

# 真菌分类研究进展

白逢彦

真菌学国家重点实验室

E-mail: baify@im.ac.cn



# 提纲

---

□ 真菌概述

□ 真菌的生物多样性与分类主要依据

□ 真菌界及其主要类群

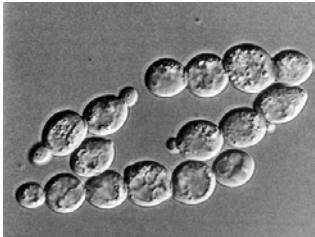
□ 真菌分子鉴定DNA条形码

□ 真菌命名法规的最新变化

# 真菌概述

□ 真菌(fungus, fungi)是真核的、能产生孢子的、无叶绿素的有机体，以吸收的方式获取营养，普遍以有性和无性两种方式进行繁殖，菌体通常由丝状、分枝的体细胞构成，细胞典型地被含几丁质的细胞壁所包裹。

- 1) 真菌属于真核(eukaryotic)生物，即具有膜包围的含有多条染色体细胞核；
- 2) 菌体除少数以单细胞(酵母)状态存在外，通常由丝状、分枝的体细胞(称为菌丝hyphae)构成，菌丝以顶端生长(apical growth)方式生长；
- 3) 细胞具有细胞壁，细胞壁通常含有几丁质(chitin)；
- 4) 营养方式为异养(heterotrophic)，即需要现成的有机物作为能源和碳源，以吸收(absorb)的方式获取营养；
- 5) 以有性和无性两种方式进行繁殖，产生形态多样并适于传播或逆境生存的孢子(spores)繁殖体。



# 真菌生物多样性：全球物种数估测

---

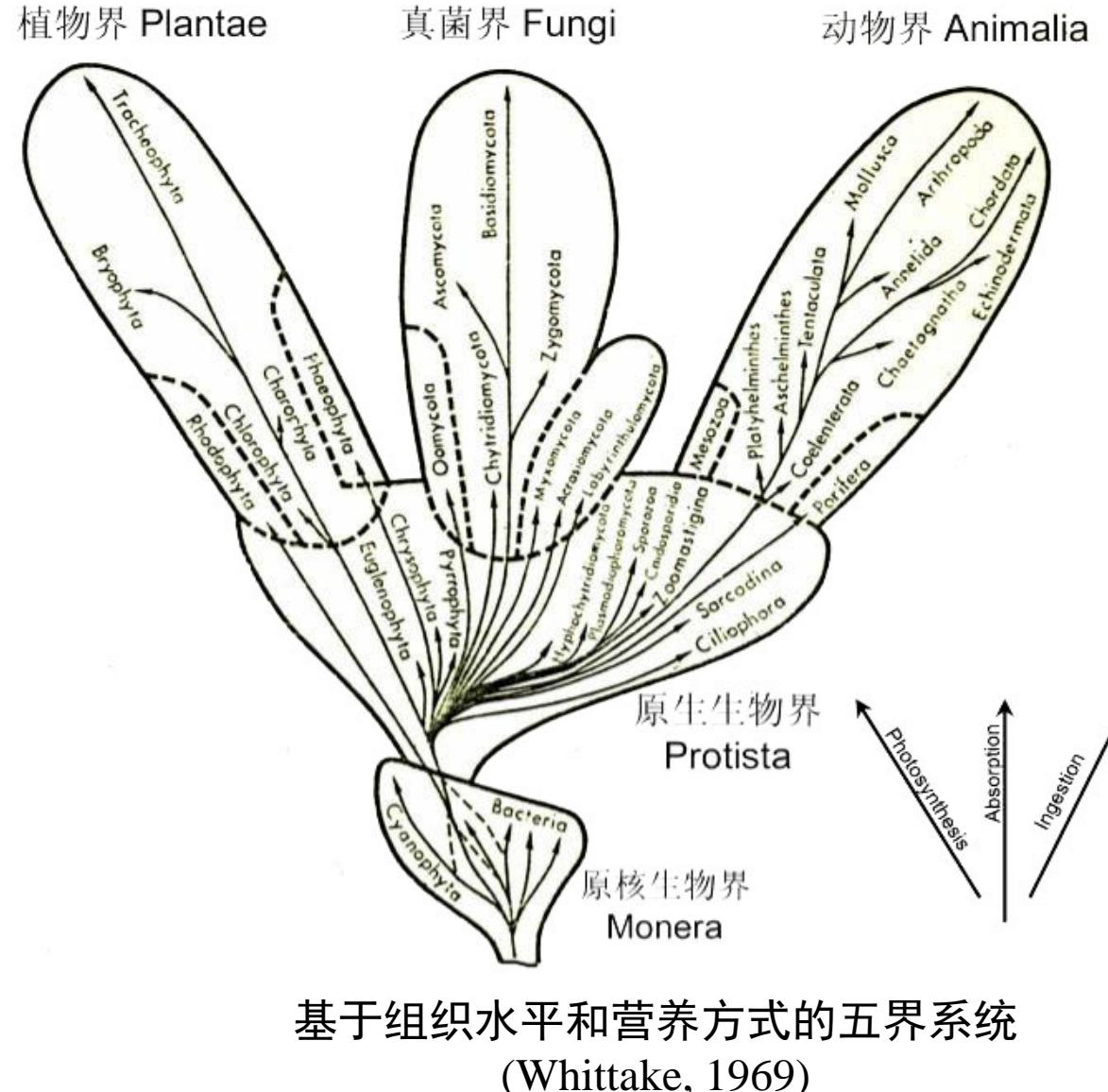
- **1.5 million species, estimated based on a fungus to plant ratio of 6 : 1 (Hawksworth, 1991).**
- **2 to 11 million species have been estimated existing on Earth (Hawksworth & Lücking 2017, Baldrian et al. 2021, Lücking et al. 2021).**
- **About 155 000 species have been formally described (Bánki et al. 2023).**
- **About 2 000 new species have been described each year in the past two decades (Cheek et al. 2020, Bhunjun et al. 2022).**

