith, Y. Yamada, T. Nakase and P.D. G. Richards. 1989c. *Lipomyces japonicus* sp. nov. from Japanese soil. Syst. Appl. Microbiol. 11, 302–304.
van der Walt, J.P., M.Th. Smith, Y. Yamada and P.D.G. Richards. 1989d. *Zygozyma arxii* sp. n. (Lipomycetaceae), a new species from southern Africa. Syst. Appl. Microbiol. 12, 288–290.
van der Walt, J.P., I. Spencer-Martins, Y. Yamada and P.D.G. Richards. 1989e. *Myxozyma kluyveri* sp. nov. (Candidaceae), a new species from southern Africa. Antonie van Leeuwenhoek 55, 297–302.
van der Walt, J.P., A. Botha and A. Eicker. 1990a. Ferrichrome production by Lipomycetaceae. Syst. Appl. Microbiol. 13, 131–135.

van der Walt, J.P., M.J. Wingfield and Y. Yamada. 1990b. *Zygozyma smithiae* sp. n. (Lipomycetaceae), a new ambrosia yeast from southern Africa. Antonie van Leeuwenhoek 58, 95–98.

van der Walt, J.P., M.Th. Smith and Y. Yamada. 1990c. *Arxula* gen. nov. (Candidaceae), a new anamorphic, arthroconidial yeast genus. Antonie van Leeuwenhoek 57, 59–61.

van der Walt, J.P., M.J. Wingfield, M.Th. Smith and W.H. Batenburg-van der Vegte. 1991. Septal micropores in *Zygozyma* and their taxonomic significance. Antonie van Leeuwenhoek 59, 77–80.

van der Walt, J.P., T. Nakase, M. Suzuki, M. Takashima and Y. Yamada. 1994. *Debaryomyces polymorphus* var. *africanus*, a new variety of ascosporogenous yeast found in South Africa. J. Gen. Appl. Microbiol. 40, 331–337.

van der Walt, J.P., A. Botha and M.Th. Smith. 1997. *Lipomyces mesembrius* sp. nov., a member of the *L. starkeyi* species complex. Antonie van Leeuwenhoek 71, 325–328.

van der Walt, J.P., M.Th. Smith and H. Roeijmans. 1999. Four new species in *Lipomyces*. System. Appl. Microbiol. 22, 229–236.

van der Westhuizen, J.P.J., J.L.F. Kock, E.J. Smit and P.M. Lategan. 1987. The value of long-chain fatty acid composition of species representing the basidiomycetous genus *Rhodosporium* Banno. Syst. Appl. Microbiol. 10, 31–34.

van Dijken, J., and A. Scheffers. 1987. Method for producing ethanol from xylose-containing substances. US Patent 4,701,414.

van Dijken, J.P., and W. Harder. 1974. Optimal conditions for the enrichment and isolation of methanol-assimilating yeasts. J. Gen. Microbiol. 84, 409–411.

van Dijken, J.P., E. van den Bosch, J.J. Hermans, L. Rodrigues de Miranda and W.A. Scheffers. 1986. Alcoholic fermentation by "non-fermentative" yeasts. Yeast 2, 123–127.

van Driel, K.G.A. 2007. Septal pore caps in Basidiomycetes: composition and ultrastructure. PhD Thesis, University Utrecht, pp. 1–133.

van Driel, K.G., A.F. van Peer, H.A. Wösten, A.J. Verkleij, T. Boekhout and W.H. Müller. 2007a. Enrichment of perforate septal pore caps from the basidiomycetous fungus *Rhizoctonia solani* by combined use of French press, isopycnic centrifugation, and Triton X-100. J. Microbiol. Meth. 71, 298–304.

van Driel, K.G., T. Boekhout, H.A.B. Wösten, A.J. Verkleij and W.H. Müller. 2007b. Laser microdissection of fungal septa as visualized by scanning electron mictroscopy. Fungal Genet. Biol. 44, 466–473.

van Driel, K.G.A., A.F. van Peer, J. Grijpstra, H.A.B. Wösten, A.J. Verkleij, W.H. Müller and T. Boekhout. 2008. The septal pore cap protein SPC18 isolated from the basidiomycetous fungus *Rhizoctonia solani* also resides in pore-plugs. Eukaryot. Cell 7, 1865–1873.

van Driel, K.G.A., B.M. Humbel, A.J. Verkleij, J. Stalpers, W.H. Müller and T. Boekhout. 2009. Variation of septal pore complex morphology in Cantharellales and Hymenochaetales (Agaricomycotina). Mycol. Res. 113, 559–576.

van Dyk, M.S., J.L.F. Kock, D.J. Coetzee, O.P.H. Augustyn and S. Nigam. 1991. Isolation of a novel arachidonic acid metabolite 3-hydroxy-5,8,11,14-eicosatetraenoic acid (3-HETE) from the yeast *Dipodascopsis uninucleata* UOFS-Y128. FEBS Lett. 283, 195–198.

van Dyk, M.S., J.L.F. Kock and A. Botha. 1994. Hydroxy long-chain fatty acids in fungi. World J. Microbiol. Biotech. 10, 495–504.

van Eck, J.H., B.A. Prior and E.V. Brandt. 1993. The water relations of growth and polyhydroxy alcohol production by ascomycetous yeasts. J. Gen. Microbiol. 139, 1047–1054.

van Eijk, G.W., and H.J. Roeymans. 1982. Distribution of carotenoids and sterols in relation to the taxonomy of *Taphrina* and *Protomyces*. Antonie van Leeuwenhoek 48, 257–264.

van Eijk, G.W., H.J. Roeijmans and A.C.M. Weijman. 1982. Biochemical characteristics: volatiles, carotenoids, sterols and fatty acids. Stud. Mycol. 22, 39–49.

van Elden, L.J., A.M. Walenkamp, M.M. Lipovsky, P. Reiss, J.F. Meis, S. de Marie, J. Dankert and A.I. Hoepelman. 2000. Declining number of patients with cryptococcosis in the Netherlands in the era of highly active antiretroviral therapy. AIDS 14, 2787–2800.

van Esch, F. 1987. Yeasts in soft drinks and fruit juice concentrates. De Ware(n) Chemicus 17, 20–31.

van Heerden, A., J.L.F. Kock, P.J. Botes, C.H. Pohl, C.J. Strauss, P.W.J. van Wyk and S. Nigam. 2005. Ascospore release from bottle-shaped asci in *Dipodascus albidus*. FEMS Yeast Res. 5, 1185–1190.

van Heerden, A., P.W.J. van Wyk, P.J. Botes, C.H. Pohl, C.J. Strauss, S. Nigam and J.L.F. Kock. 2007. The release of elongated, sheathed ascospores from bottle-shaped asci in *Dipodascus geniculatus*. FEMS Yeast Res. 7, 173–179.

van Herck, H., T. Duijser, P. Zwart, G.M. Dorrestein, M. Buitelaar and M.H. van der Hage. 1984. A bacterial proventriculitis of canaries. Avian Pathol. 13, 561–572.

van Maris, A.J., D.A. Abbott, E. Bellissimi, J. van den Brink, M. Kuyper, M.A. Luttik, H.W. Wisselink, W.A. Scheffers, J.P. van Dijken and J.T. Pronk. 2006. Alcoholic fermentation of carbon sources in biomass hydrolysates by *Saccharomyces cerevisiae*: current status. Antonie van Leeuwenhoek 90, 391–418.

van Niel, C.B. 1949. The "Delft School" and the rise of general microbiology. Bacteriol. Rev. 13, 161–174.

van Oevelen, D., M. Spaepen, P. Timmermans and H. Verachtert. 1977. Microbiological aspects of spontaneous wort fermentation in the production of Lambic and Geuze. J. Inst. Brew. 83, 356–360.

van Oorschot, C.A.N. 1980. A revision of *Chrysosporium* and allied genera. Stud. Mycol. 20, 1–89.

van Oorschot, C.A.N., and G.S. de Hoog. 1981. Dimorphic behaviour and taxonomy of *Trichosporiella sporotrichoides*. Antonie van Leeuwenhoek 47, 353–366.

van Ooyen, A.J.J., P. Dekker, M. Huang, M.M. Osthoorn, D.I. Jacobs, P.A. Colussi and C.H. Taron. 2006. Heterologous protein production in the yeast *Kluyveromyces lactis*. FEMS Yeast Res. 6, 381–392.

van Rensburg, P., M.L.A. Strauss, M.G. Lambrechts, R.R. Cordero Otero and I.S. Pretorius. 2007. The heterologous expression of polysaccharidase-encoding genes with oenological relevance in *Saccharomyces cerevisiae*. J. Appl. Microbiol. 103, 2248–2257.

van Rij, N.J.W., and O. Verona. 1949. Sopra alcuni lieviti delle olive. Atti Accad. Naz. Lincei 7, 249–253.

van Uden, N. 1952. Zur kenntnis von *Torulopsis pintolopesii* sp. nov. Arch. Mikrobiol. 17, 199–208.
van Uden, N. 1962. On the nomenclature of the genus *Metschnikowia* Kamienski. Rev. Biol. 3, 95–96.
van Uden, N., and L. Assis-Lopes. 1953a. Zur Kenntnis von *Kloeckera lodderi* sp. nov. Arch. Mikrobiol. 19, 262–266.
van Uden, N., and L. Assis-Lopes. 1953b. Zur Kenntnis von *Candida castellanii* sp. nov. Zugleich ein Beitrag zur Systematik von *Candida parakrusei* und *Candida krusoides*. Arch. Mikrobiol. 18, 356–361.
van Uden, N., and L. Assis-Lopes. 1957. Fermentation of raffinose in the absence of invertase by *Saccharomyces italicus* Castelli var. *melibiosi* nov. var. Port. Acta Biol., Ser. A, 4, 323–327.
van Uden, N., and H.R. Buckley. 1970. *Candida* Berkhout. In: J. Lodder (Ed.), The Yeasts, A Taxonomic Study, 2nd edn. North-Holland, Amsterdam, pp. 893–1087.
van Uden, N., and R. Castelo-Branco. 1961. *Metschnikowiella zobellii* sp. nov. and *M. krissii,* sp. nov., two yeasts from the Pacific Ocean pathogenic for *Daphnia magna*. J. Gen. Microbiol. 26, 141–148.
van Uden, N., and L. do Carmo-Sousa. 1957. Yeast from the bovine caecum. J. Gen. Microbiol. 16, 385–395.
van Uden, N., and L. do Carmo-Sousa. 1959. Further studies on the significance of temperature relations and vitamin deficiency patterns in yeast taxonomy. Port. Acta Biol., Ser. B 6, 239–256.
van Uden, N., and M. Farinha. 1958. On the significance of temperature relations and vitamin deficiency patterns in the delimitation of yeast species. Port. Acta Biol., Ser. B 6, 161–178.
van Uden, N., and M.C. Kolipinski. 1962. *Torulopsis haemulonii* nov. spec., a yeast from the Atlantic Ocean. Antonie van Leeuwenhoek 28, 78–80.
van Uden, N., and M. Vidal-Leiria. 1970. *Torulopsis* Berlese. In: J. Lodder (Ed.), The Yeasts, A Taxonomic Study, 2nd edn. North-Holland, Amsterdam, pp. 1235–1308.
van Uden, N., and S. Windisch. 1968. *Candida friedrichii* sp. n., a melibiose-fermenting yeast. Antonie van Leeuwenhoek 34, 270–274.
van Uden, N., and C.E. Zobell. 1962. *Candida marina* nov. spec., *Torulopsis torresii* nov. spec. and *T. maris* nov. spec., three yeasts from the Torres Strait. Antonie van Leeuwenhoek 28, 275–283.
van Vuuren, H.J.J., and B.D. Wingfield. 1986. Killer yeast. Cause of stuck fermentations in a wine cellar. S. Af. J. Enol. Vitic. 7, 113–118.
Vanbreuseghem, R. 1948. Sur une levure, *Candida truncata*, n. sp. isolée d'une dermatose présentée par le Dr. Eyckmans. Arch. Belg. Dermatol. Syphiligr. 4, 307–313.
Vanbreuseghem, R., and M. Takashio. 1970. An atypical strain of *Cryptococcus neoformans* (Sanfelice) Vuillemin 1894. Part II. *Cryptococcus neoformans* var. *gattii* var. nov. Ann. Soc. Belg. Méd. Trop. 50, 695–702.
Vancanneyt, M., R. Coopman, R. Tytgat, J.-F. Berny, G.L. Hennebert and K. Kersters. 1992. A taxonomic study of the basidiomycetous yeast genera *Rhodosporidium* Banno and *Rhodotorula* Harrison based on whole-cell protein patterns, DNA base compositions and coenzyme Q types. J. Gen. Appl. Microbiol. 38, 363–377.
Vancanneyt, M., R. Coopman, R. Tytgat, G.L. Hennebert and H. Kersters. 1994. Whole-cell protein patterns, DNA base compositions and coenzyme Q types in the yeast genus *Cryptococcus* Kützing and related taxa. Syst. Appl. Microbiol. 17, 65–75.
Vandamme, E.J. 1989. Biotechnology of Vitamins, Pigments, and Growth Factors. Elsevier Applied Science, London.
Vandamme, E.J., and W. Soetaert. 2002. Bioflavours and fragrances via fermentation and biocatalysis. J. Chem. Technol. Biotechnol. 77, 1323–1332.
Vanderhaegen, B., H. Neven, H. Verachtert and G. Derdelinckx. 2006. The chemistry of beer aging – a critical review. Food Chem. 95, 357–381.
Vanittanakom, N., C.R. Cooper Jr., M.C. Fisher and T. Sirisanthana. 2006. *Penicillium marneffei* infection and recent advances in the epidemiology and molecular biology aspects. Clin. Microbiol. Rev. 19, 95–110.
Vánky, K. 1998. The genus *Microbotryum* (smut fungi). Mycotaxon 67, 33–60.
Vánky, K. 2002. Illustrated Genera of Smut Fungi, 2nd edn. APS Press, St. Paul, MN, 238pp.
Vannelli, T., W.W. Qi, J. Sweigard, A.A. Gatenby and F.S. Sariasiani. 2007. Production of hydrocinnamic acid from glucose in *Saccharomyces cerevisiae* and *Escherichia coli* by expression of heterologous genes from plants and fungi. Metab. Eng. 9, 142–151.
Varela, C., J. Cardenas, F. Melo and E. Agosin. 2005. Quantitative analysis of wine yeast gene expression profiles under wine making conditions. Yeast 22, 369–383.
Varona, R., P. Perez and A. Duran. 1983. Effect of papulacandin B on beta-glucan synthesis in *Schizosaccharomyces pombe*. FEMS Microbiol. Lett. 20, 243–247.
Vartivarian, S.E., G.H. Reyes, E.S. Jacobson, P.G. James, R. Cherniak, V.R. Mumaw and M.J. Tingler. 1989. Localization of mannoprotein in *Cryptococcus neoformans*. J. Bacteriol. 171, 6850–6852.
Vasdinyei, R., and T. Deák. 2003. Characterization of yeast isolates originating from Hungarian dairy products using traditional and molecular identification techniques. Int. J. Food Microbiol. 86, 123–130.
Vasquez, J., A.G. Smulian, M.J. Linke and M.T. Cushion. 1996. Antigenic differences associated with genetically distinct *Pneumocystis carinii* from rats. Infect. Immun. 64, 290–297.
Vass, E., and A.J. Nappi. 1998. The effect of dietary yeast on the cellular immune response of *Drosophila melanogaster* against the larval parasitoid, *Leptopilina boulardi*. J. Parasitol. 84, 870–872.
Vasserot, Y., H. Christiaens, P. Chemardin, A. Arnaud and P. Galzy. 1989. Purification and properties of a betaglucosidase of *Hanseniaspora vineae* van der Walt and Tscheuschner with the view to its utilization in fruit aroma liberation. J. Appl. Bacteriol. 66, 271–279.
Vasserot, Y., P. Chemardin, A. Arnaud and P. Glazy. 1991. Purification and properties of the β-glucosidase of a new strain of *Candida molischiana* able to work at low pH values: possible use in the liberation of bound terpenols. J. Basic Microbiol. 31, 301–312.
Vasserot, Y., A. Arnaud and P. Glazy. 1993. Evidence for Muscat marc monoterpenol glucosides hydrolysis by free or immobilized yeast β-glucosidase. Bioresour. Technol. 43, 269–271.

Vaughan-Martini, A. 1984. Comparazione dei genomi del lievito *Pichia stipitis* e di alcune specie imperfette affini. Ann. Fac. Agrar. Univ. Perugia 66 38, 331–335.

Vaughan-Martini, A. 1989. *Saccharomyces paradoxus* comb. nov., a newly separated species of the *Saccharomyces sensu stricto* complex based upon nDNA/nDNA homologies. Syst. Appl. Microbiol. 12, 179–182.

Vaughan-Martini, A. 1991a. Evaluation of phylogenetic relationships among fission yeast by nDNA/nDNA reassociation and conventional taxonomic criteria. Yeast 7, 73–78.

Vaughan-Martini, A. 1991b. Intraspecific discontinuity within the yeast species *Cryptococcus albidus* as revealed by nDNA/nDNA reassociation. Exp. Mycol. 15, 140–145.

Vaughan-Martini, A. 1995. *Saccharomyces barnetti* and *Saccharomyces spencerorum*: two new species of *Saccharomyces sensu lato* (van der Walt). Antonie van Leeuwenhoek 68, 111–118.

Vaughan-Martini, A. 2003. Reflections on the classification of yeasts for different end-users in biotechnology, ecology, and medicine. Int. Microbiol. 6, 175–182.

Vaughan-Martini, A., and S. Barcaccia. 1996. A reconsideration of species related to *Saccharomyces dairensis* Naganishi. Int. J. Syst. Bacteriol. 46, 313–317.

Vaughan-Martini, A., and C.P. Kurtzman. 1985. Deoxyribonucleic acid relatedness among species of the genus *Saccharomyces sensu stricto*. Int. J. Syst. Bacteriol. 35, 508–511.