# 真菌分类的主要依据

- **形态特征** 是真菌，尤其是大型真菌分类的基础
- **生理学特征** 不同糖类化合物的发酵能力、对不同碳氮源化合物的利用能力、最高生长温度、对外源维生素的依赖性等
- **化学分类特征** 辅酶Q (Coenzyme Q)、脂肪酸等
- **细胞壁化学组分** 卵菌细胞壁多糖主要是纤维素，而其他真菌类群则主要含几丁质
- **蛋白质** 全蛋白质提取物的凝胶电泳图谱、或同工酶(isozymes)电泳图谱
- **核酸**
  - DNA碱基组成、DNA-DNA杂交数据（相似性或相关性）等
  - 核糖体RNA (rRNA)基因(rDNA)序列分析：ITS序列已被推荐用于真菌物种鉴定的通用DNA条形码
  - 单拷贝蛋白编码基因：EF1- $\alpha$ ,  $\beta$ -tubulin, actin, RPB1, RPB2, MCM7), calmodulin等
  - 线粒体的rRNA基因和部分蛋白基因

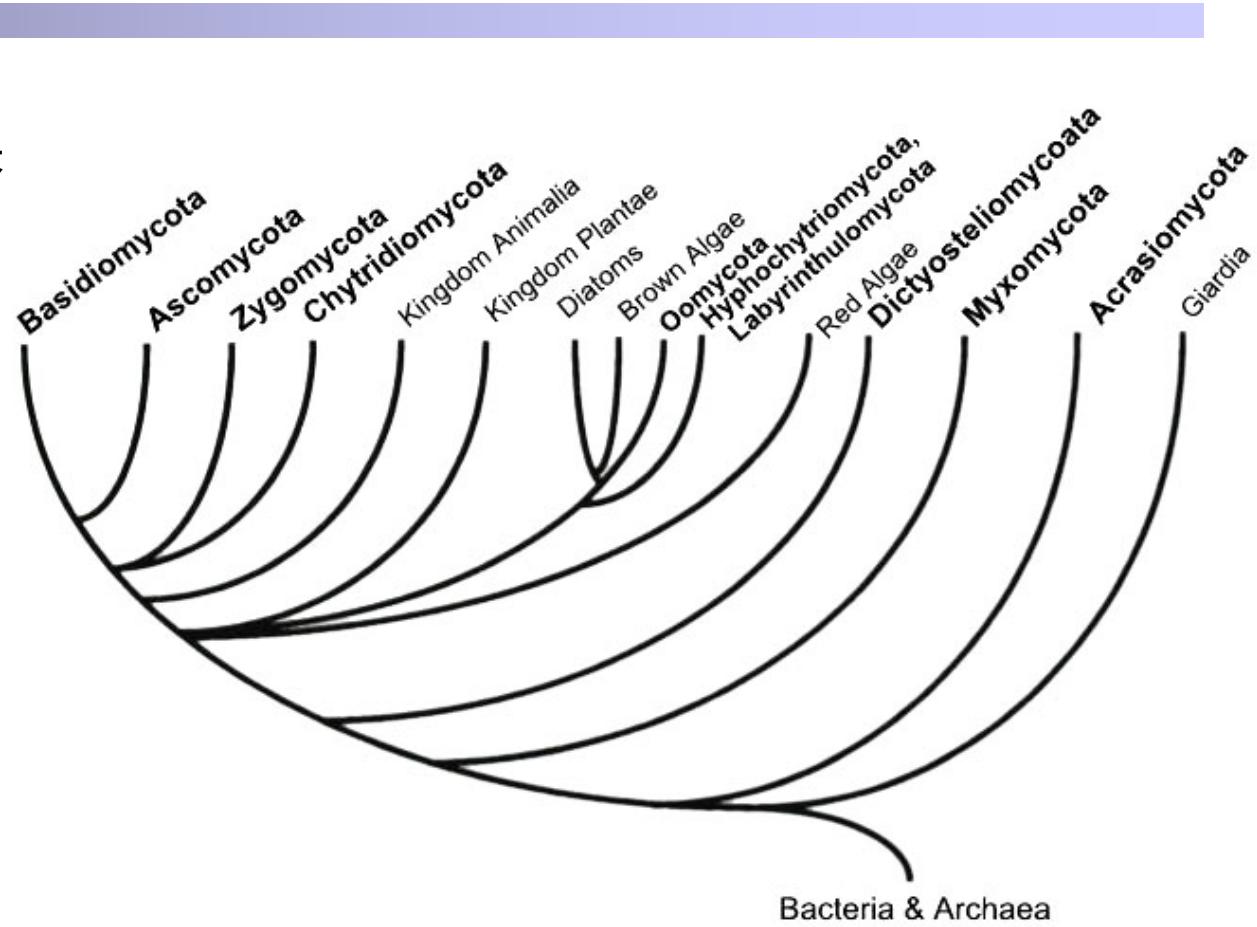
# 真菌界(Kingdom Fungi)概念的演变

- 早期真菌被归入植物界
- Whittake (1969)基于组织水平和营养方式建立了五界系统，将真菌从植物界中独立出来成为与动物界和植物界平行的真菌界
- 真菌界包括
  - 壶菌门(Chytridiomycota)
  - 接合菌门(Zygomycota)
  - 子囊菌门(Ascomycota)
  - 担子菌门(Basidiomycota)
  - 卵菌门(Oomycota)
  - 黏菌类等



# 真菌界(Kingdom Fungi)概念的演变

- 主要基于DNA序列的分子系统学研究证实原来被称为真菌的卵菌(oomycetes)和黏菌(slime moulds)等，与其他真菌没有近缘关系，被排除在真菌界之外。
- 卵菌，丝壶菌和网黏菌与硅藻类和褐藻类构成一个单元类群，被称为茸鞭生物界 (Kingdom Chromista，又称为藻物界)。
- 其他黏菌属于原生动物(Protozoa)。
- 这些生物虽不再被包括在真菌界内，但由于其在形态学、营养方式和生态学等方面与真菌核心类群相似，仍然被作为广义上的真菌由真菌学家来研究。
- 壶菌、接合菌、子囊菌和担子菌构成一个单元类群，成为真菌界的核心成员。



系统演化树，示真菌界和由真菌学者研究的各类生物  
(粗体)间的相互关系 (Berbee & Taylor, 1999)

# Assembling the Fungal Tree of Life

about  
people  
participation  
resources  
data  
links



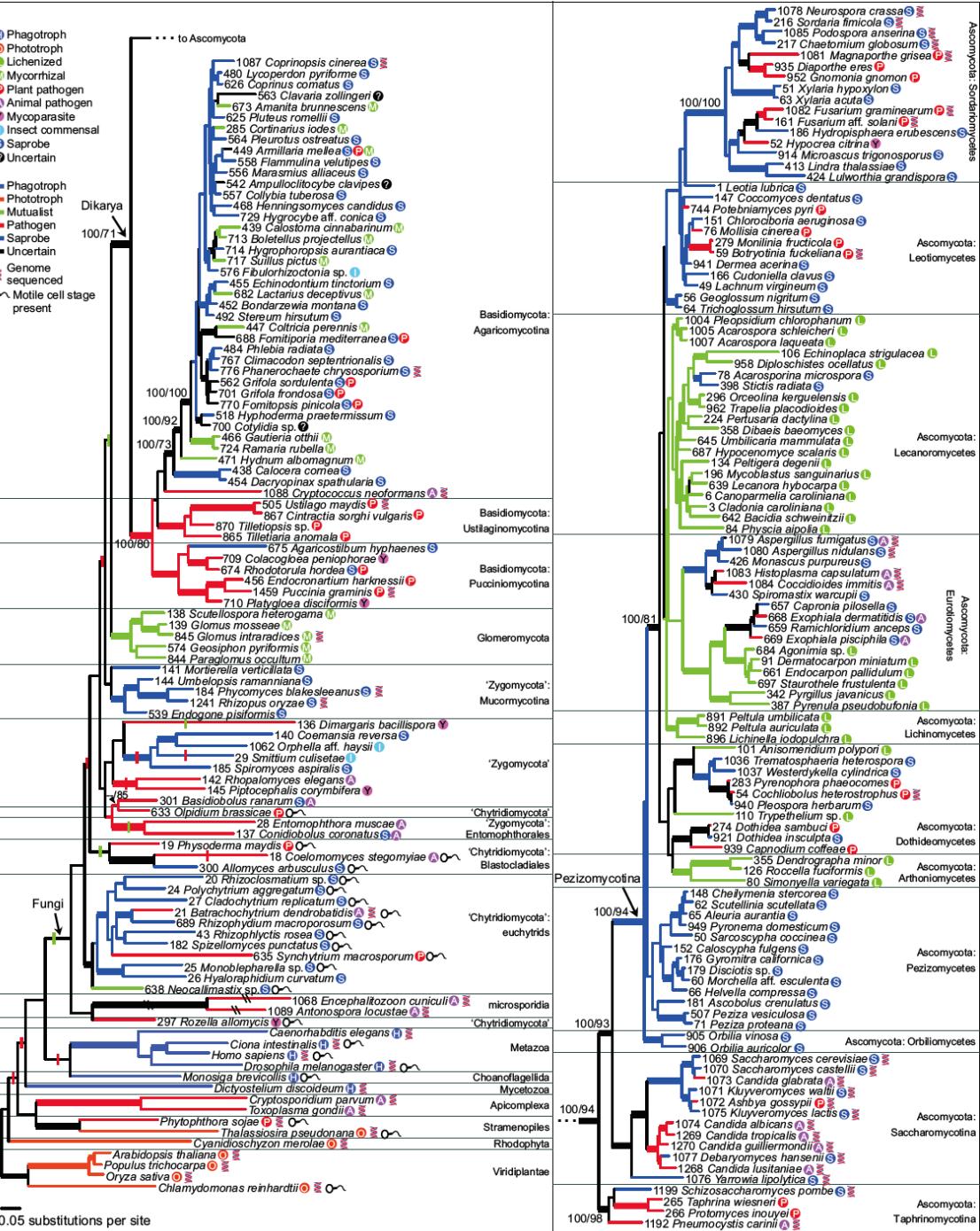
## ARTICLES

# Reconstructing the early evolution of Fungi using a six-gene phylogeny

Timothy Y. James<sup>1</sup>, Frank Kauff<sup>1</sup>, Conrad L. Schoch<sup>2\*</sup>, P. Brandon Matheny<sup>3\*</sup>, Valérie Hofstetter<sup>1\*</sup>, Cymon J. Cox<sup>1†</sup>, Gail Celio<sup>4</sup>, Cécile Gueidan<sup>1</sup>, Emily Fraker<sup>1</sup>, Jolanta Miadlikowska<sup>1</sup>, H. Thorsten Lumbsch<sup>5</sup>, Alexandra Rauhut<sup>6</sup>, Valérie Reeb<sup>1</sup>, A. Elizabeth Arnold<sup>1†</sup>, Anja Amtoft<sup>7</sup>, Jason E. Stajich<sup>8</sup>, Kentaro Hosaka<sup>2†</sup>, Gi-Ho Sung<sup>2</sup>, Desiree Johnson<sup>2</sup>, Ben O'Rourke<sup>2</sup>, Michael Crockett<sup>2</sup>, Manfred Binder<sup>3</sup>, Judd M. Curtis<sup>3</sup>, Jason C. Slot<sup>3</sup>, Zheng Wang<sup>3†</sup>, Andrew W. Wilson<sup>3</sup>, Arthur Schüßler<sup>9</sup>, Joyce E. Longcore<sup>10</sup>, Kerry O'Donnell<sup>11</sup>, Sharon Mozley-Standridge<sup>12</sup>, David Porter<sup>12</sup>, Peter M. Letcher<sup>13</sup>, Martha J. Powell<sup>13</sup>, John W. Taylor<sup>14</sup>, Merlin M. White<sup>15</sup>, Gareth W. Griffith<sup>16</sup>, David R. Davies<sup>17</sup>, Richard A. Humber<sup>18</sup>, Joseph B. Morton<sup>19</sup>, Junta Sugiyama<sup>20</sup>, Amy Y. Rossman<sup>21</sup>, Jack D. Rogers<sup>22</sup>, Don H. Pfister<sup>23</sup>, David Hewitt<sup>23</sup>, Karen Hansen<sup>23</sup>, Sarah Hambleton<sup>24</sup>, Robert A. Shoemaker<sup>24</sup>, Jan Kohlmeyer<sup>25</sup>, Brigitte Volkmann-Kohlmeyer<sup>25</sup>, Robert A. Spotts<sup>26</sup>, Maryna Serdani<sup>26</sup>, Pedro W. Crous<sup>27</sup>, Karen W. Hughes<sup>28</sup>, Kenji Matsuura<sup>29</sup>, Ewald Langer<sup>30</sup>, Gitta Langer<sup>30</sup>, Wendy A. Untereiner<sup>31</sup>, Robert Lücking<sup>5</sup>, Burkhard Büdel<sup>6</sup>, David M. Geiser<sup>32</sup>, André Aptroot<sup>33</sup>, Paul Diederich<sup>34</sup>, Imke Schmitt<sup>5†</sup>, Matthias Schultz<sup>35</sup>, Rebecca Yahr<sup>1†</sup>, David S. Hibbett<sup>3</sup>, François Lutzoni<sup>1</sup>, David J. McLaughlin<sup>4</sup>, Joseph W. Spatafora<sup>2</sup> & Rytas Vilgalys<sup>1</sup>