Vaughan-Martini, A., and C.P. Kurtzman. 1988. Deoxyribonucleic acid relatedness among species of *Saccharomyces* sensu lato. Mycologia 80, 241–243.

Vaughan-Martini, A., and A. Martini. 1987a. Three newly delimited species of *Saccharomyces sensu stricto*. Antonie van Leeuwenhoek 53, 77–84.

Vaughan-Martini, A., and A. Martini. 1987b. Taxonomic revision of the yeast genus *Kluyveromyces* by nuclear deoxyribonucleic acid reassociation. Int. J. Syst. Bacteriol. 37, 380–385.

Vaughan-Martini, A., and A. Martini. 1993. A taxonomic key to the genus *Saccharomyces*. Syst. Appl. Microbiol. 16, 113–119.

Vaughan-Martini, A., and A. Martini. 1995. Facts, myths and legends on the prime industrial microorganism. J. Ind. Microbiol. 14, 514–522.

Vaughan-Martini, A., and A. Martini. 1998. Genus *Saccharomyces*. In: C.P. Kurtzman and J.W. Fell (Eds), The Yeasts, A Taxonomic Study, 4th edn. Elsevier, Amsterdam, pp. 358–371.

Vaughan-Martini, A., and P. Pollacci. 1996. Synonymy of the yeast genera *Saccharomyces* Meyen ex Hansen and *Pachytichospora* van der Walt. Int. J. Syst. Bacteriol. 46, 318–320.

Vaughan-Martini, A., and G. Rosini. 1989. Killer relationships within the yeast genus *Kluyveromyces*. Mycologia 81, 317–321.

Vaughan-Martini, A., D.G. Sidenberg and M.A. Lachance. 1987. Analysis of a hybrid between *Kluyveromyces marxianus* and *Kluyveromyces thermotolerans* by physiological profile comparison, isoenzyme electrophoresis, DNA reassociation, and restriction mapping of ribosomal DNA. Can. J. Microbiol. 33, 971–978.

Vaughan-Martini, A., A. Martini and G. Cardinali. 1993. Electrophoretic karyotyping as a taxonomic tool in the genus *Saccharomyces*. Antonie van Leeuwenhoek 62, 145–156.

Vaughan-Martini, A., G. Cardinali and A. Martini. 1996a. Differential killer sensitivity as a tool for fingerprinting wine-yeast strains of *Saccharomyces cerevisiae*. J. Ind. Microbiol. 17, 124–127.

Vaughan-Martini, A., S. Barcaccia and P. Pollacci. 1996b. *Saccharomyces rosinii*: a new species of *Saccharomyces* sensu lato. Int. J. Syst. Bacteriol. 46, 615–618.

Vaughan-Martini, A., P. Angelini and G. Cardinali. 2000. Use of conventional taxonomy, electrophoretic karyotyping and DNA-DNA hybridization for the classification of fermentative apiculate yeasts. Int. J. Syst. Evol. Microbiol. 50, 1665–1672.

Vaughan-Martini, A., C.P. Kurtzman, S.A. Meyer and E.N. O'Neill. 2005. Two new species in the *Pichia guilliermondii* clade: *Pichia caribbica* sp. nov., the ascosporic state of *Candida fermentati*, and *Candida carpophila* comb. nov. FEMS Yeast Res. 5, 463–469.

Vazquez, F., and M.E. Toro. 1994. Occurrence of killer yeasts in Argentine wineries. World J. Microbiol. Biotechnol. 10, 358–359.

Veenhuis, M., J.P. van Dijken and W. Harder. 1983. The significance of peroxisomes in the metabolism of one-carbon compounds in yeasts. Adv. Microb. Physiol. 24, 1–82.

Veenstra, R.D. 1996. Size and selectivity of gap junction channels formed from different connexins. J. Bioenerg. Biomembr. 28, 327–337.

Vega, E.Z., B.A. Glatz and E.G. Hammond. 1988. Optimization of banana juice fermentation for the production of microbial oil. Appl. Environ. Microbiol. 54, 748–752.

Vega, F.E., M.B. Blackburn, C.P. Kurtzman and P.F. Dowd. 2003. Identification of a coffee berry borer-associated yeast: does it break down caffeine? Entomol. Exp. Appl. 107, 19–26.

Velázquez, E., J.M. Cruz- Sanchez, T. Rivas-Pala, J.L. Zurdo-Pineiro, P.F. Mateos, E. Monte, E. Martinez-Molina and A. Chordi. 2001. YeastIdent-Food/ProleFood, a new system for the identification of food yeasts based on physiological and biochemical tests. Food Microbiol. 18, 637–646.

Velázquez, E., M. del Villar, I. Grondona, E. Monte and T. González-Villa. 2006. Ultrastructural and chemotaxonomic analysis of a xylanolytic strain of *Cryptococcus adeliensis* isolated from sheep droppings in Spain. Arch. Microbiol. 186, 195–202.

Velez, A., J.C. Fernandez-Roldan, M. Linares and M. Casal. 1996. Melanonychia due to *Candida humicola*. Br. J. Dermatol. 134, 375–376.

Venitt, S., A. Myers and J.G. Manners. 1968. Studies of conjugation in *Protomyces inundatus*. Exp. Cell Res. 50, 9–18.

Venter, P., J.L.F. Kock, K.G. Sravan, A. Botha, D.J. Coetzee, P.J. Botes, R.K. Bhatt, J.R. Falck, T. Schewe and S. Nigam. 1997. Production of 3-hydroxy-polyenoic fatty acids by the yeast *Dipodascopsis uninucleata*. Lipids 32, 1277–1283.

Verbelen, P.J., D.P. de Schutter, F. Delvaux, K.J. Verstrepen and F.R. Delvaux. 2006. Immobilized yeast cell systems for continuous fermentation applications. Biotechnol. Lett. 28, 1515–1525.

Verdun, P. 1912. *Atelosaccharomyces hominis* (Vuillemin 1901.) Verdun. In: P. Verdun (Ed.), Précis de Parasitologie Humaine, 2nd edn. Doin et Fils, Paris, pp. 730–731.

Verdun, P. 1913. Précis de Parasitologie Humaine, 2nd edn. Doin et fils, Paris.
Verduyn, C., G.J. Breedveld, W.A. Scheffers and J.P. van Dijken. 1988. Metabolism of 2,3-butanediol in yeasts. Yeast 4, 135–142.
Verho, R., M. Putkonen, J. Londesborough, M. Penttilä and P. Richard. 2004. A novel NADH-linked L-xylulose reductase in the L-arabinose catabolic pathway of yeast. J. Biol. Chem. 279, 14746–14751.
Vero, S., P. Mondino, J. Burgueno, M. Soubes and M. Wisniewski. 2002. Characterization of biocontrol activity of two yeast strains from Uruguay against blue mold of apple. Postharvest Biol. Technol. 26, 91–98.
Verona, O.R. 1933. Boll. Ist. Sup. Agr., Pisa 9, p. 480.
Verona, O. 1935. Di due nuove specie di *Torulopsis* a pigmento rosso isolate dal terreno. Arch. Protistenkd. 85, 312–318.
Verona, O., and R. Ciferri. 1938. Revisione dei lievitia sporigeni del genere *Sporobolomyces* Kluyver et van Niel. Atti Ist. Bot. Univ. Pavia, Ser. IV 10, 241–255.
Verona, O., and G. Luchetti. 1941. Descrizione dei lieviti delle uve, dei mosti e dei vini. Garoglio-Tratt. Enol. 2, 288–297.
Verona, O., and G. Florenzano. 1947. Su di una nuova specie di *Brettanomyces* isolata da uva. Rend. Accad. Naz. Lincei, Ser. VIII, 3, 383–387.
Verona, O., and G. Luchetti. 1936. Ricerche microbiologiche su di alcuni vini ed alcune uve delle marche. Boll. Reg. Ist. Sup. Agr. Pisa 12, 256–311.
Verona, O., and G. Picci. 1958. A new species of *Trichosporon*: *Trichosporon hellenicum* n. sp. Ann. Microbiol. Enzimol. 8, 106–108.
Verona, O., and A. Rambelli. 1962a. Notizie intorno ai caratteri di alcune specie di *Taphrina* in fase saprofitaria (*Saprotaphrina*). Ann. Fac. Agric. Univ. Pisa n.s. 22, 1–36.
Verona, O., and A. Rambelli. 1962b. Presenza di lieviti e di specie lievitiforni in lettiere di bosco. Ann. Fac. Agric. Univ. Pisa n.s. 22, 37–46.
Verona, O., and A. Rambelli. 1962c. About two isolates labelled *Taphrina farlowii* Sad. and *Taphrina californica* Mix. Phytopathol. Z. 44, 169–272.
Verona, O., and O. Zardetto de Toledo. 1954. Indagini speciologiche sopra alcuni lieviti isolati dai fiori di vite nel territorio di S. Paolo in Brasile. Ann. Fac. Agrar. Pisa 15, 163–191.
Verona, O., and O. Zardetto de Toledo. 1959a. Considerazioni interno ad *Endomycopsis fibuliger* (Lindner) Dekker. Mycopathol. Mycol. Appl. 10, 209–215.
Verona, O., and O. Zardetto de Toledo. 1959b. Intorno ad un lievito osmofilo sistematicamente prossimo a *Saccharomyces elegans* Lodder et Kreger-van Rij. Mycopathol. Mycol. Appl. 11, 103–108.
Verrall, A.F. 1943. Fungi associated with certain ambrosia beetles. J. Agric. Res. 66, 135–144.
Verstrepen, K.J., and F.M. Klis. 2006. Flocculation, adhesion and biofilm formation in yeasts. Mol. Microbiol. 60, 5–15.
Verstrepen, K.J., P.J. Chambers and I.S. Pretorius. 2006. The development of superior yeast strains for the food and beverage industries: challenges, opportunities, and potential benefits. In: A. Querol and G.H. Fleet (Eds), Yeasts in Foods and Beverages. Springer-Verlag, Berlin, pp. 399–444.
Verwaal, R., J. Wang, J.P. Meijnen, H. Visser, G. Sandmann, J.A. van den Berg and A.J. van Ooyen. 2007. High-level production of beta-carotene in *Saccharomyces cerevisiae* by successive transformation with carotenogenic genes from *Xanthophyllomyces dendrorhous*. Appl. Environ. Microbiol. 73, 4342–4350.
Vesonder, R.F., I. Wickerham and W.K. Rohwedder. 1968. 3-D-Hydroxypalmitic acid: a metabolic product of the yeast NRRL Y-5954. Can. J. Chem. 46, 2628–2629.
Vesonder, R.F., F.H. Stodola, W.K. Rohwedder and D.B. Scott. 1970. 2-D-Hydroxyhexadecanoic acid: a metabolic product of the yeast *Hansenula sydowiorum*. Can. J. Chem. 48, 1985–1986.
Vidal-Leiria, M. 1966a. *Torulopsis mogii* sp. n. Antonie van Leeuwenhoek 32, 312–314.
Vidal-Leiria, M. 1966b. *Torulopsis vanderwaltii* sp. nov. Antonie van Leeuwenhoek 32, 447–449.
Vidal-Leiria, M. 1967. *Candida mogii* sp. n., a halotolerant yeast associated with miso fermentation. Antonie van Leeuwenhoek 33, 341–344.
Vidal-Leiria, M. 1976. Oxidation of *myo*-inositol by two yeast enzymes. Rev. Port. Quimica 18, 214–216.
Vidal-Leiria, M., and N. van Uden. 1963. *Candida silvae* sp. n., a yeast isolated from humans and horses. Antonie van Leeuwenhoek 29, 261–264.
Vidal-Leiria, M., and N. van Uden. 1973. Inositol dehydrogenase from the yeast *Cryptococcus melibiosum*. Biochim. Biophys. Acta 293, 295–303.
Vigentini, I., L. Brambilla, P. Branduardi, A. Merico, D. Porro and C. Compagno. 2005. Heterologous protein production in *Zygosaccharomyces bailii*: physiological effects and fermentative strategies. FEMS Yeast Res. 5, 647–652.
Vijayalakshmi, G., B. Shobha, V. Vanajakshi, S. Divakar and B. Manohar. 2001. Response surface methodology for optimization of growth parameters for the production of carotenoids by a mutant strain of *Rhodotorula gracilis*. Eur. Food Res. Technol. 213, 234–239.
Vilela, R., L. Mendoza, P.S. Rosa, A.F. Belone, S. Madeira, D.V. Opromolla and M.A. de Resende. 2005. Molecular model for studying the uncultivated fungal pathogen *Lacazia loboi*. J. Clin. Microbiol. 43, 3657–3661.
Vilgalys, R., and D. Gonzalez. 1990. Organization of ribosomal DNA in the basidiomycete *Thanatephorus praticola*. Curr. Genet. 18, 277–280.
Viljoen, B. 2006. Yeast ecological interactions. Yeast–yeast, yeast-bacteria, yeast-fungi interactions and yeasts as biocontrol agents. In: A. Querol and G.H. Fleet (Eds), Yeasts in Food and Beverages. Springer-Verlag, Berlin, pp. 83–110.
Villa-Carvajal, M., J.J.R. Coque, M.L. Alvarez-Rodriguez, F. Uruburu and C. Belloch. 2004. Polyphasic identification of yeasts isolated from bark of cork oak during the manufacturing process of cork stoppers. FEMS Yeast Res. 4, 745–750.
Villarruel, G., D.M. Rubio, F. Lopez, J. Cintioni, R. Gurevech, R. G. Romero and Y. Vandenplas. 2007. *Saccharomyces boulardii* in acute childhood diarrhea: a randomized, placebo controlled study. Acta Paediatr. 96, 538–541.
Villas-Bôas, S., E. Esposoito and M. de Mendonça. 2002. Novel lignocellulolytic ability of *Candida utilis* during solid-substrate cultivation on apple pomace. World J. Microbiol. Biotechnol. 18, 541–545.

Vinga, S., and J. Almeida. 2003. Alignment-free sequence comparison – a review. Bioinformatics 19, 513–523.

Visbal, G., G. San-Blas, J. Murgich and H. Franco. 2005. *Paracoccidioides brasiliensis*, paracoccidioidomycosis, and antifungal antibiotics. Curr. Drug Targets Infect. Disord. 5, 211–226.

Vishnevskaya, A.B., V.V. Kushnirov and M.D. Ter-Avanesyan. 2007. Neurogenerative amyloidoses: yeast model. Mol. Biol. 41, 308–315.

Vishniac, H.S. 1983. An enation system for the isolation of Antarctic yeasts inhibited by conventional media. Can. J. Microbiol. 29, 90–95.

Vishniac, H.S. 1985a. *Cryptococcus socialis* sp. nov. and *Cryptococcus consortionis* sp. nov. Int. J. Syst. Bacteriol. 35, 119–122.

Vishniac, H.S. 1985b. *Cryptococcus friedmannii*, a new species of yeast from the Antarctic. Mycologia 77, 149–153.

Vishniac, H.S. 1995. Simulated *in situ* competitive ability and survival of a representative soil yeast, *Cryptococcus albidus*. Microb. Ecol. 30, 309–320.

Vishniac, H.S. 2002. *Cryptococcus tephrensis*, sp. nov. and *Cryptococcus heimaeyensis*, sp. nov.; new anamorphic basidiomycetous yeast species from Iceland. Can. J. Microbiol. 48, 463–467.

Vishniac, H.S. 2006a. A multivariate analysis of soil yeasts isolated from a latitudinal gradient. Microb. Ecol. 52, 90–103.

Vishniac, H.S. 2006b. Yeast biodiversity in the Antarctic. In: G. Peter and C.A. Rosa (Eds), Biodiversity and Ecophysiology of Yeasts. Springer, Berlin, pp. 428–440.

Vishniac, H.S., and S. Baharaeen. 1982. Five new basidioblastomycetous yeast species segregated from *Cryptococcus vishniacii* emend. auct., an Antarctic yeast species comprising four new varieties. Int. J. Syst. Bacteriol. 32, 437–445.

Vishniac, H.S., and W.P. Hempfling. 1979a. Evidence of an indigenous microbiota (yeasts) in the dry valleys of Antarctica. J. Gen. Microbiol. 112, 301–314.

Vishniac, H.S., and W.P. Hempfling. 1979b. *Cryptococcus vishniacii* sp. nov., an Antarctic yeast. Int. J. Syst. Bacteriol. 29, 153–158.

Vishniac, H.S., and C.P. Kurtzman. 1992. *Cryptococcus antarcticus* sp. nov. and *Cryptococcus albidosimilis* sp. nov., basidioblastomycetes from Antarctic soils. Int. J. Syst. Bacteriol. 42, 547–553.

Vishniac, H.S., and S. Onofri. 2002. *Cryptococcus antarcticus* var. *circumpolaris* var. nov., a basidiomycetous yeast from Antarctica. Antonie van Leeuwenhoek 83, 231–233.

Vishniac, H.S., J.A. Anderson and A.B. Filonow. 1997. Assimilation of volatiles from ripe apples by *Sporidiobolus salmonicolor* and *Tilletiopsis washingtonensis*. Antonie van Leeuwenhoek 72, 201–207.

Visser, H., A.J.J. van Ooyen and J.C. Verdoes. 2003. Metabolic engineering of the astaxanthin-biosynthetic pathway of *Xanthophyllomyes dendrorhous*. FEMS Yeast Res. 4, 221–231.

Viswanathan, R., and H.S. Randhawa. 1959. *Candida viswanathii* sp. nov. isolated from a case of meningitis. Sci. Cult. 25, 86.

Vitovskaia, G., G.M. Samarkina, E.P. Anan'eva, A.S. Shashkov and A. Goncharov. 1988. The structure of extracellular heteroglycans in various *Cryptococcus* species. Bioorg. Khim. 14, 1405–1412.

Viviani, M.A., and N. Vanittanakom. 2005. Penicilliosis. In: W. G. Merz and R.J. Hay (Eds), Medical Mycology, 10th edn. Hodder Arnold, London, pp. 560–575.

Viviani, M.A., M. Cogliati, M.C. Esposto, K. Lemmer, K. Tintelnot, M.F. Valiente, D. Swinne, A. Velgraki, R. Velho and the ECMM Cryptococcosis Working Group. 2006. Molecular analysis of 311 *Cryptococcus neoformans* isolates from a 30 month ECMM survey of cryptococcosis in Europe. FEMS Yeast Res. 6, 614–619.

Vivoli, D., R. Avellaneda and E. de Bardessi. 1932. Glositis ulcerosa por *Monilia argentina* (n. sp.). Soc. Argent. Patol. Regional del Norte, Séptima Reunión, pp. 239–277.

Vlchkova-Lashkoska, M., S. Kamberova, A. Starova, L. Goleva-Mishevska, N. Tsatsa-Biljanovska, V. Janevska and M. Petrovska. 2004. Cutaneous *Cryptococcus laurentii* infection in a human immunodeficiency virus-negative subject. J. Eur. Acad. Dermatol. Venereol. 18, 99–100.

Vogel, C., A. Rogerson, S. Schatz, H. Laubach, A. Statzell-Tallman and J.W. Fell. 2007. Prevalence of yeasts in beach sand at three bathing beaches in South Florida. Water Res. 41, 1915–1920.

Vohra, A., and T. Satyanarayana. 2004. A cost-effective cane molasses medium for enhanced cell-bound phytase production by *Pichia anomala*. J. Appl. Microbiol. 97, 471–476.

Volkert, F.C., D.W. Wilson and J.R. Broach. 1989. Deoxyribonucleic acid plasmids in yeasts. Microbiol. Rev. 53, 299–317.

Volz, P.A., and S.L. Parent. 1998. Space flight micro-fungi after 27 years storage in water and continuous culture. Microbios 96, 111–125.

von Arx, J.A. 1972. On *Endomyces*, *Endomycopsis* and related yeast-like fungi. Antonie van Leeuwenhoek 38, 289–309.

von Arx, J.A. 1977a. Notes on *Dipodascus*, *Endomyces* and *Geotrichum* with the description of two new species. Antonie van Leeuwenhoek 43, 333–340.

von Arx, J.A. 1977b. Centraalbureau voor Schimmelcultures Baarn and Delft Progress Report 1976. Verh. K. Ned. Akad. Wet. Afd. Natuurkd. Reeks 2, 68, 84–107.

von Arx, J.A. 1978. Centraalbureau voor Schimmelcultures Baarn and Delft Progress Report 1977. Verh. K. Ned. Akad. Wet. Afd. Natuurkd. Reeks 2, 71, 175–195.

von Arx, J.A. 1979a. Centraalbureau voor Schimmelcultures Progress Report 1978. Verh. K. Ned. Akad. Wet. Amsterdam Afd. Natuurkd. Reeks 2, 73, 101–125.

von Arx, J.A. 1979b. Propagation in the yeasts and yeast-like fungi. In: B. Kendrick (Ed.), The Whole Fungus, Proc. 2nd Int. Mycol. Conf., Kananaskis, Vol. 2. National Museums of Canada, Ottawa, pp. 555–571.

von Arx, J.A. 1981. The genera of fungi sporulating in pure culture. J. Cramer, Vaduz, Switzerland.

von Arx, J.A., and E. Müller. 1984. Notes on some Ascomycetes. Sydowia Ann. Mycol. 37, 6–10.

von Arx, J.A., and J.P. van der Walt. 1976. The ascigerous state of *Candida chodatii*. Antonie van Leeuwenhoek 42, 309–314.

von Arx, J.A., and J.P. van der Walt. 1986. Are yeast cells of Endomycetales homologues of conidia of Eurotiales? Persoonia 13, 161–171.

von Arx, J.A., and J.P. van der Walt. 1987. Ophiostomatales and Endomycetales. In: G.S. de Hoog, M.Th. Smith and A. C.M. Weijman (Eds), The Expanding Realm of Yeast-like Fungi. Elsevier, Amsterdam, pp. 167–176. (Stud. Mycol. 30, 167–176).

von Arx, J.A., and A.C.M. Weijman. 1979. Conidiation and carbohydrate composition in some *Candida* and *Torulopsis* species. Antonie van Leeuwenhoek 45, 547–555.
von Arx, J.A., and D. Yarrow. 1984. The adventures of the yeast genus *Endomycopsis* Dekker. Antonie van Leeuwenhoek 50, 799–805.
von Arx, J.A., L. Rodrigues de Miranda, M.Th. Smith and D. Yarrow. 1977. The genera of yeasts and the yeast-like fungi. Stud. Mycol. 14, 1–42.
von Arx, J.A., J.P. van der Walt and N.V.D.M. Liebenberg. 1982. The classification of *Taphrina* and other fungi with yeast-like cultural states. Mycologia 74, 285–296.
von der Haar, T., L. Josse, P. Wright, J. Zenbthon and M.F. Tufte. 2007. Development of a novel yeast cell-based assay for studying the aggregation of Alzheimer's disease-associated A beta peptides *in vivo*. Neurodegener. Dis. 4, 136–147.
von Höhnel, F.X.R. 1917. Mycologische Fragmente. Ann. Mycol. 15, 293.
von Klopotek, A. 1967. *Blastobotrys nivea*, gen. nov., sp. nov. Arch. Mikrobiol. 58, 92–96.
von Nägeli, C. 1879. Theorie der Gahrung. Ein Beitrag zur Molekularphysiologie. München.
von Richter, A.A. 1912. Über einen osmophilen Organismus den Hefepilz *Zygosaccharomyces mellis acidi* sp. n. Mycol. Zentralbl. 1, 67–76.
von Stosch, H.A. 1966. Eine algologische Seltenheit, *Saprochaete saccharophila* Coker u. Shanor, in Hessen. Hess. Flor. Briefe 15, 21–28.
von Stosch, H.A. 1967. Bemerkungen zur Physiologie und Morphologie der pigmentfreien Alga *Saprochaete saccharophila* Coker und Shanor. Le Botaniste 50, 437–455.
von Szilvinyi, A. 1934. *Blastodendrion canis* nov. sp.; ein Beitrag zur Diagnose und Systematik der asporogenen Sprosspilze. Zentralbl. Bakteriol. Parasitenkd., Abt. II, 89, 284–299.
von Szilvinyi, A., and L. Kaulich. 1948. Zur Kenntnis der Mikroflora Österreichischer Kernobstmoste. Mitt. Versuchsanst. Gärungsgewerbe Inst. angew. Mikrobiol. Hochschule Bodenkultur 4, 1–3.
von Thümen, F.K.A.E.J. 1874. Hedwigia 13, 97 (cited by Reddy and Kramer 1975).
von Thümen, F.K.A.E.J. 1875. Mycotheca Universalis, No. 289.
von Wettstein, F. 1921. Das Vorkommen von Chitin und seine Verwertung als systematisch-phylogenetisches Merkmal im Pflanzenreich. Sitzungsber. Akad. Wiss. Wien, Math.-Naturw. Kl., Abt. I, 130, 3–20.
von Wettstein, R. 1885. Untersuchungen über einen neuen pflanzlichen Parasiten des menschlichen Körpers. Sitzungsber. Akad. Wiss. Wien, Abt. I, 19, 33–59.
Vörös-Felkai, G. 1961. Studies on arthrosporogenous yeasts. Acta Microbiol. Hung. 8, 95–102.
Vuillemin, P. 1898. Les caractères spécifiques du champignon du muguet (*Endomyces albicans*). C.R. Acad. Sci. 127, 630–633.
Vuillemin, P. 1901. Les blastomycètes pathogènes. Rev. Gen. Sci. 12, 732–751.
Vuillemin, P. 1902. *Trichosporum* et trichospories. Arch. Parasitol. 5, 38–66.
Vuillemin, P. 1911. Différence fondamentale entre le genre *Monilia* et les genres *Scopulariopsis*, *Acrosporium* et *Catenularia*. Bull. Soc. Mycol. Fr. 27, 137–152.
Vuillemin, P. 1931. Les Champignons Parasites et les Mycoses de l'Homme. Encyclopédie Mycologique, Vol. 2. Lechedevalier, Paris.
Vustin, M.M., G.I. Naumov, I.P. Bab'eva and T.I. Naumova. 1982. Genosystematics of the yeast *Williopsis saturnus* – new biological species. Dokl. Akad. Nauk. SSSR 267, 1481–1484. In Russian.
Vustin, M.M., T.M. Shemiakina, I.P. Bab'eva, I.S. Reshetova and E.A. Timokhina. 1988. A new antibiotic produced by the yeast *Williopsis pratensis* Babjeva et Reshetova. Dokl. Akad. Nauk. SSSR 302, 724–727.
Waché, Y., G. Husson, G. Feron and J.-M. Belin. 2006. Yeast as an efficient biocatalyst for the production of lipid-derived flavours and fragrances. Antonie van Leeuwenhoek 89, 405–416.
Wada, M., K. Okabe, M. Kataoka, S. Shimizu, A. Yokota and H. Takagi. 2008. Distribution of L-azetidine-2-carboxylate *N*-acetyltransferase in yeast. Biosci. Biotechnol. Biochem. 72, 582–586.
Wada, Y., T. Kobayashi, M. Takahashi, H. Nakanishi, S. Mori and N.K. Nishizawa. 2006. Metabolic engineering of *Saccharomyces cerevisiae* producing nicotianamine: potential for industrial biosynthesis of a novel antihypertensive substrate. Biosci. Biotechnol. Biochem. 70, 1408–1415.
Wade, W.N., R. Vasdinnyei, T. Deák and L.R. Beuchat. 2003. Proteolytic yeasts isolated from raw, ripe tomatoes and metabolic association of *Geotrichum candidum* with *Salmonella*. Int. J. Food Microbiol. 86, 101–112.
Wagner, D.T.S., and C.J. Dawes. 1970. Revision of the systematic position of *Saprochaete saccharophila*. Mycologia 62, 791–796.
Wagner, R.P. 1944. The nutrition of *Drosophila mulleri* and *D. aldrichi*. Growth of larvae on cactus extract and microorganisms found in cactus. Univ. Texas Publ. 4445, 104–128.
Wagner, R.P. 1949. Nutritional differences in the *mulleri* group. Univ. Texas Publ. 4920, 39–41.
Wahyuningsih, R., I.N. SahBandar, B. Theelen, F. Hagen, G. Poot, J.F. Meis, A. Rozalyani, R. Sjam, D. Widodo, S. Djauzi and T. Boekhout. 2008. *Candida nivariensis* isolated from an Indonesian HIV-infected patient suffering from oropharyngeal candidiasis. J. Clin. Microbiol. 46, 388–391.
Wainwright, M. 1992. The impact of fungi on environmental biogeochemistry. In: G.C. Carroll and D.T. Wicklow (Eds), The Fungal Community, Its Organization and Role in the Ecosystem, 2nd edn. Marcel Dekker, New York, pp. 601–618.
Wainwright, M., and A.M.K. Falih. 1996. Involvement of yeasts in urea hydrolysis and nitrification in soil amended with a natural source of sucrose. Mycol. Res. 100, 307–310.
Walker, G.M. 1998. Yeast. Physiology and Biotechnology. John Wiley & Sons, Chichester.
Walker, G., and P. van Dijck. 2006. Physiological and molecular responses of yeasts to the environment. In: A. Querol and G.H. Fleet (Eds), Yeasts in Food and Beverages. Springer-Verlag, Berlin, pp. 111–152.
Walker, G.M., A.H. McLeod and V.J. Hodgson. 1995. Interactions between killer yeasts and pathogenic fungi. FEMS Microbiol. Lett. 127, 213–222.
Walker, H.W. 1977. Spoilage of food by yeasts. Food Technol. 65 31, 57–61.
Walker, H.W., and J.C. Ayres. 1970. Yeasts as spoilage organisms. In: A.H. Rose and J.S. Harrison (Eds), The Yeasts, Vol. 3. Academic Press, London, pp. 463–528.

Walker, J.D., and R.S. Pore. 1978. Growth of *Prototheca* isolates on *n*-hexadecane and mixed-hydrocarbon substrate. Appl. Environ. Microbiol. 35, 694–697.

Walker, J.D., R.R. Colwell, Z. Vaituzis and S.S. Meyer. 1975. Petroleum-degrading achlorophyllous alga *Prototheca zopfii*. Nature 254, 423–424.

Walker, L.B. 1931. Studies on *Ascoidea rubescens*. I. History and development. Mycologia 23, 51–76.

Walker, L.B. 1935. Studies on *Ascoidea rubescens*. II. Cytological observations. Mycologia 27, 102–127.

Walker, W.F. 1984. 5S rRNA sequences from Atractiellales, and basidiomycetous yeasts and fungi imperfecti. Syst. Appl. Microbiol. 5, 352–359.

Walker, W.F. 1985. 5S ribosomal RNA sequences from ascomycetes and evolutionary implications. Syst. Appl. Microbiol. 6, 48–53.

Walker, W.F., and W.F. Doolittle. 1982. Redividing the basidiomycetes on the basis of 5S rRNA nucleotide sequences. Nature (London) 299, 723–724.

Wall, M.J., A.J. Quinn and G.B. D'Cunha. 2008. Manganese (Mn^{2+})-dependent storage stabilization of *Rhodotorula glutinis* phenylalanine ammonia-lyase activity. J. Agric. Food Chem. 56, 894–902.

Walsh, G. 2003. Biopharmaceuticals. Biochemistry and Biotechnology, 2nd edn. John Wiley and Son, Chichester.

Walsh, G. 2005. Biopharmaceuticals: recent approvals and likely directions. Trends Biotechnol. 23, 553–558.

Walsh, G. 2006. Biopharmaceutical benchmarks 2006. Nat. Biotechnol. 24, 769–776.

Walsh, T.J., A. Groll, J. Hiemenz, R. Fleming, E. Roilides and E. Anaissie. 2004. Infections due to emerging and uncommon medically important fungal pathogens. Clin. Microbiol. Infect. 10, 48–66.

Walters, L.S. 1943. Studies of yeast causing defects in beer II. The distinguishing characters of *Torulopsis cylindrica* nov. sp., a yeast causing a turbidity and unpleasant taste and smell in beer. J. Inst. Brew. 59, 253–256.

Walzer, P.D., V. Schnelle, D. Armstrong and P.P. Rosen. 1977. Nude mouse: a new experimental model for *Pneumocystis carinii* infection. Science 197, 177–179.

Wan, Y., and S. Tian. 2005. Integrated control of postharvest diseases of pear fruits using antagonistic yeasts in combination with ammonium molybdate. J. Sci. Food Agric. 85, 2605–2610.

Wan, Y., S. Tian and G.Z. Qin. 2003. Enhancement of biocontrol activity of yeasts by adding sodium bicarbonate or ammonium molybdate to control postharvest diseases of pears. Lett. Appl. Microbiol. 37, 249–253.

Wanderley, K.J., F.A. Torres, L.M. Moraes and C.J. Ujhoa. 2004. Biochemical characterization of alpha-amylase from the yeast *Cryptococcus flavus*. FEMS Microbiol. Lett. 231, 165–169.

Wang, C.J.K., and R.A. Zabel. 1990. Identification Manual for Fungi from Utility Poles in the Eastern United States. Allen Press, Lawrence.

Wang, Q.-M., and F.-Y. Bai. 2004. Four new species of the genus *Sporobolomyces* from plant leaves. FEMS Yeast Res. 4, 579–586.

Wang, Q.-M., F.-Y. Bai, B. Fungsin, T. Boekhout and T. Nakase. 2010. Proposal of Mingxiaea gen. nov. for the anamorphic basidiomycetous yeast species in the Bulleribasidium clade (Tremellales) based on molecular phylogenetic analysis and description of four novel Mingxiaea species. Int. J. Syst. Evol. Microbiol. (Epub ahead of print).

Wang, Q.-M., and F.-Y. Bai. 2008. Molecular phylogeny of basidiomycetous yeasts in the *Cryptococcus luteolus* lineage (Tremellales) based on nuclear rRNA and mitochondrial cytochrome b gene sequence analyses: proposal of *Derxomyces* gen. nov. and *Hannaella* gen. nov., and description of eight novel *Derxomyces* species. FEMS Yeast Res. 8, 799–814.

Wang, Q.-M., F.-Y. Bai, J.-H. Zhao and J.-H. Jia. 2003a. *Bensingtonia changbaiensis* sp. nov. and *Bensingtonia sorbi* sp. nov., novel ballistoconidium-forming yeast species from plant leaves. Int. J. Syst. Evol. Microbiol. 53, 2085–2089.

Wang, Q.-M., F.-Y. Bai, J.-H. Zhao and J.-H. Jia. 2003b. *Dioszegia changbaiensis* sp. nov., a basidiomycetous yeast species isolated from northeast China. J. Gen. Appl. Microbiol. 49, 295–299.

Wang, Q.-M., F.-Y. Bai, H.-Z. Lu, J.-H. Jia and M. Takashima. 2004. *Bullera cylindrica* sp. nov., *Bullera hubeiensis* sp. nov. and *Bullera nakasei* sp. nov., ballistoconidium-forming yeast species from plant leaves. Int. J. Syst. Evol. Microbiol. 54, 1877–1882.

Wang, Q.-M., J.-H. Jia and F.-Y. Bai. 2006a. *Bensingtonia pseudonaganoensis* sp. nov., a novel ballistoconidium-forming yeast species isolated from plant leaves. Antonie van Leeuwenhoek 89, 261–266.

Wang, Q.-M., J.-H. Jia and F.-Y. Bai. 2006b. *Pseudozyma hubeiensis* sp. nov. and *Pseudozyma shanxiensis* sp. nov., novel ustilaginomycous anamorphic yeast species from plant leaves. Int. J. Syst. Evol. Microbiol. 56, 289–293.

Wang, Q.-M., S.-A. Wang, J.-H. Jia and F.-Y. Bai. 2007. *Cryptococcus tibetensis* sp. nov., a novel basidiomycetous anamorphic yeast species isolated from plant leaves. J. Gen. Appl. Microbiol. 53, 281–285.