**Phylogeny of the kingdom Fungi using bayesian analysis of the combined six-gene data set (18S, 28S and 5.8S rRNA; EF1 $\alpha$ , RPB1 and RPB2).**

James et al. 2006. NATURE 443:818-822



# Assembling the Fungal Tree of Life (AFTOL) Classification

Hibbett DS et al. (67 authors). 2007. A higher-level phylogenetic classification of the Fungi. *Mycol Res* 111: 509–547

## Kingdom FUNGI (basal fungi)

### Phylum

**CHYTRIDIOMYCOTA**

**NEOCALLIMASTIGOMYCOTA**

**BLASTOCLADIOMYCOTA**

**MICROSPORIDIA**

**GLOMEROMYCOTA**

### Subphylum

**Mucoromycotina**

**Entomophthoromycotina**

**Zoopagomycotina**

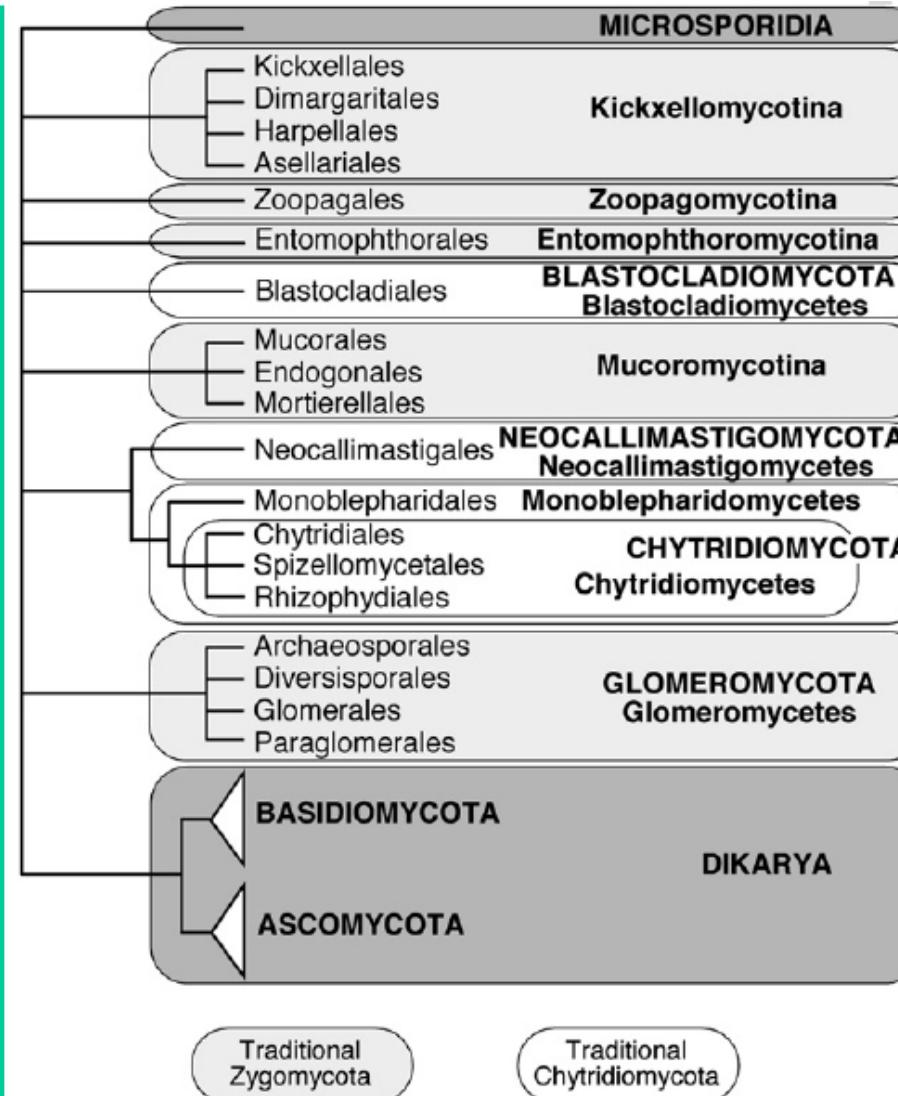
**Kickxellomycotina**

### Subkingdom DIKARYA

### Phylum

**ASCOMYCOTA**

**BASIDIOMYCOTA**



## Discovery of novel intermediate forms redefines the fungal tree of life

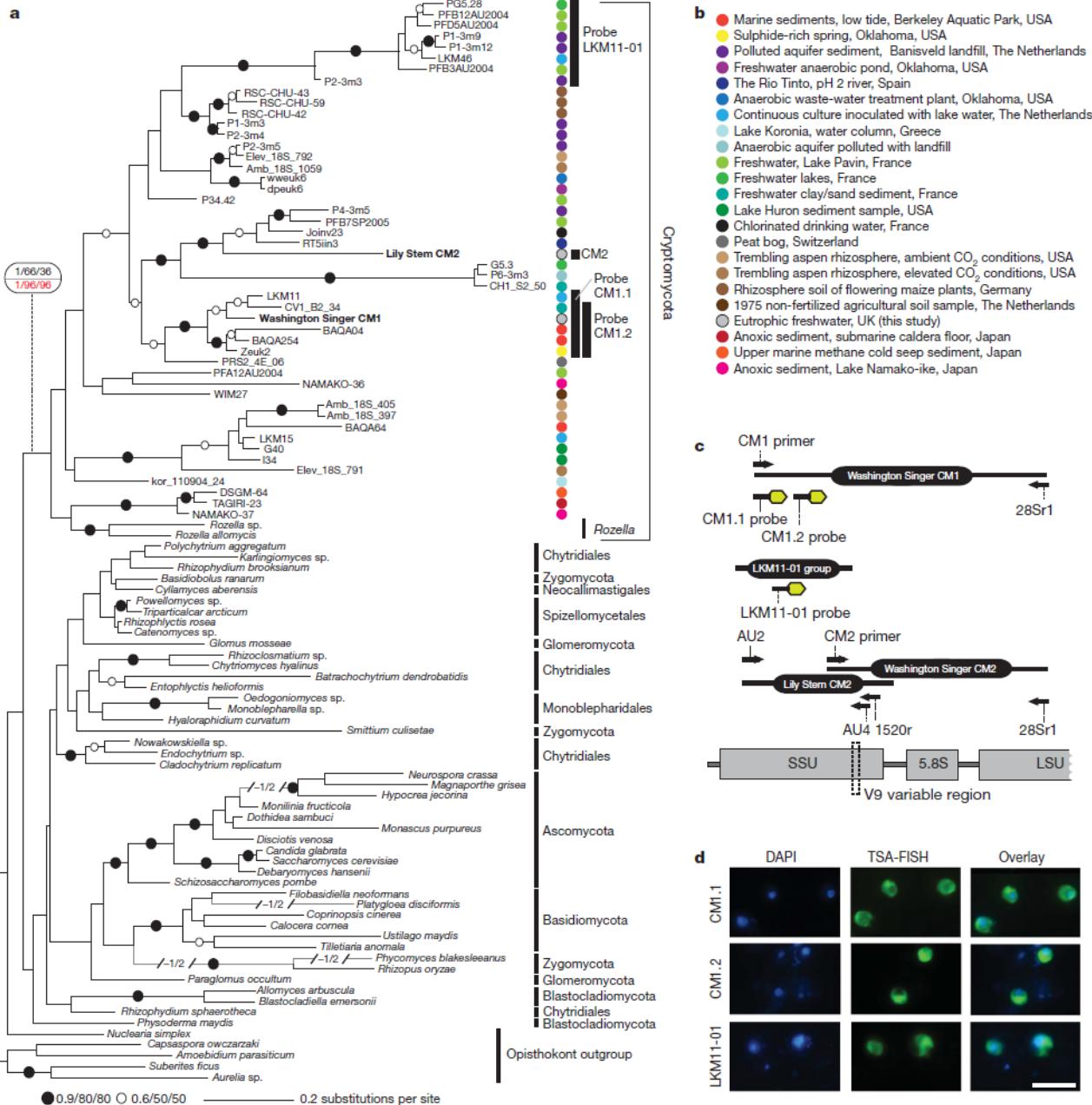
Meredith D. M. Jones<sup>1,2</sup>, Irene Forn<sup>3</sup>, Catarina Gadelha<sup>4</sup>, Martin J. Egan<sup>1,5</sup>, David Bass<sup>2</sup>, Ramon Massana<sup>3</sup> & Thomas A. Richards<sup>1,2</sup>

## Discovery and Identification of the Cryptomycota

A highly diverse form of eukaryotic life that branches with the Fungi, using environmental DNA analyses combined with fluorescent detection via DNA probes.

This clade is present in numerous ecosystems including soil, freshwater and aquatic sediments. The cells are small eukaryotes of 3–5 µm in length, capable of forming a microtubule-based flagellum, but do not produce a chitin-rich cell wall.

Phylogenetic analyses using multiple ribosomal RNA genes place this clade with *Rozella*, the putative primary branch of the fungal kingdom.

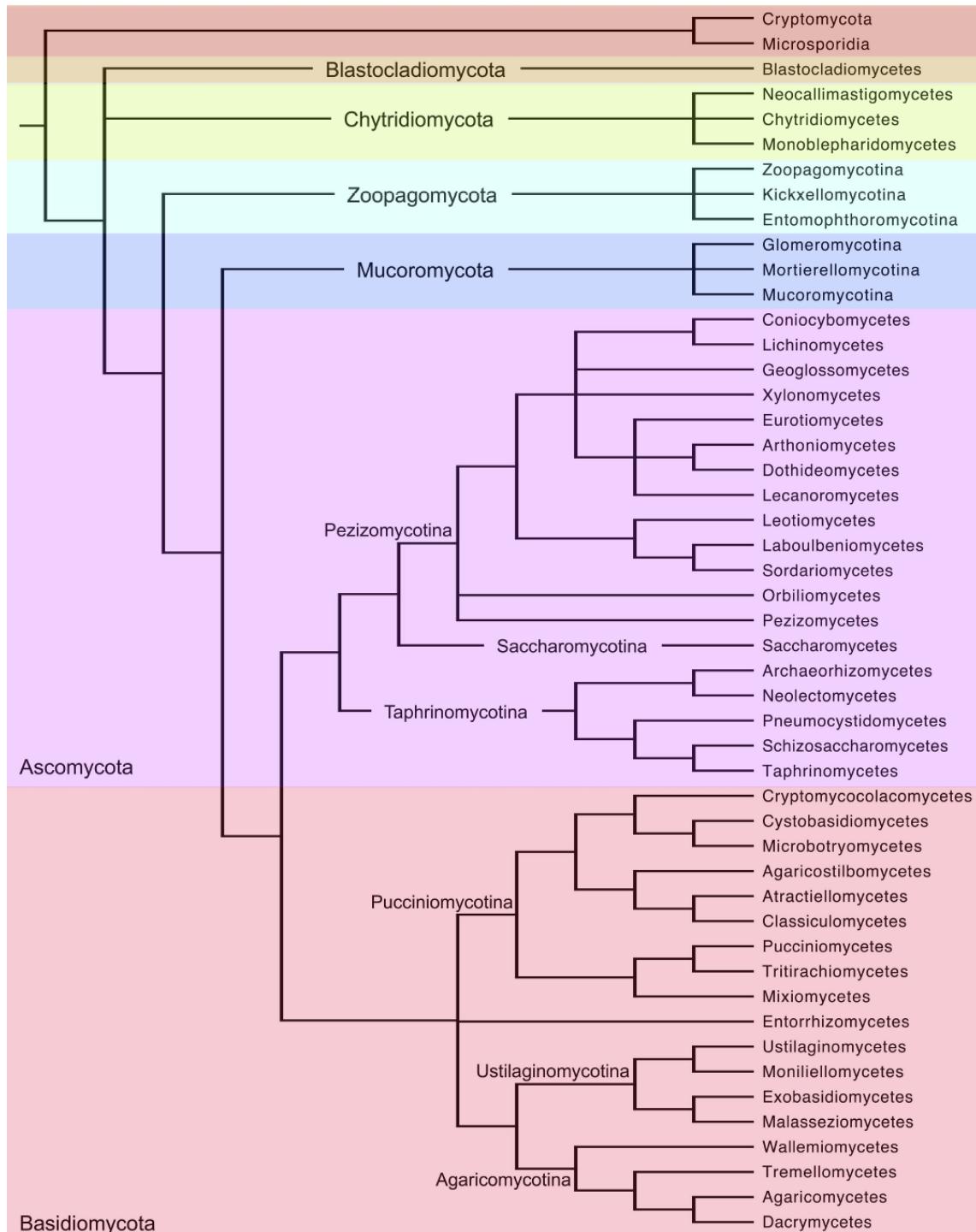


## The Fungal Tree of Life: from Molecular Systematics to Genome-Scale Phylogenies

JOSEPH W. SPATAFORA,<sup>1</sup> M. CATHERINE AIME,<sup>2</sup> IGOR V. GRIGORIEV,<sup>3</sup>  