Wang, L., A. Gamez, C.N. Sarkissian, M. Straub, M.G. Patch, G. W. Han, S. Striepeke, P. Fitzpatrick, C.R. Scriver and R.C. Stevens. 2005. Structure-based chemical modification strategy for enzyme replacement treatment of phenylketonuria. Mol. Genet. Metab. 86, 134–140.

Wang, S.-A., and F.-Y. Bai. 2008. *Saccharomyces arboricolus* sp. nov., a yeast species from tree bark. Int. J. Syst. Evol. Microbiol. 58, 510–514.

Wang, S.A., J.H. Jia and F.Y. Bai. 2008. *Candida alocasiicola* sp. nov., *Candida hainanensis* sp. nov., *Candida heveicola* sp. nov. and *Candida musiphila* sp. nov., novel anamorphic, ascomycetous yeast species isolated from plants. Antonie van Leeuwenhoek 94, 257–265.

Wang, T.T., C.F. Lee and B.H. Lee. 1999. The molecular biology of *Schwanniomyces occidentalis* Klöecker. Crit. Rev. Biotechnol. 19, 113–143.

Ward, H.M. 1892. The ginger-beer plant, and the organisms composing it: a contribution to the study of fermentation – yeasts and bacteria. Philos. Trans. R. Soc. London 183, 125–197.

Ward, T.J., and J.L. Baker. 1929. *Saccharomyces festinans*. J. Inst. Brew. 35, 466–468.

Wardlaw, A.M., T.E. Berkers, K.C. Man and M.A. Lachance. 2009. Population structure of two beetle-associated yeasts: comparison of a New World asexual and an endemic Nearctic sexual species in the *Metschnikowia* clade. Antonie van Leeuwenhoek 96, 1–15.

Warrand, J. 2006. Healthy polysaccharides – the next chapter in food products. Food Technol. Biotechnol. 44, 355–370.

Warren, R.C. 1972. Interference by common leaf saprophytic fungi with the development of *Phoma betae* lesions on sugar beet leaves. Ann. Appl. Biol. 72, 137–144.

Warth, A.D. 1977. Mechanism of resistance of *Saccharomyces bailii* to benzoic, sorbic and other weak acids used as food preservatives. J. Appl. Bacteriol. 43, 215–230.

Wartmann, T., and G. Kunze. 2003. Expression of heterologous genes in *Arxula adeninivorans* budding cells and mycelia. In: K. Wolf, K. Breunig and G. Barth (Eds), Nonconventional Yeasts in Genetics, Biochemistry and Biotechnology. Springer Verlag, Berlin, pp. 7–12.

Wartmann, T., E. Boër, A.H. Pico, H. Sieber, O. Bartelsen, G. Gellissen and G. Kunze. 2002. High-level production and secretion of recombinant proteins by the dimorphic yeast *Arxula adeninivorans*. FEMS Yeast Res. 2, 363–369.

Watanabe, K., Y. Shimada, K. Kawaharada, K. Suzuki and F. Tanaka. 1973. Process for fermentative production of yeast cells. US Patent 3725200.

Waterham, H.R., and R.J.A. Wanders. 2007. *Saccharomyces cerevisiae* as a tool for human gene function discovery. Methods Microbiol. 36, 577–595.

Waters, M.D., and J.M. Fostel. 2004. Toxicogenomics and systems toxicology: aims and prospects. Nat. Rev. Genet. 5, 936–948.

Watson, K.G. 1987. Temperature relations. In: A.H. Rose and J.S. Harrison (Eds), The Yeasts, 2nd edn. Vol. 1. Academic Press, London, pp. 41–71.

Watson, K., H. Arthur and H. Morton. 1978. Thermal adaptation in yeast: obligate psychrophiles are obligate aerobes, and obligate thermophiles are facultative anaerobes. J. Bacteriol. 136, 815–817.

Wattanachaisaereekul, S., A.E. Lantz, M.L. Nielsen, O.S. Andresson and J. Nielsen. 2007. Optimization of heterologous production of the polyketide 6-MSA in *Saccharomyces cerevisiae*. Biotechnol. Bioeng. 97, 893–900.

Wazir, J.F., and N.A. Ansari. 2004. *Pneumocystis carinii* infection. Update and review. Arch. Pathol. Lab. Med. 128, 1023–1027.

Webb, J.S., M. Nixon, I.M. Eastwood, M. Greenhalgh, G.D. Robson and P.S. Handley. 2000. Fungal colonization and biodeterioration of plasticized polyvinyl chloride. Appl. Environ. Microbiol. 66, 3194–3200.

Weber, G., F. Spaaij and J.P. van der Walt. 1992. *Kluyveromyces piceae* sp. nov., a new yeast species isolated from the rhizosphere of *Picea abies* (L.) Karst. Antonie van Leeuwenhoek 63, 239–244.

Weber, R.W.S., and P. Davoli. 2003. Teaching techniques for mycology: 20. Astaxanthin, a carotenoid of biotechnological potential importance from yeast and salmonid fish. Mycologist 17, 30–34.

Weber, R.W.S., P. Davoli and H. Anke. 2006. A microbial consortium involving the astaxanthin producer *Xanthophyllomyces dendrorhous* on freshly cut birch stumps in Germany. Mycologist 20, 57–61.

Weber, R.W.S., J. Becerra, M.J. Silva and P. Davoli. 2008. An unusual *Xanthophyllomyces* strain from leaves of *Eucalyptus globulus* in Chile. Mycol. Res. 112, 861–867.

Weber, U. 1922. Beitrag zur Kenntnis der esterbildenden Hefen. Biochem. Z. 129, 208–216.

Webster, A.J., R.J. Payne and M. Pagel. 2003. Molecular phylogenies link rates of evolution and speciation. Science 301, 478.

Webster, J., R.A. Davey, G.A. Duller and C.T. Ingold. 1984. Ballistospore discharge in *Itersonilia perplexans*. Trans. Br. Mycol. Soc. 82, 13–29.

Wegner, G.H. 1983. Biochemical conversions by yeast fermentation at high cell densities. US Patent 4,329,414.

Wegner, G.H. 1990. Emerging applications of the methylotropic yeasts. FEMS Microbiol. Rev. 87, 279–284.

Wehmer, C. 1906. Durch Pilzenzyme bewirkte Stärkeverzuckerung im Brennereigewerbe. Mycologie der Rumbrennerei und der Arrakbereitung. In: F. Lafar (Ed.), Handbuch der Technischen Mycologie. G. Fischer, Jena, pp. 319–342.

Wei, Y.-H., F.-L. Lee, W.-H. Hsu, S.-R. Chen, C.-C. Chen, C.-Y. Wen, S.-J. Lin, W.-S. Chu, G.-F. Yuan and G.-Y. Liou. 2005. *Pseudozyma antarctica* in Taiwan: a description based on morphological, physiological and molecular characteristics. Bot. Bull. Acad. Sin. 46, 223–229.

Wei, Y.-H., G-Y. Liou, H.-Y., Liu and F.-L. Lee. 2010. *Sympodiomycopsis kandeliae* sp. nov., a novel basidiomycetous anamorphic fungus from mangroves in Taiwan. Int. J. Sysy. Evol. Microbiol., March 26, doi:10.1099/ijs.0.021865-0.

Weidman, F.D. 1925. Exfoliative dermatitis in the Indian rhinoceros (*Rhinoceros unicornis*), with description of a new yeast species, *Pityrosporum pachydermatis*. In: H. Fox (Ed.), Report of the Laboratory and Museum of Comparative Pathology of the Zoological Society of Philadelphia, pp. 36–44.

Weig, M., and A.J.P. Brown. 2007. Genomics and the development of new diagnostics and anti-*Candida* drugs. Trends Microbiol. 15, 310–317.

Weig, M., L. Jansch, U. Gross, C.G. de Koster, F.M. Klis and P.W.J. de Groot. 2004. Systematic identification *in silico* of covalently bound cell wall proteins and analysis of protein–polysaccharide linkages of the human pathogen *Candida glabrata*. Microbiology 150, 3129–3144.

Weigmann, H., and A. Wolff. 1909. Uber einige zum "Rübengeschmack" der Butter beitragende Mycelpilze. Zentralbl. Bakteriol. Parasitenkd. Abt. 2, 22, 657–671.

Weiher, E., and P. Keddy. 2001. Ecological Assembly Rules: Perspectives, Advances, Retreats. Cambridge University Press, Cambridge.

Weijman, A.C.M. 1979b. Carbohydrate composition and taxonomy of *Geotrichum*, *Trichosporon* and allied genera. Antonie van Leeuwenhoek 45, 43–51.

Weijman, A.C.M. 1976. Cell wall composition and taxonomy of *Cephaloascus fragrans* and some Ophiostomataceae. Antonie van Leeuwenhoek 42, 315–324.

Weijman, A.C.M. 1977. Carbohydrate composition and taxonomy of the genus *Dipodascus*. Antonie van Leeuwenhoek 43, 323–331.

Weijman, A.C.M. 1979a. Carbohydrate patterns of *Moniliella*, *Trichosporonoides* and *Hyalodendron*. Stud. Mycol. 19, 76–80.

Weijman, A.C.M., and G.S. de Hoog. 1985. Carbohydrate patterns and taxonomy of *Sporothrix* and *Blastobotrys*. Antonie van Leeuwenhoek 51, 111–120.

Weijman, A.C.M., and W.I. Golubev. 1987. Carbohydrate patterns and taxonomy of yeasts and yeast-like fungi. In: G.S. de Hoog, M.Th. Smith and A.C.M. Weijman (Eds), The

Expanding Realm of Yeast-like Fungi. Elsevier, Amsterdam, pp. 361–371. (Stud. Mycol. 30, 361–371).
Weijman, A.C.M., and L. Rodrigues de Miranda. 1983. Xylose distribution within and taxonomy of the genera *Bullera* and *Sporobolomyces*. Antonie van Leeuwenhoek 49, 559–562.
Weijman, A.C.M., and L. Rodrigues de Miranda. 1988. Carbohydrate patterns of *Candida*, *Cryptococcus* and *Rhodotorula* species. Antonie van Leeuwenhoek 54, 535–543.
Weijman, A.C.M., and J.P. van der Walt. 1989. Carbohydrate profiles and the taxonomic concept of the Lipomycetaceae. Stud. Mycol. 31, 193–199.
Weijman, A.C.M., L. Rodrigues de Miranda and J.P. van der Walt. 1988. Redefinition of *Candida* Berkhout and the consequent emendation of *Cryptococcus* Kützing and *Rhodotorula* Harrison. Antonie van Leeuwenhoek 54, 545–553.
Weiler, F., and M.J. Schmitt. 2003. *Zygo*cin, a secreted antifungal toxin of the yeast *Zygosaccharomyces bailii*, and its effect on sensitive fungal cells. FEMS Yeast Res. 3, 69–76.
Weis, J.D. 1902. Four pathogenic torulae (Blastomycetes). J. Med. Res. 7, 280–311.
Weiser, J., R. Wegensteiner, U. Händel and Z. Žižka. 2003. Infections with the ascomycete fungus *Metschnikowia typographi* sp. nov. in the bark beetles Ips *typographicus* and *Ips amitinus* (Coleoptera, Scolytidae). Folia Microbiol. 48, 611–618.
Weiss, A., J. Delproposto and C.N. Giroux. 2004a. High-throughput phenotypic profiling of gene–environment interactions by quantitative growth curve analysis in *Saccharomyces cerevisiae*. Anal. Biochem. 327, 23–34.
Weissß, M., R. Bauer and D. Begerow. 2004b. Spotlights on Heterobasidiomycetes. In: R. Agerer, P. Blanz and M. Piepenbring (Eds), Frontiers in Basidiomycote Mycology. IHW-Verlag, Eching, pp. 7–48.
Weissß, S.J., P.E. Schoch and B.A. Cunha. 1991. *Malassezia furfur* fungemia associated with central venous catheter lipid emulsion infusion. Heart Lung 20, 87–90.
Wellinghausen, N., D. Siegel, J. Winter and S. Gebert. 2009. Rapid diagnosis of candidaemia by real-time PCR detection of *Candida* DNA in blood samples. J. Med. Microbiol. 58, 1106–1111.
Wells, D.E. 1954. *Ascocybe*, a new genus of lower ascomycetes. Mycologia 46, 37–51.
Wells, G.M., A. Gajjar, T.A. Pearson, K.L. Hale and J.L. Shenep. 1998. Pulmonary cryptosporidiosis and *Cryptococcus albidus* fungemia in a child with acute lymphocytic leukemia. Med. Pediatr. Oncol. 31, 544–546.
Wells, J.M. 1977. Sour rot of peaches caused by *Monilia implicata* and *Geotrichum candidum*. Phytopathology 67, 404–408.
Wells, K. 1994. Jelly fungi, then and now. Mycologia 86, 18–48.
Wells, K., and R.J. Bandoni. 2001. Heterobasidiomycetes. In: D.J. McLaughlin, E.G. McLaughlin and P.A. Lemke (Eds), The Mycota VII, Systematics and Evolution, Part B. Springer-Verlag, Berlin, pp. 85–120.
Welthagen, J.J., and B.C. Viljoen. 1998. Yeast profile in Gouda cheese during processing and ripening. Int. J. Food Microbiol. 41, 185–194.
Went, F.A.F.C., and H.C. Prinsen Geerligs. 1894. Over suikeren alcoholvorming door organismen in verband met de verwerking der naproducten in rietsuikerfabrieken. Arch. Suikerind. Ned. Indie III. Meded. Proefst. Java-Suikerind. 13, 529–549.
Wertheim, B., L.E.M. Vet and M. Dicke. 2003. Increased risk of parasitism as ecological costs of using aggregation pheromones: laboratory and field study of *Drosophila*–*Leptoppilina* interaction. Oikos 100, 269–282.
West, G.S. 1916. Algae Vol. 1, Cambridge University Press, Cambridge, 475pp.
Wheals, A.E., L.C. Basso, D.M. Alves and H.V. Amorim. 1999. Fuel ethanol after 25 years. Trends Biotechnol. 12, 482–487.
Wheat, L.J. 2006. Histoplasmosis: a review for clinicians from non-endemic areas. Mycoses 49, 274–282.
Wheeler, W.C., J. Gatesy and R. DeSalle. 1995. Elision: a method for accommodating multiple molecular sequence alignments with alignment-ambiguous sites. Mol. Phylogenet. Evol. 4, 1–9.
Whelan, S. 2007. New approaches to phylogenetic tree search and their application to large numbers of protein alignments. Syst. Biol. 56, 727–740.
Whelan, S., and N. Goldman. 2001. A general empirical model of protein evolution derived from multiple protein families using a maximum-likelihood approach. Mol. Biol. Evol. 18, 691–699.
Whelan, S., P. Liò and N. Goldman. 2001. Molecular phylogenetics: state-of-the-art methods for looking into the past. Trends Genet. 17, 262–272.
Whelden, R.M. 1935. Observations on the cytology of *Sebacina globospora*, n. sp. Rhodora 37, 121–128.
Whiffen, A.J. 1948. The production, assay and antibiotic activity of actidione, an antibiotic from *Streptomyces griseus*. J. Bacteriol. 56, 283–291.
White, J.H., A.R. Butler and M.J.R. Stark. 1989. *Kluyveromyces lactis* toxin does not inhibit yeast adenyl cyclase. Nature 341, 666–668.
White, W.L. 1942. A new hemiascomycete. Can. J. Res. (Sect. C) 20, 389–395.
Wickerham, L.J. 1946. A critical evaluation of the nitrogen assimilation tests commonly used in the classification of yeasts. J. Bacteriol. 52, 293–301.
Wickerham, L.J. 1951. Taxonomy of yeasts. Techn. Bull. 1029, U.S. Deptartment of Agriculture, Washington, DC.
Wickerham, L.J. 1952. Recent advances in the taxonomy of yeasts. Annu. Rev. Microbiol. 6, 317–332.
Wickerham, L.J. 1956. Influence of agglutination on zygote formation in *Hansenula wingei*, a new species of yeast. C.R. Trav. Lab. Carlsberg, Ser. Physiol. 26, 423–433.
Wickerham, L.J. 1958. Sexual agglutination of heterothallic yeasts in diverse taxonomic areas. Science 128, 1504–1505.
Wickerham, L.J. 1960. *Hansenula holstii*, a new yeast important in the early evolution of the heterothallic species of its genus. Mycologia 52, 171–183.
Wickerham, L.J. 1964a. A preliminary report on a perfect family of exclusively protosexual yeasts. Mycologia 56, 253–266.
Wickerham, L.J. 1964b. A cadaver yeast and related species. Mycologia 56, 398–414.

Wickerham, L.J. 1965a. New heterothallic species of *Hansenula*. I. *Hansenula fabianii*. Mycopathol. Mycol. Appl. 26, 79–86.
Wickerham, L.J. 1965b. New heterothallic species of *Hansenula*. II. *Hansenula bimundalis* and variety *americana*. Mycopathol. Mycol. Appl. 26, 87–103.
Wickerham, L.J. 1966. Validation of the species *Pichia guilliermondii*. J. Bacteriol. 92, 12–69.
Wickerham, L.J. 1969a. Hybridization as a basis for speciation in the genus *Hansenula*. Proc. II Int. Symp. Yeasts, 1966, Bratislava, pp. 41–44.
Wickerham, L.J. 1969b. New homothallic taxa of *Hansenula*. Mycopathol. Mycol. Appl. 37, 15–32.
Wickerham, L.J. 1970a. *Hansenula* H. et P. Sydow. In: J. Lodder (Ed.), The Yeasts, A Taxonomic Study, 2nd edn. North-Holland, Amsterdam, pp. 226–315.
Wickerham, L.J. 1970b. *Pachysolen* Boidin et Adzet. In: J. Lodder (Ed.), The Yeasts, A Taxonomic Study, 2nd edn. North-Holland, Amsterdam, pp. 448–454.
Wickerham, L.J., and K.A. Burton. 1948. Carbon assimilation tests for the classification of yeasts. J. Bacteriol. 56, 363–371.
Wickerham, L.J., and K.A. Burton. 1952. Occurrence of yeast mating types in nature. J. Bacteriol. 63, 449–451.
Wickerham, L.J., and K.A. Burton. 1954a. A simple technique for obtaining mating types in heterothallic diploid yeasts, with special reference to their uses in the genus *Hansenula*. J. Bacteriol. 67, 303–308.
Wickerham, L.J., and K.A. Burton. 1954b. A clarification of the relationships of *Candida guilliermondii* to other yeasts by a study of their mating types. J. Bacteriol. 68, 594–597.
Wickerham, L.J., and K.A. Burton. 1960. Heterothallism in *Saccharomyces rouxii*. J. Bacteriol. 80, 492–495.
Wickerham, L.J., and K.A. Burton. 1961. Phylogeny of phosphomannan-producing yeasts. 1. The genera. J. Bacteriol. 82, 265–268.
Wickerham, L.J., and K.A. Burton. 1962. Phylogeny and biochemistry of the genus *Hansenula*. Bacteriol. Rev. 26, 382–397.
Wickerham, L.J., and E. Duprat. 1945. A remarkable fission yeast, *Schizosaccharomyces versatilis* nov. sp. J. Bacteriol. 50, 597–607.
Wickerham, L.J., and C.P. Kurtzman. 1971. Two new saturn-spored species of *Pichia*. Mycologia 63, 1013–1018.
Wickerham, L.J., and F.H. Stodola. 1960. Formation of extracellular sphingolipids by microorganisms. I. Tetraacetylphytosphingosine from *Hansenula ciferrii*. J. Bacteriol. 80, 484–491.
Wickerham, L.J., L.B. Lockwood, O.G. Pettijohn and G.E. Ward. 1944. Starch hydrolysis and fermentation by the yeast *Endomycopsis fibuliger*. J. Bacteriol. 48, 413–427.
Wickerham, L.J., M.H. Flickinger and R.M. Johnston. 1946. The production of riboflavin by *Ashbya gossypii*. Arch. Biochem. 9, 95–98.
Wickerham, L.J., C.P. Kurtzman and A.I. Herman. 1970a. Sexual reproduction in *Candida lipolytica*. Science 167, 11–41.
Wickerham, L.J., C.P. Kurtzman and A.I. Herman. 1970b. Sexuality in *Candida lipolytica*. In: D.G. Ahearn (Ed.), Recent Trends in Yeast Research, Spectrum, Vol. I. Georgia State University, Atlanta, GA, pp. 81–92.
Wickes, B.L., T.D. Moor and K.J. Kwon-Chung. 1994. Comparison of the electrophoretic karyotypes and chromosomal location of ten genes in the two varieties of *Cryptococcus neoformans*. Microbiologia 140, 543–550.
Wickes, B.L., M.E. Mayorga, U. Edman and J.C. Edman. 1996. Dimorphism and haploid fruiting in *Cryptococcus neoformans*: association with the alpha-mating type. Proc. Natl. Acad. Sci. USA 93, 7327–7331.
Wickes, B.L., U. Edman and J.C. Edman. 1997. The *Cryptococcus neoformans* STE12alpha gene: a putative *Saccharomyces cerevisiae* STE12 homologue that is mating type specific. Mol. Microbiologia 26, 951–960.
Wicklow, D.T., and G.C. Carroll. 1981. The Fungal Community, Its Organization and Role in the Ecosystem. Marcel Dekker, New York.
Wickner, R.B. 1986. Double-stranded RNA replication in yeast, the killer system. Annu. Rev. Biochem. 55, 373–395.
Wickner, R.B. 1992. Double-stranded and single-stranded RNA viruses of *Saccharomyces cerevisiae*. Annu. Rev. Microbiol. 46, 347–375.
Wickner, R.B. 1996. Double-stranded RNA viruses of *Saccharomyces cerevisiae*. Microbiol. Rev. 60, 250–265.
Wickner, R.B., H.K. Edskes, F. Shewmaker and T. Nakayashiki. 2007. Prions of fungi: inherited structures and biological roles. Nat. Rev. Microbiol. 5, 611–618.
Wieringa, K.T. 1956. The micro-organisms decomposing pectic substances in the dew retting process of flax. Neth. J. Agri. Sci. 4, 204–209.
Wild, B.L. 1987. Comparison of bioassay and chemical determination of the activity of the fungicide guazatine used in a post-harvest citrus dip. Ann. Appl. Biol. 111, 553–559.
Wildt, S., and T. Gerngross. 2005. The humanization of N-glycosylation pathways in yeast. Nat. Rev. Microbiol. 3, 119–128.
Wiley, A.S. 2007. The globalization of cow's milk production and consumption: biocultural perspectives. Ecol. Food Nutr. 46, 281–312.
Wilhelmi, A. 1898. Beiträge zur Kenntnis des *Saccharomyces guttulatus* Buscalioni. Zentralbl. Backtenol., Abt. II, 305–309.
Will, H. 1910. Beiträge zur Kenntnis der Gattung *Mycoderma* nach Untersuchungen von Hans Leberle. Zentralbl. Bakteriol. Parasitenkd., Abt. II, 28, 1–37.
Will, H. 1913. *Saccharomyces anamensis*, die Hefe des neueren Amyloverfahrens. Zentralbl. Bakteriol. Parasitenkd., Abt. II, 39, 26–53.
Will, H. 1916. Beiträge zur Kenntnis der Sprosspilze ohne Sporenbildung, welche in Brauereibetrieben und in deren Umgebung vorkommen. VI. (Schluss)-Mitteilung. Zentralbl. Bakteriol. Parasitenkd., Abt. II, 46, 226–281.
Willaert, R., and V.A. Nedovic. 2006. Primary beer fermentation by immobilised yeast – a review on flavour formation and control strategies. J. Chem. Technol. Biotechnol. 81, 1353–1367.
Williamson, M.A., and N.J. Fokkema. 1985. Phyllosphere yeasts antagonize penetration from appressoria and subsequent infection of maize leaves by *Colletotrichum graminicola*. Eur. J. Plant Pathol. 91, 265–276.
Williamson, P.R. 1994. Biochemical and molecular characterization of the diphenol oxidase of *Cryptococcus neoformans*: identification as a laccase. J. Bacteriol. 176, 656–664.

Wilmotte, A., Y. van de Peer, A. Goris, S. Chapelle, R. de Baere, B. Nelissen, J. Neefs, G.L. Hennebert and R. de Wachter. 1993. Evolutionary relationships among higher fungi inferred from small ribosomal subunit RNA sequence analysis. Syst. Appl. Microbiol. 16, 436–444.

Wilsenach, R., and M. Kessel. 1965. On the function and structure of the septal pore of *Polyporus rugulosus*. J. Gen. Microbiol. 40, 397–400.

Wilson, C.L., A. El Ghaouth, E. Chalutz, S. Droby, C. Stevens, J. Y. Lu, V. Khan and J. Arul. 1994. Potential of induced resistance to control postharvest diseases of fruits and vegetables. Plant Dis. 78, 837–944.

Wilson, C.M. 1961. A cytological study of *Ascocybe*. Can. J. Bot. 39, 1605–1607.

Wilson, D.E., J.E. Bennett and J.W. Bailey. 1968. Serologic grouping of *Cryptococcus neoformans*. Proc. Soc. Exp. Biol. Med. 127, 820–823.

Wilson, C.L., and E. Chalutz. 1989. Postharvest biological control of *Penicillium* rots of citrus with antagonistic yeasts and bacteria. Sci. Hortic. 40, 105–112.

Windisch, S. 1940. Entwicklungsgeschichtliche Untersuchungen an *Torulopsis pulcherrima* (Lindner) Saccardo und *Candida tropicalis* (Castellani) Berkhout. Ein Beitrag zur Systematik der Gärungsmonilien. Arch. Mikrobiol. 11, 368–390.

Windisch, S. 1949. *Sporobolomyces holsaticus* n. sp. Arch. Mikrobiol. 14, 287–290.

Windisch, S. 1951. Zur Biologie und Systematik des Milchschimmels und ähnlicher Formen. I. Der Milchschimmel (*Endomyces lactis*) und *Endomyces magnusii*. Beitr. Biol. Pfl. 28, 69–130.

Windisch, S. 1952. Zur Biologie und Systematik des Milchschimmels und einiger ähnlicher Formen. II. Milchschimmel ähnliche Pilze. Beitr. Biol. Pflanz. 29, 143–170.

Windisch, S. 1953. Zur Biologie und Systematik der *Pseudomonilia albomarginata* Geiger. Zentralbl. Bakteriol. Parasitenkd., Abt. II, 107, 84–98.

Windisch, S. 1965. Über zwei neue Pilzarten, *Protendomycopsis domschii* n. g., n. sp. und *Endomyces laibachii* n. sp. Beitr. Biol. Pflanz. 41, 337–358.

Winey, M., C.L. Mamay, E.T. O'Toole, D.N. Mastronarde, T.H. Giddings Jr., K.L. McDonald and J.R. McIntosh. 1995. Three-dimensional ultrastructural analysis of the *Saccharomyces cerevisiae* mitotic spindle. J. Cell Biol. 129, 1601–1615.

Wingard, S.A. 1922. Yeast-spot of lima beans. Phytopathology 12, 525–532.

Winge, O., and O. Laustsen. 1937. On two types of spore germination, and on genetic segregations in *Saccharomyces*, demonstrated through single-spore cultures. C.R. Trav. Lab. Carlsberg, Ser. Physiol. 22, 99–116.

Winter, G.L. 1884. Rabenhorsts's Kryptogamen Flora van Deutschland, Österreich und der Schweiz, Band I. Die Pilze Abt. I. Leipzig.

Wisniewski, M., C. Biles, S. Droby, R. McLaughlin, C. Wilson and E. Chalutz. 1991. Mode of action of the postharvest biocontrol yeast, *Pichia guilliermondii*. 1. Characterization of attachment to *Botrytis cinerea*. Physiol. Mol. Plant Pathol. 39, 245–258.

Wisniewski, M., S. Droby, E. Chalutz and Y. Eilam. 1995. Effects of Ca^{2+} and Mg^{2+} on *Botrytis cinerea* and *Penicillium expansum in vitro* and on the biocontrol activity of *Candida oleophila*. Plant Pathol. 44, 1016–1024.

Withers, S.T., and J.D. Keasling. 2007. Biosynthesis and engineering of isoprenoid small molecules. Appl. Microb. Biotechnol. 73, 980–990.

Witt, S.N., and T.R. Flower. 2006. α-Synuclein, oxidative stress and apoptosis from the perspective a yeast model of Parkinson's disease. FEMS Yeast Res. 6, 1107–1116.

Wittig, H.P.P., K.B. Johnson and J.W. Pscheidt. 1997. Effect of epiphytic fungi on brown rot blossom blight and latent infections in sweet cherry. Plant Dis. 81, 383–387.

Wojewoda, W. 1977. Grzyby (Mycota), Vol 8: Podstaswczaki (Basidiomycetes), Trzesakowe (Tremellales), Uszakowe (Auriculariales), Czerwcogrzybowe (Septobasidiales). Panstwowe Wydawnictwo Naukowe, Warsaw, 334pp.

Wojewoda, W. 1981. Basidiomycetes (Podstawczaki), Tremellales (Trzçsakowe), Auriculariales (Uzakowe), Septobasidiales (Czerwcogrzybowe). In: S. Domanski (Ed.), Mala Flora Grzybó, Vol. 2. Pánstwowe Wydawnictwo Naukowe, Warsaw.

Wolf, D.G., R. Falk, M. Hacham, B. Theelen, T. Boekhout, G. Scorzetti, M. Shapiro, C. Block, I.F. Salkin and I. Polacheck. 2001. Multidrug-resistant *Trichosporon asahii* infection of nongranulocytopenic patients in three intensive care units. J. Clin. Microbiol. 39, 4420–4425.

Wolf, K. (Ed.) 1996. Nonconventional Yeasts in Biotechnology. Springer, Berlin.

Wolfe, D.M., and D.A. Pearce. 2006. Channeling studies in yeast – yeast as a model for channelopathies. Neuromol. Med. 8, 279–306.

Wolfe, K.H. 2001. Yesterday's polyploids and the mystery of diploidization. Nat. Rev. Gen. 2, 333–341.

Wolfe, K.H. 2006. Comparative genomics and genome evolution in yeasts. Philos. Trans. R. Soc. B Biol. Sci. 361, 403–412.

Wolfram, S., and F. Zach. 1934a. Über einige durch niedere Pilze verursachte Nagelerkrankungen beim Menschen. Arch. Dermatol. Syph. 169, 95–104.

Wolfram, S., and F. Zach. 1934b. Über durch niedere Pilze verursachte Nagelerkrankungen beim Menschen. Arch. Dermatol. Syph. 170, 681–694.

Wong, G., K. Wells and R.J. Bandoni. 1985. Interfertility and comparative morphological studies of *Tremella mesenterica*. Mycologia 77, 36–49.

Wong, S., M.A. Fares, W. Zimmermann, G. Butler and K.H. Wolfe. 2003. Evidence from comparative genomics for a complete sexual cycle in the "asexual" pathogenic yeast *Candida glabrata*. Genome Biol. 4, R10.

Woo, P.C., H. Zhen, J.J. Cai, J. Yu, S.K. Lau, J. Wang, J.L. Teng, S.S. Wong, R.H. Tse, R. Chen, H. Yang, B. Liu and K.Y. Yuen. 2003. The mitochondrial genome of the thermal dimorphic fungus *Penicillium marneffei* is more closely related to those of molds than yeasts. FEBS Lett. 555, 469–477.

Woo, P.C., K.T. Chong, H. Tse, J.J. Cai, C.C. Lau, A.C. Zhou, S.K. Lau and K.Y. Yuen. 2006. Genomic and experimental evidence for a potential sexual cycle in the pathogenic thermal dimorphic fungus *Penicillium marneffei*. FEBS Lett. 580, 3409–3416.

Wood, V., R. Gwilliam, M.A. Rajandream, M. Lyne, R. Lyne and A. Stewart., et al. 2002. The genome sequence of *Schizosaccharomyces pombe*. Nature 415, 871–880.

Woodley, J.M. 2006. Microbial catalytic processes and their development. Adv. Appl. Microbiol. 60, 1–15.

Woods, J.P. 2006. Molecular deteminants of *Histoplasma capsulatum* pathogenesis. In: J. Heitman, S.G. Filler, J.E. Edwards, Jr. and A.P. Mitchell (Eds), Molecular Principles of Fungal Pathogenesis. ASM Press, Washington, DC, pp. 321–331.

Woolfit, M., E. Rozpędowska, J. Piśkur and K.H. Wolfe. 2007. Genome survey sequencing of the wine spoilage yeast *Dekkera* (*Brettanomyces*) *bruxellensis*. Eukaryot. Cell 6, 721–733.

Woolfolk, S., and G.D. Inglis. 2004. Microorganisms associated with field-collected *Chrysoperla rufilabris* (Neuroptera: Chrysopidae) adults with emphasis on yeast symbionts. Biol. Control 29, 155–168.

Woronin, M. 1986. Zur Entwicklunggeschichte des *Ascobolus pulcherrimus* Cr. und Pezizen. Abh. Senkenb. Naturforsch. 5, 333–344.

Worsham, P.L., and P.L. Bolen. 1990. Killer toxin production in *Pichia acaciae* is associated with linear DNA plasmids. Curr. Genet. 18, 77–80.

Wright, J.E. 1970. *Agaricostilbum*, a new genus of Deuteromycetes on palm spathes from Argentina. Mycologia 62, 679–682.

Wright, J.E., R.J. Bandoni and F. Oberwinkler. 1981. *Agaricostilbum*: an auricularioid basidiomycete. Mycologia 73, 880–886.

Wszelaki, A.L., and E.J. Mitcham. 2003. Effect of combination of hot water dips, biological control and controlled atmospheres for control of gray mold on harvested strawberries. Postharvest Biol. Technol. 27, 255–264.

Wu, H., X.-H. Zheng, Y. Araki, H. Sahara, H. Takagi and H. Shimoi. 2006. Global gene expression analysis of yeast cells during sake brewing. Appl. Environ. Microbiol. 72, 7353–7358.

Wu, Z.-W., and F.-Y. Bai. 2005a. *Kazachstania aquatica* sp. nov., and *Kazachstania solicola* sp. nov., novel ascomycetous yeast species. Int. J. Syst. Evol. Microbiol. 55, 2219–2224.

Wu, Z.-W., and F.-Y. Bai. 2005b. ITS sequence and electrophoretic karyotype comparisons of *Candida ethanolica* with *Pichia deserticola* and *Candida odintsovae* with *Pichia rabaulensis*. J. Gen. App. Microbiol. 51, 319–322.

Wu, Z.-W., and F.Y. Bai. 2006. *Candida tibetensis* sp. nov. and *Candida linzhiensis* sp. nov., novel anamorphic, ascomycetous yeast species from Tibet. Int. J. Syst. Evol. Microbiol. 56, 1153–1156.

Wu, Z.-W., V. Robert and F.-Y. Bai. 2006. Genetic diversity of the *Pichia membranifaciens* strains revealed from rRNA gene sequencing and electrophoretic karyotyping, and the proposal of *Candida californica* comb. nov. FEMS Yeast Res. 6, 305–311.

Wuczkowski, M., and H. Prillinger. 2004. Molecular identification of yeasts from soils of the alluvial forest national park along the river Danube downstream of Vienna, Austria ("Nationalpark Donauauen"). Microbiol. Res. 159, 263–275.

Wuczkowski, M., E. Metzger, K. Sterflinger and H. Prillinger. 2005. Diversity of yeasts isolated from litter and soil of different natural forest sites in Austria. Die Bodenkultur 56, 201–208.