FRANCIS MARTIN,<sup>4</sup> JASON E. STAJICH,<sup>5</sup> and MEREDITH BLACKWELL<sup>6</sup>

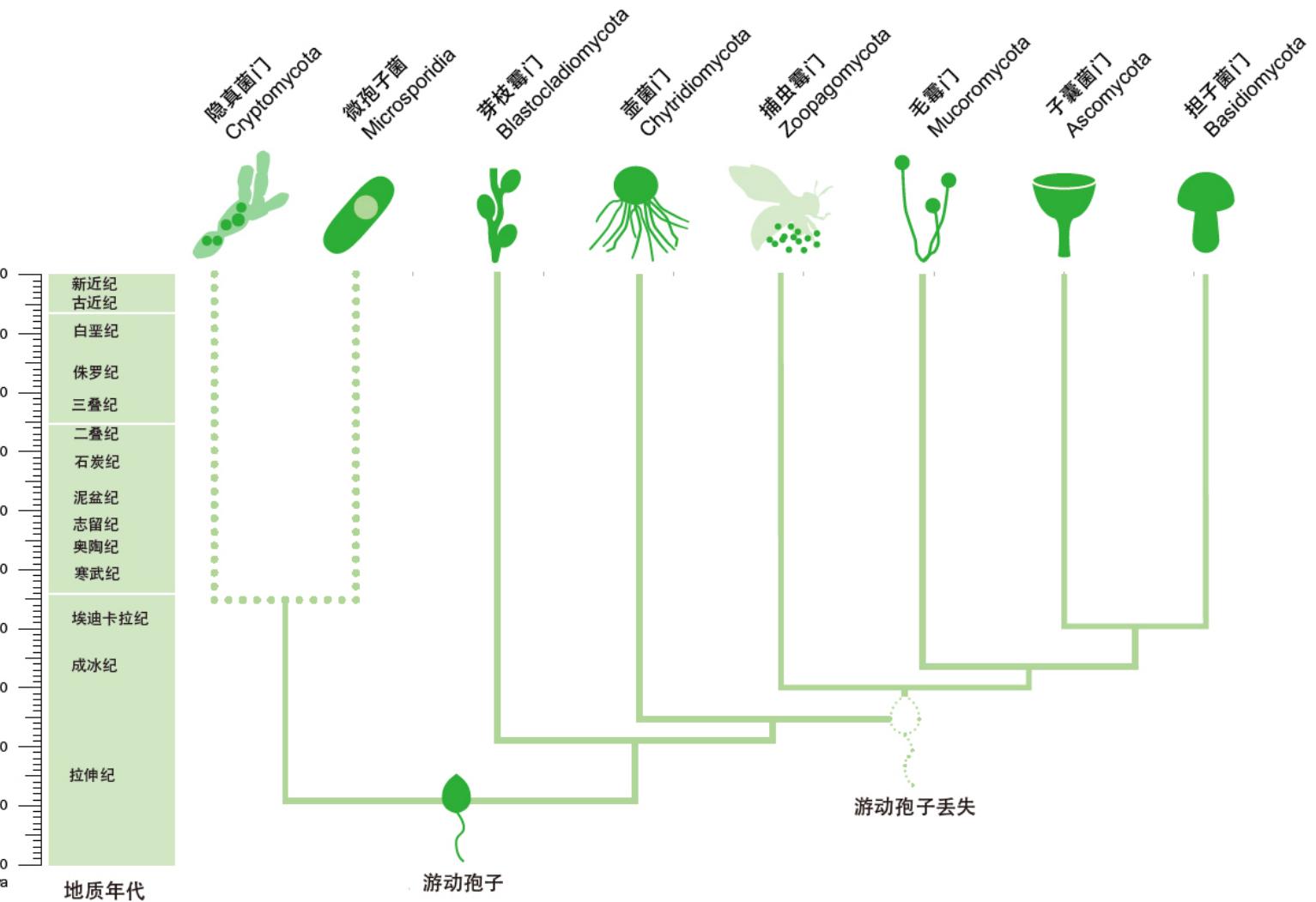
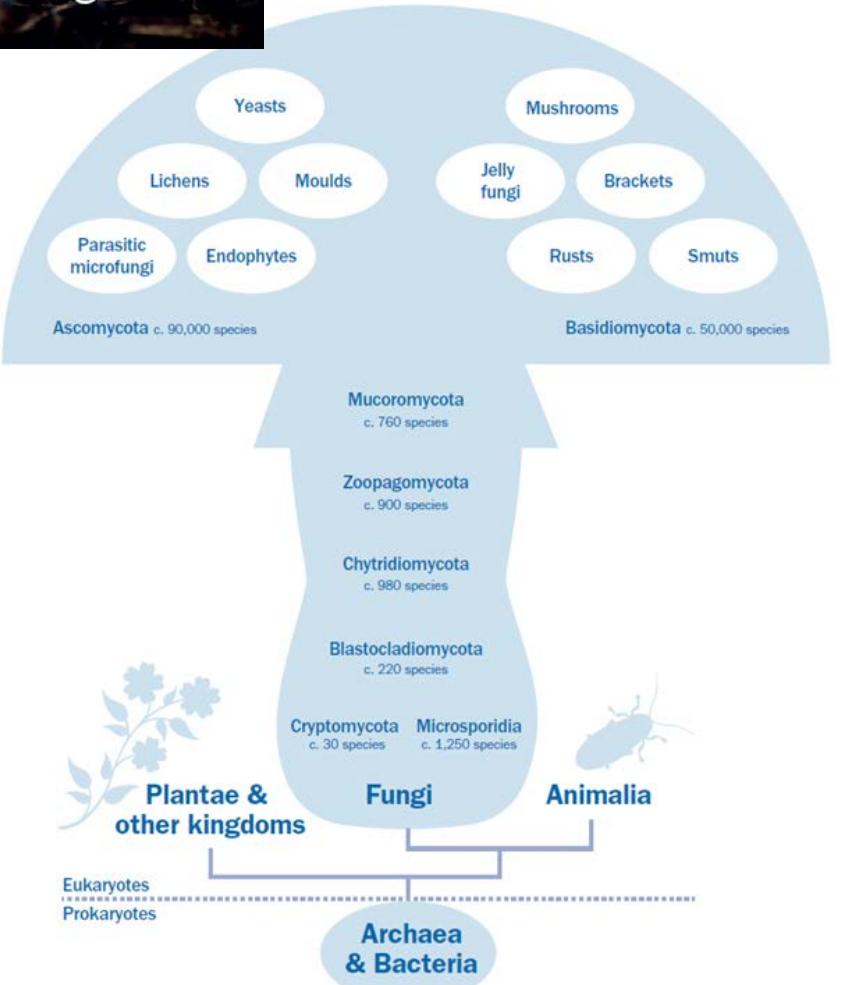
In the current classification, 8 phyla, 12 subphyla, and 46 classes within the fungal kingdom are recognized.