Wuczkowski, M., C. Bond and H. Prillinger. 2006. *Geotrichum vulgare*, a novel asexual arthroconidial yeast. Int. J. Syst. Evol. Microbiol. 56, 301–303.

Wuczkowski, M., V. Passoth., B. Turchetti, A.-C., Andersson, M. Olstorpe, A. Laitila, B. Theelen, M. van Broock, P. Buzzini, H. Prillinger, K. Sterflinger, J. Schnürer, T. Boekhout and D. Libkind. 2010. Description of *Holtermanniella takashima*sp. nov., *Holtermanniella* gen. nov. and proposal of the order Holtermanniales to accommodate Tremellomycetous yeasts of the *Holtermania* clade. Int. J. Syst. Evol. Microbiol. Apr. 9 [epub ahead of point].

Wyder, M.-T., H. Spillmann and Z. Puhan. 1997. Investigation of the yeast flora in dairy products: a case study of kefyr. Food Technol. Biotechnol. 35, 299–304.

Wyder, M.-T., L. Meile and M. Teuber. 1999. Description of *Saccharomyces turicensis* sp. nov., a new species from kefyr. Syst. Appl. Microbiol. 22, 420–425.

Xie, H., X. Zhuang, Z. Bai, H. Qi and H. Zhang. 2006. Isolation of levoglucosan-assimilating microorganisms from soil and an investigation of their levoglucosan kinases. World J. Microbiol. Biotechnol. 22, 887–892.

Xin, M., and P. Zhou. 2007. *Mrakia psychrophila* sp. nov., a new species isolated from Antarctic soil. J. Zhejiang Univ. Sci. B 8, 260–265.

Xu, J., and T.G. Mitchell. 2003. Comparative gene genealogical analyses of strains of serotype AD identify recombination in populations of serotypes A and D in the human pathogenic yeast *Cryptococcus neoformans*. Microbiology (UK) 149, 2147–2154.

Xu, J., R. Vilgalys and T.G. Mitchell. 2000. Multiple gene genealogies reveal recent dispersion and hybridization in the human pathogenic fungus *Cryptococcus neoformans*. Mol. Ecol. 9, 1471–1481.

Xu, J., G. Luo, R.J. Vilgalys, M.E. Brandt and T.G. Mitchell. 2002. Multiple origins of hybrid strains of *Cryptococcus neoformans* with serotype AD. Microbiology (UK) 148, 203–212.

Xu, J., C.W. Saunders, P. Hu, R.A. Grant, T. Boekhout, E.E. Kuramae, J.W. Kronstad, Y.M. DeAngelis, N.L. Reeder, K.R. Johnstone, M. Leland, A.M. Fieno, W.M. Begley, Y. Sun, M. P. Lacey, T. Chaudhary, T. Keough, L. Chu, R. Sears, B. Yuan and T.L. Dawson Jr. 2007. Dandruff-associated *Malassezia* species reveals convergent and divergent virulence traits with plant and human fungal pathogens. Proc. Natl. Acad. Sci. USA 104, 18730–18735.

Xu, Y., W. Du, D. Liu and J. Zeng. 2003. A novel enzymatic route for biodiesel production from renewable oils in a solvent-free medium. Biotechnol. Lett. 25, 1239–1241.

Xu, Y., G.A. Zhao and L.P. Wang. 2006. Controlled formation of volatile components in cider making using a combination of *Saccharomyces cerevisiae* and *Hanseniaspora valbyensis* yeast species. J. Ind. Microbiol. Biotechnol. 33, 192–196.

Xue, C., Y. Tada, X. Dong and J. Heitman. 2007. The human fungal pathogen *Cryptococcus* can complete its sexual cycle during a pathogenic association with plants. Cell Host Microbe 14, 263–273.

Xue, M.-L., L.-Q. Zhang, Q.-M. Wang, J.-S. Zhang and F.-Y. Bai. 2006. *Metschnikowia sinensis* sp. nov., *Metschnikowia zizyphicola* sp. nov. and *Metschnikowia shanxiensis* sp. nov., novel yeast species from jujube fruit. Int. J. Syst. Evol. Microbiol. 56, 2245–2250.

Yabe, K. 1897. On the origin of sake yeast (*Sacch. sake*). Bull. Imp. Univ. Tokyo Coll. Agric. 3, 221–233.

Yamada, Y., K. Aida and T. Uemura. 1969. Enzymatic studies on the oxidation of sugar and sugar alcohol. V.

Ubiquinone of acetic acid bacteria and its relation to classification of genera *Gluconobacter* and *Acetobacter*, especially of the so-called intermediate strains. J. Gen. Appl. Microbiol. 15, 181–196.

Yamada, K. 1977. Japan's most advanced industrial fermentation technology and industry. Int. Technol. Inf. Inst., Tokyo.

Yamada, K., and H. Machida. 1962. Studies on the production of lipase by microorganisms. Part I. The selection and identification of a new strain. Nippon Nogeikagaku Kaishii 36, 858–860. In Japanese.

Yamada, K., and Y. Ota. 1963. Studies on the production of lipase by microorganisms. Part IV. Identification of a new strain and determination of its lipase activity. J. Agric. Chem. Soc. Jpn 37, 649–652.

Yamada, R.H., H. Ujiie, Y. Kera, T. Nakase, K. Kitagawa, T. Imasaka, K. Arimoto, M. Takahashi and Y. Matsumura. 1996. Purification and properties of D-aspartate oxidase from *Cryptococcus humicolus* UJ1. Biochim. Biophys. Acta 1294, 153–158.

Yamada, Y. 1986a. The coenzyme Q system in strains of species in the anamorphic yeast genus *Myxozyma*. J. Gen. Appl. Microbiol. 32, 259–261.

Yamada, Y. 1986b. *Holleya* gen. nov., an ascosporogenous yeast genus for the Q9-equipped organism whose ascospores are needle shaped with smooth surfaces in their anterior half and concentric ridges in their posterior half and without appendage. J. Gen. Appl. Microbiol. 32, 447–449.

Yamada, Y. 1998. Identification of coenzyme Q (ubiquinone) homologs. In: C.P. Kurtzman and J.W. Fell (Eds), The Yeasts, A Taxonomic Study. Elsevier, Amsterdam, pp. 101–102.

Yamada, Y., and K. Aizawa. 1987. Electrophoretic comparison of enzymes in strains of species in the genera *Myxozyma* (Cryptococcaceae) and *Zygozyma* (Lipomycetaceae). Trans. Mycol. Soc. Jpn 28, 163–170.

Yamada, Y., and I. Banno. 1984a. *Fellomyces*, a new anamorphic yeast genus for the Q10-equipped organisms whose conidium is freed by an end-break in the sterigma. J. Gen. Appl. Microbiol. 30, 523–525.

Yamada, Y., and I. Banno. 1984b. The coenzyme Q system in strains of species in the genus *Sterigmatomyces* (Cryptococcaceae) and its teleomorphic genus Sterigmatosporidium. Trans. Mycol. Soc. Jpn 25, 455–460.

Yamada, Y., and I. Banno. 1987a. *Hasegawaea* gen. nov., an ascosporogenous yeast genus for the organism whose ascospores have smooth surfaces without papillae and which are characterised by the absence of coenzyme Q and by the presence of linoleic acid in cellular fatty acid composition. J. Gen. Appl. Microbiol. 33, 295–298.

Yamada, Y., and I. Banno. 1987b. *Hasegawaea japonica* var. *versatilis*, a new combination for *Schizosaccharomyces japonicus* var. *versatilis*. J. Gen. Appl. Microbiol. 33, 547–548.

Yamada, Y., and I. Banno. 1998. *Tsuchiyaea* Y. Yamada, Kawasaki, M. Itoh, Banno and Nakase. In: C.P. Kurtzman and J.W. Fell (Eds), The Yeasts, A Taxonomic Study, 4th edn. Elsevier, Amsterdam, pp. 878–879.

Yamada, Y., and H. Kawasaki. 1989. The molecular phylogeny of the Q8-equipped basidiomycetous yeast genera *Mrakia* Yamada et Komagata and *Cystofilobasidium* Oberwinkler et Bandoni based on the partial sequences of 18S and 26S ribosomal ribonucleic acids. J. Gen. Appl. Microbiol. 35, 173–183.

Yamada, Y., and K. Komagata. 1983. *Rhodotorula hasegawae* sp. nov., a new asporogenous yeast species. J. Gen. Appl. Microbiol. 29, 323–326.

Yamada, Y., and K. Komagata. 1987. *Mrakia* gen. nov., a heterobasidiomycetous yeast genus for the Q8-equipped, self-sporulating organisms which produce a unicellular metabasidium, formerly classified in the genus *Leucosporidium*. J. Gen. Appl. Microbiol. 33, 455–457.

Yamada, Y., and T. Konda. 1984. The coenzyme Q system in strains of species in the genus *Itersonilia*, Sporobolomycetaceae. J. Gen. Appl. Microbiol. 30, 313–315.

Yamada, Y., and K. Kondo. 1972a. Taxonomic significance of coenzyme Q system in yeasts and yeast-like fungi (1). In: A. Kocková-Kratochvílová and E. Minarik (Eds.), Yeasts. Models in Science and Technics, Proc. 1st Spec. Int. Symp. on Yeasts. Slovak Academy of Sciences, Bratislava, pp. 363–373.

Yamada, Y., and K. Kondo. 1972b. Taxonomic significance of the coenzyme Q system in yeasts and yeast-like fungi (2). In: G. Terui (Ed.), Fermentation Technology Today, Proc. IVth Int. Ferment. Symp., Soc. Ferment. Technol., Osaka, Japan, pp. 781–784.

Yamada, Y., and K. Kondo. 1972c. In: A. Kockova-Kratochvilova and E. Minarik (Eds.), Yeasts. Models in Science and Technics, Proc. 1st Spec. Int. Symp. on Yeasts. Slovak Academy of Sciences, Bratislava, pp. 363–373.

Yamada, Y., and K. Kondo. 1973. Coenzyme Q system in the classification of the yeast genera *Rhodotorula* and *Cryptococcus*, and the yeast-like genera *Sporobolomyces and Rhodosporidium*. J. Gen. Appl. Microbiol. 19, 59–77.

Yamada, Y., and A. Matsumoto. 1988a. An electrophoretic comparison of enzymes in strains of species in the genus *Mrakia* Yamada et Komagata (Filobasidiaceae). J. Gen. Appl. Microbiol. 34, 201–208.

Yamada, Y., and A. Matsumoto. 1988b. An electrophoretic comparison of enzymes in strains of species in the genera *Lipomyces* Lodder et Kreger-van Rij and *Waltomyces* Yamada et Nakase (Lipomycetaceae). Agric. Biol. Chem. 52, 2525–2530.

Yamada, Y., and T. Nagahama. 1991. The molecular phylogeny of the ascomycetous yeast genus *Holleya* Yamada based on the partial sequences of 18S and 26S ribosomal ribonucleic acids. J. Gen. Appl. Microbiol. 37, 199–206.

Yamada, Y., and Y. Nakagawa. 1988. An electrophoretic comparison of enzymes in strains of the Q9-equipped species in the genus *Sporobolomyces* Kluyver et van Niel (Sporobolomycetaceae). J. Gen. Appl. Microbiol. 34, 289–295.

Yamada, Y., K. Sugihara, G.W. van Eijk, H.J. Roeijmans and G.S. de Hoog. 1989c. Coenzyme Q systems in ascomycetous black yeasts. Antonie van Leeuwenhoek 56, 349–356.

Yamada, Y., and Y. Nakagawa. 1990. The molecular phylogeny of the basidiomycetous yeast species *Leucosporidium scottii* based on the partial sequences of 18S and 26S ribosomal nucleic acids. J. Gen. Appl. Microbiol. 36, 63–68.

Yamada, Y., and Y. Nakagawa. 1992. The phylogenetic relationships of some heterobasidiomycetous yeast species based on the partial sequences of 18S and 26S ribosomal RNAs. J. Gen Appl. Microbiol. 38, 559–565.

Yamada, Y., and T. Nakase. 1985. *Waltomyces*, a new ascosporogenous yeast genus for the Q10-equipped, slime-producing organisms whose asexual reproduction is by multilateral budding and whose ascospores have smooth surfaces. J. Gen. Appl. Microbiol. 31, 491–492.

Yamada, Y., and C. Nogawa. 1990. The molecular phylogeny of the lipomycetaceous yeasts based on partial sequences of 18S and 26S ribosomal ribonucleic acids. In: A. Reisinger and A. Bresinsky (Eds.), Abstracts 4th Int. Mycol. Congress, Regensburg, Germany, Aug. 28–Sept. 3. University of Regensburg, p. 63.

Yamada, Y., and C. Nogawa. 1995a. The phylogeny of the lipomycetaceous yeasts based on the partial sequences of 18S and 25S ribosomal RNAs. Bull. Fac. Agric. Shizuoka Univ. 45, 13–23.

Yamada, Y., and C. Nogawa. 1995b. *Kawasakia* gen. nov. for *Zygozyma arxii*, the Q9-equipped species in the genus *Zygozyma* (Lipomycetaceae). Bull. Fac. Agric. Shizuoka Univ. 45, 31–34.

Yamada, Y., and M.Th. Smith. 1985. The coenzyme Q system in strains of species in the genera *Stephanoascus* and *Sporopachydermia* (Saccharomycetaceae). Trans. Mycol. Soc. Jpn 26, 247–251.

Yamada, Y., K. Aida and T. Uemura. 1969. Enzymatic studies on the oxidation of sugar and sugar alcohol. V. Ubiquinone of acetic acid bacteria and its relation to classification of genera *Gluconobacter* and *Acetobacter*, especially of the so-called intermediate strains. J. Gen. Appl. Microbiol. 15, 181–196.

Yamada, Y., T. Okada, O. Ueshima and K. Kondo. 1973a. Coenzyme Q system in the classification of the ascosporogenous yeast genera *Hansenula* and *Pichia*. J. Gen. Appl. Microbiol. 19, 189–208.

Yamada, Y., M. Arimoto and K. Kondo. 1973b. Coenzyme Q system in the classification of the ascosporogenous yeast genus *Schizosaccharomyces* and yeast-like genus *Endomyces*. J. Gen. Appl. Microbiol. 19, 353–358.

Yamada, Y., Y. Kanematsu, M. Ohashi and K. Kondo. 1973c. On the partly reduced coenzyme Q isolated from *Rhodotorula lactosa* IFO1058 and its relation to the taxonomic position. Agric. Biol. Chem. 37, 621–628.

Yamada, Y., M. Arimoto and K. Kondo. 1976a. Coenzyme Q system in the classification of apiculate yeasts in the genera *Nadsonia*, *Saccharomycodes, Hanseniaspora, Kloeckera* and *Wickerhamia*. J. Gen. Appl. Microbiol. 22, 293–299.

Yamada, Y., M. Nojiri, M. Matsuyama and K. Kondo. 1976b. Coenzyme Q system in the classification of the ascosporogenous yeast genera *Debaryomyces, Saccharomyces, Kluyveromyces*, and *Endomycopsis*. J. Gen. Appl. Microbiol. 22, 325–337.

Yamada, Y., M. Arimoto and K. Kondo. 1977. Coenzyme Q system in the classification of some ascosporogenous yeast genera in the families Saccharomycetaceae and Spermophthoraceae. Antonie van Leeuwenhoek 43, 65–71.

Yamada, Y., H. Takinami-Nakamura, Y. Tahara and M.T. Smith. 1980. The coenzyme Q system in the classification of the ascosporogenous yeast genus *Dekkera* and the asporogenous yeast genus *Brettanomyces*. Antonie van Leeuwenhoek 46, 595–599.

Yamada, Y., J. Sasaki, C.F. Hou, Y. Tahara, M. Miranda and H.J. Phaff. 1981. A new natural quinone, ubiquinone-5, isolated from an ascosporogenous yeast species *Nematospora coryli*. Agric. Biol. Chem. 45, 2671–2673.

Yamada, Y., E. Nakazawa and K. Kondo. 1982. The coenzyme Q system in strains of *Trichosporon* species and related organisms. J. Gen. Appl. Microbiol. 28, 355–358.

Yamada, Y., T. Ohishi and K. Kondo. 1983. The coenzyme Q system in strains of some yeasts and yeast-like fungi. J. Gen. Appl. Microbiol. 29, 51–57.

Yamada, Y., T. Nakase and J.P. van der Walt. 1986a. The coenzyme Q system in strains of species in the ascosporogenous yeast genera *Lipomyces* and *Waltomyces*. Trans. Mycol. Soc. Jpn 27, 313–319.

Yamada, Y., K. Aizawa and I. Banno. 1986b. The coenzyme Q system and an electrophoretic comparison of enzymes in the strain of the anamorphic yeast species, *Sterigmatomyces fuzhouensis*. J. Gen. Appl. Microbiol. 32, 367–370.

Yamada, Y., K. Aizawa, A. Matsumoto, Y. Nakagawa and I. Banno. 1987a. An electrophoretic comparison of enzymes in strains of species in the fission yeast genera *Schizosaccharomyces, Octosporomyces*, and *Hasegawaea*. J. Gen. Appl. Microbiol. 33, 363–369.

Yamada, Y., I. Banno, J.A. von Arx and J.P. van der Walt. 1987b. Taxonomic significance of the coenzyme Q system in yeasts and yeast-like fungi. In: G.S. de Hoog, M.Th. Smith and A.C.M. Weijman (Eds), The Expanding Realm of Yeast-like Fungi. Elsevier, Amsterdam, pp. 299–308. (Stud. Mycol. 30, 299–308).

Yamada, Y., M. Itoh, H. Kawasaki, I. Banno and T. Nakase. 1988a. *Kurtzmanomyces* gen. nov., an anamorphic yeast genus for the Q10-equipped organism whose conidium is freed by an end-break in the sterigma which branches or elongates to produce additional conidia and whose cells contain no xylose. J. Gen. Appl. Microbiol. 34, 503–506.

Yamada, Y., H. Kawasaki, M. Itoh, I. Banno and T. Nakase. 1988b. *Tsuchiyaea* gen. nov., an anamorphic yeast genus for the Q9-equipped organism whose reproduction is either by enteroblastic budding or by the formation of conidia which are disjointed at a septum in the mid-region of the sterigmata and whose cells contain xylose. J. Gen. Appl. Microbiol. 34, 507–510.

Yamada, Y., Y. Nakagawa and J.P. van der Walt. 1988c. *Bensingtonia phyllades*, a new combination for the Q9-equipped species, *Sporobolomyces phyllades*. Agric. Biol. Chem. 52, 3203.

Yamada, Y., Y. Nakagawa and I. Banno. 1989a. The phylogenetic relationship of the Q9-equipped species of the heterobasidiomycetous yeast genera *Rhodosporidium* and *Leucosporidium* based on the partial sequences of 18S and 26S ribosomal ribonucleic acids: the proposal of a new genus *Kondoa*. J. Gen. Appl. Microbiol. 35, 377–385.

Yamada, Y., H. Kawasaki, T. Nakase and I. Banno. 1989b. The phylogenetic relationship of the conidium-forming anamorphic yeast genera *Sterigmatomyces*, *Kurtzmanomyces, Tsuchiyaea* and *Fellomyces* and the telemorphic yeast genus *Sterigmatosporidium* on the basis of the partial sequences of 18S and 26S ribosomal ribonucleic acids. Agric. Biol. Chem. 53, 2993–3001.

Yamada, Y., K. Sugihara, G.W. van Eijk, H.J. Roeijmans and G.S. de Hoog. 1989c. Coenzyme Q systems in ascomycetous black yeasts. Antonie van Leeuwenhoek 56, 349–356.

Yamada, Y., T. Nagahama, H. Kawasaki and I. Banno. 1990a. The phylogenetic relationship of the genera *Phaffia* Miller, Yoneyama et Soneda and *Cryptococcus* Kützing emend. Phaff et Spencer (Cryptococcaceae) based on the partial sequences of 18S and 26S ribosomal ribonucleic acids. J. Gen. Appl. Microbiol. 36, 403–414.

Yamada, Y., Y. Nakagawa and I. Banno. 1990b. The molecular phylogeny of the Q10-equipped species of the heterobasidiomycetous yeast genus *Rhodosporidium* Banno based on the partial sequences of 18S and 26S ribosomal nucleic acids. J. Gen. Appl. Microbiol. 36, 435–444.

Yamada, Y., T. Nagahama and I. Banno. 1991a. The molecular phylogeny of the Q9-equipped ascomycetous teleomorphic yeast genus *Debaryomyces* Lodder et Kreger-van Rij based on the partial sequences of 18S and 26S ribosomal ribonucleic acids. J. Gen. Appl. Microbiol. 37, 277–288.

Yamada, Y., K. Maeda, T. Nagahama and I. Banno. 1991b. The phylogenetic relationships of the Q6-equipped genera *Torulaspora* Lindner and *Zygosaccharomyces* Barker (Saccharomycetaceae) based on the partial sequences of 18S and 26S ribosomal ribonucleic acids. J. Gen. Appl. Microbiol. 37, 503–513.

Yamada, Y., K. Maeda, T. Nagahama and I. Banno. 1991c. The phylogenetic relationships of the Q9-equipped genus *Schwanniomyces* Klöcker (Saccharomycetaceae) based on the partial sequences of 18S and 26S ribosomal RNAs. J. Gen. Appl. Microbiol. 37, 523–528.

Yamada, Y., K. Maeda and I. Banno. 1992a. An emendation of *Kloeckeraspora* Niehaus with the type species *Kloeckeraspora osmophila* Niehaus, and the proposals of two new combinations, *Kloeckeraspora occidentalis* and *Kloeckeraspora vineae* (Saccharomycetaceae). Bull. Jpn. Fed. Cult. Collect. 8, 79–85.

Yamada, Y., K. Maeda and I. Banno. 1992b. The phylogenetic relationships of the Q9-equipped, spheroidal ascospore-forming *Pichia* species based on the partial sequences of 18S and 26S ribosomal RNAs. J. Gen. Appl. Microbiol. 38, 247–252.

Yamada, Y., K. Maeda and I. Banno. 1992c. The phylogenetic relationships of the Q6-equipped species in the teleomorphic apiculate yeast genera *Hanseniaspora*, *Nadsonia*, and *Saccharomycodes* based on the partial sequences of 18S and 26S ribosomal ribonucleic acids. J. Gen. Appl. Microbiol. 38, 585–596.

Yamada, Y., K. Maeda, I. Banno and J.P. van der Walt. 1992d. An emendation of the genus *Debaryomyces* Lodder et Kreger-van Rij and the proposals of two new combinations, *Debaryomyces carsonii* and *Debaryomyces etchellsii* (Saccharomycetaceae). J. Gen. Appl. Microbiol. 38, 623–626.

Yamada, Y., K. Mikata and I. Banno. 1993a. Reidentification of 121 strains of the genus *Saccharomyces*. Bull. Jpn. Fed. Cult. Collect 9, 95–119.

Yamada, Y., K. Maeda and K. Mikita. 1993b. The phylogenetic relationships of species of the apiculate yeast genera *Wickerhamia* Soneda and *Kloeckera* Janke based on the partial sequences of 18S and 26S ribosomal RNAs. Bull. Fac. Agric. Shizuoka Univ. 43, 19–28.

Yamada, Y., K. Maeda and K. Mikata. 1994a. The phylogenetic relationships of *Rhodosporidium dacryoideum* Fell, Hunter et Tallman based on the partial sequences of 18S and 26S ribosomal RNAs: the proposal of *Sakaguchia* gen. nov., a heterobasidiomycetous yeast genus. Biosci. Biotechnol. Biochem. 58, 99–103.

Yamada, Y., M. Matsuda, K. Maeda, C. Sakakibara and K. Mikata. 1994b. The phylogenetic relationships of the Saturn-shaped ascospore-forming species of the genus *Williopsis* Zender and related genera based on the partial sequences of 18S and 26S ribosomal RNAs (Saccharomycetaceae): the proposal of *Komagataea* gen. nov. Biosci. Biotechnol. Biochem. 58, 1236–1244.

Yamada, Y., K. Maeda and K. Mikata. 1994c. The phylogenetic relationships of the hat-shaped ascospore-forming, nitrate-assimilating *Pichia* species, formerly classified in the genus *Hansenula* Sydow et Sydow, based on the partial sequences of 18S and 26S ribosomal RNAs (Saccharomycetaceae): the proposals of three new genera, *Ogataea, Kuraishia*, and *Nakazawaea*. Biosci. Biotechnol. Biochem. 58, 1245–1257.

Yamada, Y., M. Matsuda, K. Maeda and K. Mikata. 1994d. The phylogenetic relationships of species of the genus *Dekkera* van der Walt based on the partial sequences of 18S and 26S ribosomal RNAs (Saccharomycetaceae). Biosci. Biotechnol. Biochem. 58, 1803–1808.

Yamada, Y., M. Matsuda, K. Maeda and K. Mikata. 1995a. The phylogenetic relationships of methanol-assimilating yeasts based on the partial sequences of 18S and 26S ribosomal RNAs: the proposal of *Komagataella* gen. nov. (Saccharomycetaceae). Biosci. Biotechnol. Biochem. 59, 439–444.

Yamada, Y., T. Suzuki, M. Matsuda and K. Mikata. 1995b. The phylogeny of *Yamadazyma ohmeri* (Etchells et Bell) Billon-Grand based on partial sequences of 18S and 26S ribosomal RNAs: the proposal of *Kodamaea* gen. nov. (Saccharomycetaceae). Biosci. Biotechnol. Biochem. 59, 1172–1174.

Yamada, Y., M. Matsuda and K. Mikita. 1995c. The phylogenetic relationships of *Eeniella nana* Smith, Batenburg-van der Vegte et Scheffers based on the partial sequences of 18S and 26S ribosomal RNAs (Candidaceae). J. Ind. Microbiol. 14, 456–460.

Yamada, Y., T. Higashi, S. Ando and K. Mikata. 1997. The phylogeny of strains of species of the genus *Pichia* Hansen (Saccharomycetaceae) based on the partial sequences of 18S ribosomal RNA: the proposals of *Phaffomyces* and *Starmera*, the new genera. Bull. Fac. Agric. Shizuoka Univ. 47, 23–35.

Yamada, Y., H. Kawasaki, Y. Nagatsuka, K. Mikata and T. Seki. 1999. The phylogeny of the cactophilic yeasts based on the 18S ribosomal RNA gene sequences: the proposals of *Phaffomyces antillensis* and *Starmera caribaea*, new combinations. Biosci. Biotechnol. Biochem. 63, 827–832.

Yamada-Onodera, K., M. Fukui and Y. Tani. 2007. Purification and characterization of alcohol dehydrogenase reducing *N*-benzyl-3-pyrrolidinone from *Geotrichum capitatum*. J. Biosc. Bioeng. 103, 174–178.

Yamagishi, H., and T. Ogata. 1999. Chromosomal structures of bottom fermenting yeasts. Syst. Appl. Microbiol. 22, 341–353.

Yamaguchi, H., T. Hiratani, K. Iwata and Y. Yamamoto. 1982. Studies on the mechanism of antifungal action of aculeacin A. J. Antibiot. 35, 210–219.

Yamaguchi, K. 1943. A new pentose-assimilating yeast. (1) *Mycotorula japonica* n. sp. J. Agric. Chem. Soc. Jpn 19, 800–804. In Japanese.

Yamaguchi, M., S.K. Biswas, S. Kita, E. Aikawa and K. Takeo. 2002. Electron microscopy of pathogenic yeasts *Cryptococcus neoformans* and *Exophiala dermatitidis* by high-pressure freezing. J. Electron Microsc. (Tokyo) 51, 21–27.

Yamaguchi, T., M. Ishida and T. Suzuki. 1999. Biodegradation of hydrocarbons by *Prototheca zopfii* in rotating biological contractors. Proc. Biochem. 35, 403–409.

Yamamoto, T., T. Hiratani, H. Hirata, M. Imai and H. Yamaguchi. 1986. Killer toxin from *Hansenula mrakii* selectively inhibits cell wall synthesis in a sensitive yeast. FEBS Lett. 197, 50–54.

Yamane, N., and Y. Saitoh. 1985. Isolation and detection of multiple yeasts from a single clinical sample by use of Pagano-Levin agar medium. J. Clin. Microbiol. 21, 276–277.

Yamasaki, I., and H. Fujii. 1950. Studies on *Sporobolomyces* red yeast. Part 7. Classification of the genera *Sporobolomyces* and *Bullera*. Bull. Agric. Chem. Soc. Jpn 24, 11–15.

Yamatoya, K., J. Sugiyama and H. Kuraishi. 1990. Electrophoretic comparison of enzymes as a chemotaxonomic aid among *Aspergillus* taxa: (2) *Aspergillus* sect. Flavi. In: R.A. Samson and J.I. Pitt (Eds), Modern Concepts in *Penicillium* and *Aspergillus* Classification. Plenum Press, New York, pp. 395–405.

Yamazaki, M., and S. Goto. 1985. An electrophoretic comparison of enzymes in the genera *Lipomyces* and *Myxozyma*. J. Gen. Appl. Microbiol. 31, 313–321.

Yamazaki, M., and K. Komagata. 1981. Taxonomic significance of electrophoretic comparison of enzymes in the genera *Rhodotorula* and *Rhodosporidium*. Int. J. Syst. Bacteriol. 31, 361–381.

Yamazaki, M., and K. Komagata. 1982a. Asporogenous yeasts and their supposed ascosporogenous states: an electrophoretic comparison of enzymes. J. Gen. Appl. Microbiol. 28, 119–138.

Yamazaki, M., and K. Komagata. 1982b. An electrophoretic comparison of enzymes in the genus *Cryptococcus* and related microorganisms. J. Gen. Appl. Microbiol. 28, 429–449.

Yamazaki, M., and K. Komagata. 1983a. An electrophoretic comparison of enzymes of ballistosporogenous yeasts. J. Gen. Appl. Microbiol. 29, 115–143.

Yamazaki, M., and K. Komagata. 1983b. An eletrophoretic comparison of the enzymes of *Hansenula* yeasts. J. Gen. Appl. Microbiol. 29, 365–378.

Yamazaki, M., S. Goto and K. Komagata. 1982. Comparison of enzymes from strains of wine yeast and their related yeasts on electrophoresis. J. Inst. Vitic. Yamanashi Univ. 17, 11–19. In Japanese.

Yamazaki, M., S. Goto and K. Komagata. 1983. An electrophoretic comparison of the enzymes of *Saccharomyces* yeasts. J. Gen. Appl. Microbiol. 29, 305–318.

Yamazaki, M., S. Goto and K. Komagata. 1985. Taxonomical studies of the genus *Tilletiopsis* on physiological properties and electrophoretic comparison of enzymes. Trans. Mycol. Soc. Jpn 26, 13–22.

Yamazaki, M., C.P. Kurtzman and J. Sugiyama. 1998. Electrophoretic comparisons of enzymes. In: C.P. Kurtzman and J.W. Fell (Eds), The Yeasts, A Taxonomic Study. Elesvier, Amsterdam, pp. 49–53.

Yamazaki, T., and Y. Oshima. 1979. Direct diploidization and occurrence of polyploidy in *Saccharomycodes ludwigii*. J. Gen. Microbiol. 111, 271–281.

Yamazaki, T., and Y. Oshima. 1996. *Saccharomycodes ludwigii* has seven chromosomes. Yeast 12, 237–240.

Yamazaki, T., Y. Ohara and Y. Oshima. 1976. Rare occurrence of the tetratype tetrads in *Saccharomycodes ludwigii*. J. Bacteriol. 125, 461–466.

Yamazaki, T., Y. Nakagawa, M. Hayakawa and Y. Iimura. 2005. Phylogenetic position of the yeast strain *Saccharomycodes sinensis* IFO 10111. J. Gen. Appl. Microbiol. 51, 35–39.

Yamazaki, Y., and K. Hosono. 1988. Microbial asymmetric reduction of organometallic ketones: acetylferrocene and (acetophenone)-tricarbonylchromium. Agric. Biol. Chem. 52, 3239–3240.

Yan, H., P. He, H.R. Cheng, A. Shen and N. Jiang. 2007. Cloning, sequencing and characterization of the alpha-aminoadipate reductase gene (LYS2) from *Saccharomycopsis fibuligera*. Yeast 24, 189–199.

Yanai, T., and M. Sato. 2000. Purification and characterization of a novel α-L-arabino-furanosidase from *Pichia capsulata* X91. Biosci. Biotechnol. Biochem. 64, 1181–1188.

Yang, Q., M. Yang, L. Hei and S. Zheng. 2003. Using ammonium-tolerant yeast isolates: *Candida halophila* and *Rhodotorula glutinis* to treat high strength fermentative wastewater. Environ. Technol. 24, 383–390.

Yang, S.-H., and P.-H. Wang. 2003. Three species of yeasts new to Taiwan. Taiwania 48, 99–105.

Yang, S.-W., J.-B. Park, N.-S. Han, Y.-W. Ryu and J.-H. Seo. 1999. Production of erythritol from glucose by an osmophilic mutant of *Candida magnoliae*. Biotechnol. Lett. 21, 887–890.

Yang, Z. 1993. Maximum-likelihood estimation of phylogeny from DNA sequences when substitution rates differ over sites. Mol. Biol. Evol. 10, 1396–1401.

Yang, Z., and W.B. Pan. 2005. Ionic liquids: green solvents for nonaqueous biocatalysis. Enzyme Microb. Technol. 37, 19–28.

Yang, Z., and B. Rannala. 1997. Bayesian phylogenetics inference using DNA sequences: a Markov chain Monte Carlo method. Mol. Biol. Evol. 14, 717–724.

Yang, Z., and B. Rannala. 2005. Branch-length prior influences Bayesian posterior probability of phylogeny. Syst. Biol. 54, 455–470.

Yao, H.J., and S.P. Tian. 2005. Effects of a biocontrol agent and methyl jasmonate on postharvest diseases of peach fruit and the possible mechanisms involved. J. Appl. Microbiol. 98, 941–950.

Yao, H., S. Tian and Y. Wang. 2004. Sodium bicarbonate enhances biocontrol efficacy of yeasts on fungal spoilage of pears. Int. J. Food Microbiol. 93, 297–304.

Yarrow, D. 1965. *Pichia onychis* sp. n. Antonie van Leeuwenhoek 31, 465–467.

Yarrow, D. 1968. *Torulopsis peltata* sp. n. Antonie van Leeuwenhoek 34, 81–84.

Yarrow, D. 1969a. *Candida steatolytica* sp. n. Antonie van Leeuwenhoek 35, 24–28.

Yarrow, D. 1969b. *Selenotila peltata* comb. n. Antonie van Leeuwenhoek 35, 418–420.

Yarrow, D. 1972. Four new combinations in yeasts. Antonie van Leeuwenhoek 38, 357–360.

Yarrow, D. 1978. *Candida milleri* spec. nov. Int. J. Syst. Bacteriol. 28, 608–610.

Yarrow, D. 1984a. *Saccharomyces* Meyen ex Reess. In: N.J.W. Kreger-van Rij (Ed.), The Yeasts, A Taxonomic Study, 3rd edn. Elsevier, Amsterdam, pp. 379–395.

Yarrow, D. 1984b. *Schizosaccharomyces* Lindner. In: N.J.W. Kreger-van Rij (Ed.), The Yeasts, A Taxonomic Study, 3rd edn. Elsevier, Amsterdam, pp. 414–422.

Yarrow, D. 1984c. *Torulaspora* Lindner. In: N.J.W. Kreger-van Rij (Ed.), The Yeasts, A Taxonomic Study, 3rd edn. Elsevier, Amsterdam, pp. 434–439.

Yarrow, D. 1984d. *Zygosaccharomyces* Barker. In: N.J.W. Kreger-van Rij (Ed.), The Yeasts, A Taxonomic Study, 3rd edn. Elsevier, Amsterdam, pp. 449–465.