Microbiol Spectrum 5(5): FUNK-0053-2016, 2017.  
DOI:10.1128/microbiolspec.FUNK-0053-2016.





# The Fungal Tree of Life (2018)

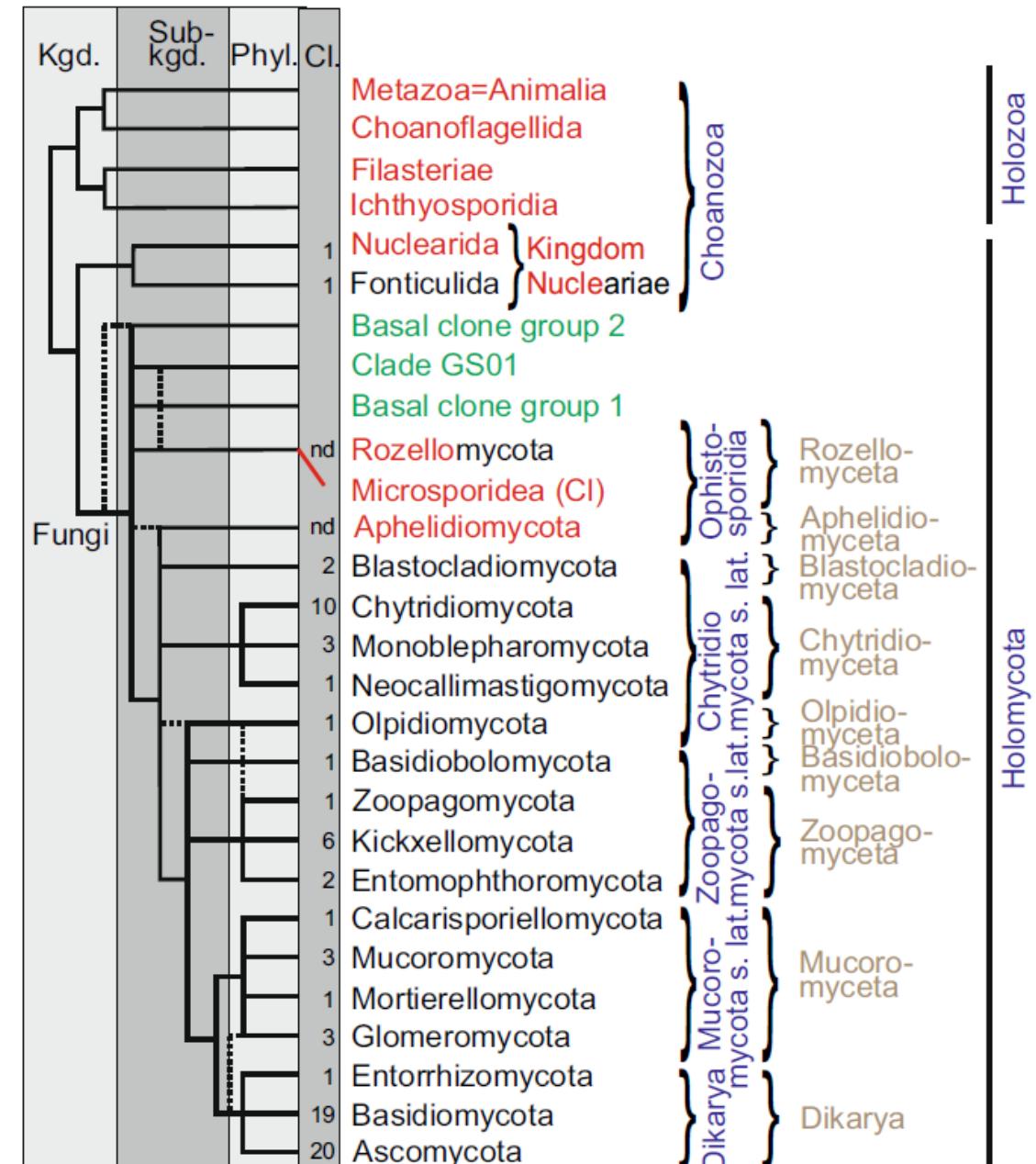


Willis, K. J. (ed.) (2018). State of the World's Fungi 2018. Report. Royal Botanic Gardens, Kew.