Yarrow, D. 1998. Methods for the isolation, maintenance and identification of yeasts. In: C.P. Kurtzman and J.W. Fell (Eds), The Yeasts, A Taxonomic Study, 4th edn. Elsevier, Amsterdam, pp. 77–100.

Yarrow, D., and D.G. Ahearn. 1971. *Brettanomyces abstinens* sp. n. Antonie van Leeuwenhoek 37, 296–298.

Yarrow, D., and D.G. Ahearn. 1984. *Malassezia* Baillon. In: N.J.W. Kreger-van Rij (Ed.), The Yeasts, A Taxonomic Study, 3rd edn. Elsevier, Amsterdam, pp. 882–885.

Yarrow, D., and J.W. Fell. 1980. Validation of the name of the yeast *Sporobolomyces holsaticus* Windisch. Mycotaxon 12, 253–254.

Yarrow, D., and S.A. Meyer. 1978. Proposal for amendment of the diagnosis of the genus *Candida* Berkhout nom. cons. Int. J. Syst. Bacteriol. 28, 611–615.

Yarrow, D., and T. Nakase. 1975. DNA base composition of species of the genus *Saccharomyces*. Antonie van Leeuwenhoek 41, 81–88.

Yasuda, F., D. Yamagishi, H. Akamatsu, H. Izawa, M. Kodama and H. Otani. 2005. Fruit stain of Japanese pear caused by basidiomycetous, yeast-like fungi, *Acaromyces ingoldii* and *Meira* sp. Jpn. J. Phytopathol. 71, 156–165.

Yasuda, F., D. Yamagishi, H. Akamatsu, H. Izawa, M. Kodama and H. Otani. 2006. *Meira nashicola* sp. nov., a novel basidiomycetous, anamorphic yeastlike fungus isolated from Japanese pear fruit with reddish stain. Mycoscience 47, 36–40.

Yasui, M., S. Shibasaki, K. Kuroda, M. Ueda, N. Kawada, J. Nishikawa, T. Nishihara and A. Tanaka. 2004. An arming yeast with the ability to entrap fluorescent 17-beta-estradiol on the cell surface. Appl. Microbiol. Biotechnol. 59, 329–331.

Yazbeck, D.R., C.A. Martinez, S. Hu and J. Tao. 2004. Challenges in the development of an efficient enzymatic process in the pharmaceutical industry. Tetrahedron Asymmetry 15, 2757–2764.

Yeh, B.J., and W.A. Lim. 2007. Synthetic biology: lessons from the history of synthetic organic chemistry. Nat. Chem. Biol. 3, 521–525.

Yehuda, H., S. Droby, M. Bar-Shimon, M. Wisniewski and M. Goldway. 2003. The effect of under- and overexpressed CoEXG1-encoded exoglucanase secreted by *Candida oleophila* on the biocontrol of *Penicillium digitatum*. 20, 771–780.

Yildirim, M., I. Sahin, A. Kucukbayrak, D. Ozdemir, M. Tevfik Yavuz, S. Oksuz and S. Cakir. 2007. Hand carriage of *Candida* species and risk factors in hospital personnel. Mycoses 50, 189–192.

Yin, Q.Y., P.W.J. de Groot, H.L. Dekker, L. de Jong, F.M. Klis and C.G. de Koster. 2005. Comprehensive proteomic analysis of *Saccharomyces cerevisiae* cell walls: identification of proteins covalently attached via glycosylphosphatidylinositol remnants or mild alkali–sensitive linkages. J. Biol. Chem. 280, 20894–20901.

Yin, Q.Y., P.W. de Groot, L. de Jong, F.M. Klis and C.G. de Koster. 2007. Mass spectrometric quantification of covalently bound cell wall proteins in *Saccharomyces cerevisiae*. FEMS Yeast Res. 7, 887–896.

Yin, Q.Y., P.W. de Groot, C.G. de Koster and F.M. Klis. 2008. Mass spectrometry-based proteomics of fungal cell wall glycoprotein. Trends Microbiol. 16, 20–26.

Ykema, A. 1989. Lipid production in the oleaginous yeast *Apiotrichum curvatum*. PhD Thesis, Free University Amsterdam, The Netherlands.

Ykema, A., E.C. Verbree, M.M. Kater and H. Smit. 1988. Optimization of lipid production in the oleaginous yeast *Apiotrichum curvatum* in whey permeate. Appl. Microbiol. Biotechnol. 29, 211–218.

Ykema, A., E.C. Verbree, H.J.J. Nijkamp and H. Smit. 1989. Isolation and characterization of fatty acid auxotrophs from the oleaginous yeast *Apiotrichum curvatum*. Appl. Microbiol. Biotechnol. 32, 76–84.

Yokote, Y., M. Sugimoto and S. Abe. 1974. Yeasts utilizing methanol as a sole carbon source. J. Ferment. Technol. 52, 201–209.

Yokotsuka, I., and S. Goto. 1955. Studies on Japanese wine film yeasts. Part 4. On new species of genus *Candida* and *Trichosporon*. J. Agric. Chem. Soc. Jpn 29, 132–135.

Yong, P.V.C., P.P. Chong, L.Y. Lau, R.S.C. Yeoh and F. Jamal. 2008. Molecular identification of *Candida orthopsilosis* isolated from blood culture. Mycopathologia 165, 81–87.

Yoshida, K., T. Hisatomi and N. Yanagishima. 1989. Sexual behavior and its pheromonal regulation in ascosporogenous yeasts. J. Basic Microbiol. 29, 99–128.

Yoshida, S., K. Hashimoto, E. Shimada, T. Ishiguro, T. Minato, S. Mizutani, H. Yoshimoto, K. Tashiro, S. Kuhara and O. Kobayashi. 2007. Identification of bottom-fermenting yeast genes expressed during lager beer fermentation. Yeast 24, 599–606.

Yoshiuchi, K., M. Watanabe and A. Nishimura. 2000. Breeding of a non-urea producing sake yeast with killer character using a kar1-1 mutant as a killer donor. J. Ind. Microbiol. Biotechnol. 24, 203–209.

Youssef, B.M., A.A. Asker, S.K. el-Samahy and H.M. Swailam. 2002. Combined effect of steaming and gamma irradiation on the quality of mango pulp stored at refrigerated temperature. Food Res. Int. 35, 1–13.

Yu, T., and X.D. Zheng. 2007. Indole-3-acetic acid enhances the biocontrol of *Penicillium expansum* and *Botrytis cinerea* on pear fruit by *Cryptococcus laurentii*. FEMS Yeast Res 7, 459–464.

Yu, T., P.G. Wu, J.J. Qi, X.D. Zheng, F. Jiang and X. Zhan. 2006. Improved control of postharvest blue mold in pear fruit by a combination of *Cryptococcus laurentii* and gibberellic acid. Biol. Control 39, 128–134.

Yuan, P., G. Jedd, D. Kumaran, S. Swaminathan, H. Shio, D. Hewitt, N.H. Chua and K. Swaminathan. 2003. A HEX-1 crystal lattice required for Woronin body function in *Neurospora crassa*. Nat. Struct. Biol. 10, 264–270.

Yuan, L., I. Kurek, J. English and R. Keenan. 2005. Laboratory-directed protein evolution. Microbiol. Mol. Biol. Rev. 68, 373–392.

Yue, J.-Z. 1977. *Saccharomycodes sinensis* sp. nov. A new species of yeast from soil of Hainan Island, China. Acta Microbiol. Sin. 17, 89–95. In Chinese.

Yue, J.-Z. 1982. A new species of *Sterigmatomyces*. Acta Mycol. Sin. 1, 79–87. In Chinese.

Yue, J.-Z., and Y. Pna. 1984. A new species of *Candida* – *Candida* b*eijingensis*. Acta Mycol. Sin. 3, 157–168. In Chinese.

Yui, T., K. Ogawa, M. Kakuta and A. Misaki. 1995. Chain conformation of a glucuronoxylomannan isolated from fruit body of *Tremella fuciformis* Berk. J. Carbohydr. Res. 14, 255–263.

Yukawa, M., and T. Maki, 1931. *Schizosaccharomyces japonicus* nov. spec. La. Bul. Sci. Fakultato Terkultura, Kjusu Imp. Univ., Fukuoka, Japan 4, 218–226. In Japanese; English summary. (Cited by Wickerham and Duprat 1945.)

Yurkevich, D.I., and V.P. Kutyshenko. 1998. Study of glucose utilization during growth of tea fungus by ^{1}H NMR spectroscopy. Biofizica 43, 319–322.

Yurkov, A.M., and I.Y. Chernov. 2005. Geographical races of certain species of ascomycetous yeasts in the Moscow and Novosibirsk regions. Microbiology (Moscow) 74, 597–601.

Yurkov, A.M., I.A. Maksimova and I.Yu. Chernov. 2004. The comparative analysis of yeast communities structure in birch forests of European Russia and Western Siberia. Mikol. Fitopatol. 38, 71–79. In Russian.

Zambino, P.J., and T.C. Harrington. 1992. Correspondence of isozyme characterization with morphology in the sexual genus *Leptographium* and taxonomic implications. Mycologia 84, 12–25.

Zambonelli, C., G. Montanari, P. Passatelli and S. Rainieri. 1996. The yeasts from Parmigiano-Reggiano whey. Scienza e Tecnica Latteria Casearia 47, 261–270.

Zamir, D., and I. Chet. 1985. Application of enzyme eletrophoresis for the identification of isolates in *Trichoderma harizianum*. Can. J. Microbiol. 31, 578–580.

Zancopé-Oliveira, R.M., M.J. James, A.P. Derossi, J.L.M. Sampaio, M.M. Muniz, R.K. Li, A.S.A. Nascimento, J.M. Peralta and E. Reiss. 2000. Strain characterization of *Candida parapsilosis* fungemia by molecular typing methods. Eur. J. Clin. Microbiol. Infect. Dis. 19, 514–520.

Zander, R.H. 2004. Minimal values for reliability of bootstrap and jackknife proportions, decay index, and Bayesian posterior probability. Phyloinformatics 2, 1–13.

Zang, M. 1999. A new taxon, *Filobasidiella xianghuijun* Zang, associated with *Tremella fuciformis*. Edible Fungi of China 18, 43–44.

Zargari, A., G. Midgley, O. Back, S.G. Johansson and A. Scheynius. 2003. IgE-reactivity to seven *Malassezia* species. Allergy 58, 306–311.

Zeikus, J.G., and E.A. Johnson. 1991. Mixed Cultures in Biotechnology. McGraw Hill, New York.

Zender, J. 1925a. Sur quelques nouvelles espèces de levures et d'*Endomyces*. Bull. Soc. Bot. Genève 17, 258–271.

Zender, J. 1925b. Sur la classification des Endomycétacés. Bull. Soc. Bot. Genève 17, 272–302.

Zhang, H., C. Fu, X. Zheng, Y. Xi, W. Jiang and Y. Wang. 2004. Control of postharvest *Rhizopus* rot of peach by microwave treatment and yeast antagonist. Eur. Food Res. Technol. 218, 568–572.

Zhang, H., C. Fu, X. Zheng, C. Fu and Y. Xi. 2005. Postharvest biological control of gray mold rot of pear with *Cryptococcus laurentii*. Postharvest Biol. Technol. 35, 79–86.

Zhang, H., X. Zheng, L. Wang, S. Li and R. Liu. 2007. Effect of yeast antagonist in combination with hot water dips on postharvest *Rhizopus* rot of strawberries. J. Food Eng. 78, 281–287.

Zhang, L.H., Y. Wangjing, Ohta and Y.J. Wang. 2003. Expression of the inulinase gene from *Aspergillus niger* in *Pichia pastoris*. Process Biochem. 38, 1209–1212.

Zhang, N., S.-O. Suh and M. Blackwell. 2003. Microorganisms in the gut of beetles: evidence from molecular cloning. J. Invertebr. Pathol. 84, 226–233.

Zhang, S., D.A. Schisler, M.J. Boehm and P.J. Slininger. 2005. Carbon-to-nitrogen ratio and carbon loading of production media influence freeze-drying survival and biocontrol efficacy of *Cryptococcus nodaensis* OH 182.9. Phytopathology 95, 626–631.

Zhang, S., D.A. Schisler, M.A. Jackson, M.J. Boehm, P.J. Slininger and Z.L. Liu. 2006. Cold shock during liquid production increases storage shelf-life of *Cryptococcus nodaensis* OH 182.9 after air-drying. Biocontrol Sci. Technol. 16, 281–293.

Zhao, J., and G.H. Fleet. 2005. Degradation of RNA during the autolysis of *Saccharomyces cerevisiae* produces predominantly ribonucleotides. J. Ind. Microbiol. Biotechnol. 32, 415–423.

Zhao, J.-H., F.-Y. Bai, L.-D. Guo and J.-H. Jia. 2002. *Rhodotorula pinicola* sp. nov., a basidiomycetous yeast species isolated from xylem of pine twigs. FEMS Yeast Res. 2, 159–163.

Zhao, J.-H., F.-Y. Bai, Q.-M. Wang and J.-H. Jia. 2003. *Sporobolomyces bannaensis*, a novel ballistoconidium-forming yeast species in the *Sporidiobolus* lineage. Int. J. Syst. Evol. Microbiol. 53, 2091–2093.

Zharkikh, A. 1994. Estimation of evolutionary distances between nucleotide sequences. J. Mol. Evol. 39, 315–329.

Zheng, X., H. Zhang and Y. Xi. 2004. Effects of *Cryptococcus laurentii* (Kufferath) Skinner on biocontrol of postharvest decay of arbutus berries. Bot. Bull. Acad. Sin. 45, 55–60.

Zhong, W.Y., M.W. Jeffries and N.H. Georgopapadakou. 2000. Inhibition of inositol phosphorylceramide synthase by aurobasidin A in *Candida* and *Aspergillus* spp. Antimicrob. Agents Chemother. 44, 651–653.

Zierdt, C.H., C. Detlefson, J. Muller and K.S. Waggie. 1988. *Cyniclomyces guttulatus* (*Saccharomycopsis guttulata*) –culture, ultrastructure and physiology. Antonie van Leeuwenhoek 54, 357–366.

Zikes, H. 1911. Über eine Struktur in der Zellhaut mancher Schleimhefen. Zentralbl. Bakteriol. Parasitenkd., Abt. II, 30, 625–639.

Zimmermann, J. 1938. Sprosspilze im Wein und deren Bestimmung. Zentralbl. Bakteriol. Parasitenkd., Abt. II, 98, 36–65.

Zironi, R., P. Romano, G. Suzzi, F. Battistutta and G. Comi. 1993. Volatile metabolites produced in wine by mixed and sequential cultures of *Hanseniaspora guilliermondii* or *Kloeckera apiculata* and *Saccharomyces cerevisiae*. Biotechnol. Lett. 15, 235–238.

Zlatanov, M., K. Pavlova and D. Grigorova. 2001. Lipid composition of some yeast strains from Livingston Island, Antarctica. Folia Microbiol. 46, 402–406.

Zook, C.D., M.E. Parrish, R.J. Bradock and M.D. Balaban. 1999. High pressure inactivation kinetics of *Saccharomyces cerevisiae* ascospores in orange and apple juices. J. Food Sci. 64, 533–535.

Zopf, W. 1889. Oxalsäuregährung (an Stelle von Alcoholgährung) bei einem typischen (endosporen) Saccharomyceten (*S. hansenii* n. spec.). Ber. Dtsch. Bot. Ges. 7, 94–97.

Zopf, W. 1890. Die Pilze in morphologischer, physiologischer, biologischer und systematischer Richtung. Trewendt, Breslau.

Zorg, J., S. Kilian and F. Radler. 1988. Killer toxin producing strains of the yeasts *Hanseniaspora uvarum* and *Pichia kluyveri*. Arch. Microbiol. 149, 261–267.

Zou, Z.H., F.S. Li and L.B. Buck. 2005. Odor maps in the olfactory cortex. Proc. Natl. Acad. Sci. USA 102, 7724–7729.

Zsolt, J. 1957. A new yeast: *Dioszegia hungarica* nov. gen. et sp. Bot. Kozl. 47, 63–66.

Zsolt, J. 1963. Morphological and physiological investigations of a *Dipodascus* strain isolated in Hungary. Acta Bot. Hung. 9, 217–226.

Zubkova, R. 1971. Genus novum Saccharomycetacearum e *Kazachstania*. Bot. Mat. Gerb. Inst. Bot. AN. Kazakh. SSR. 7, 53–56. In Russian.

Zubkova, R.D., and L.M. Lukasheva, 1979. Species nova generis Vanderwaltiae Novák et Zsolt. Bot. Mat. Gerb. Inst. Bot. Kazakh. SSR 11, 108–110. In Russian.

Zugmaier, W., R. Bauer and F. Oberwinkler. 1994. Mycoparasitism of some *Tremella* species. Mycologia 86, 49–56.

Zuzuarregul, A., P. Carrasco, A. Palacios, A. Julien and M. del Olmo. 2005. Analysis of the expression of some stress induced genes in several commercial wine yeast strains at the beginning of vinification. J. Appl. Microbiol. 98, 299–307.

Zwart, C., M. Veenhuis and W. Harder. 1970. Biogenesis and breakdown of peroxisomes in the yeast *Hansenula polymorpha* in relation to environmental changes. Antonie van Leeuwenhoek 45, 331–332.

Zwickl, D.J. 2006. Genetic algorithm approaches for the phylogenetic analysis of large biological sequence datasets under the maximum likelihood criterion. Thesis, University of Texas at Austin, TX.

Zwickl, D.J., and M.T. Holder. 2004. Model parameterization, prior distributions, and the general time-reversible model in Bayesian phylogenetics. Syst. Biol. 53, 877–888.

Zwillenberg, L.O. 1966. *Torulopsis anatomiae*, a new yeast resistant against low concentrations of formalin. Antonie van Leeuwenhoek 32, 135–138.