## High-level classification of the Fungi and a tool for evolutionary ecological analyses

Leho Tedersoo<sup>1,2,3</sup> · Santiago Sánchez-Ramírez<sup>4</sup> · Urmas Köljalg<sup>1,2</sup> · Mohammad Bahram<sup>3,5</sup> ·  
Markus Döring<sup>6</sup> · Dmitry Schigel<sup>6,7</sup> · Tom May<sup>8</sup> · Martin Ryberg<sup>5</sup> · Kessy Abarenkov<sup>1</sup>

- Nine subkingdoms accommodating 18 phyla are accepted.



Phylum-level classification of fungi (Tedersoo et al. 2018)

*Annual Review of Microbiology*  
Toward a Fully Resolved  
Fungal Tree of Life

Timothy Y. James,<sup>1</sup> Jason E. Stajich,<sup>2</sup>  
Chris Todd Hittinger,<sup>3</sup> and Antonis Rokas<sup>4</sup>

<sup>1</sup>Department of Ecology and Evolutionary Biology, University of Michigan, Ann Arbor, Michigan 48109, USA; email: tyjames@umich.edu

<sup>2</sup>Department of Microbiology and Plant Pathology, Institute for Integrative Genome Biology, University of California, Riverside, California 92521, USA; email: jason.stajich@ucr.edu

<sup>3</sup>Laboratory of Genetics, DOE Great Lakes Bioenergy Research Center, Wisconsin Energy Institute, Center for Genomic Science and Innovation, J.F. Crow Institute for the Study of Evolution, University of Wisconsin–Madison, Madison, Wisconsin 53726, USA; email: cthittinger@wisc.edu

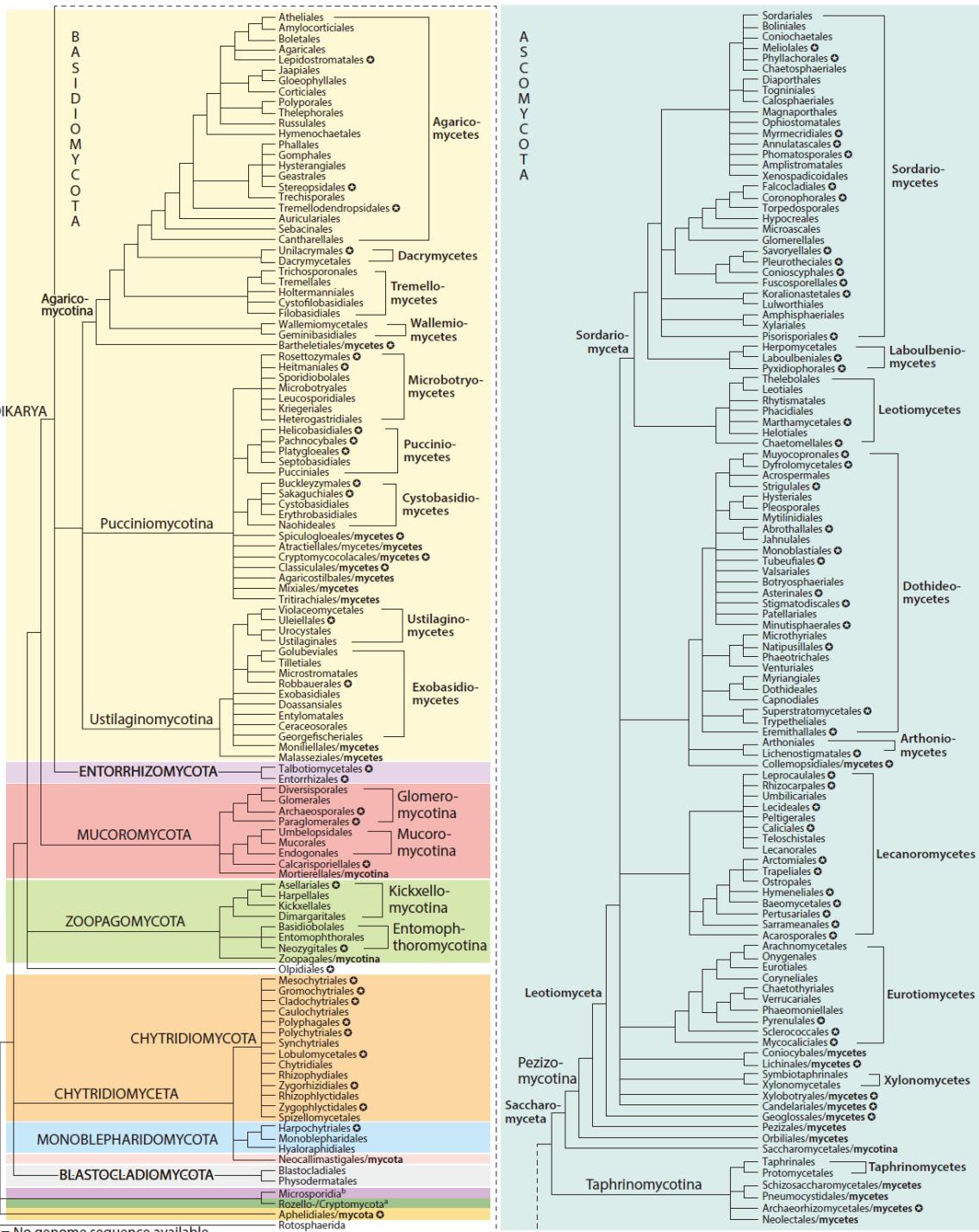
<sup>4</sup>Department of Biological Sciences, Vanderbilt University, Nashville, Tennessee 37235, USA; email: antonis.rokas@vanderbilt.edu

# The Current Status of the Fungal Tree of Life

(James et al., 2020)

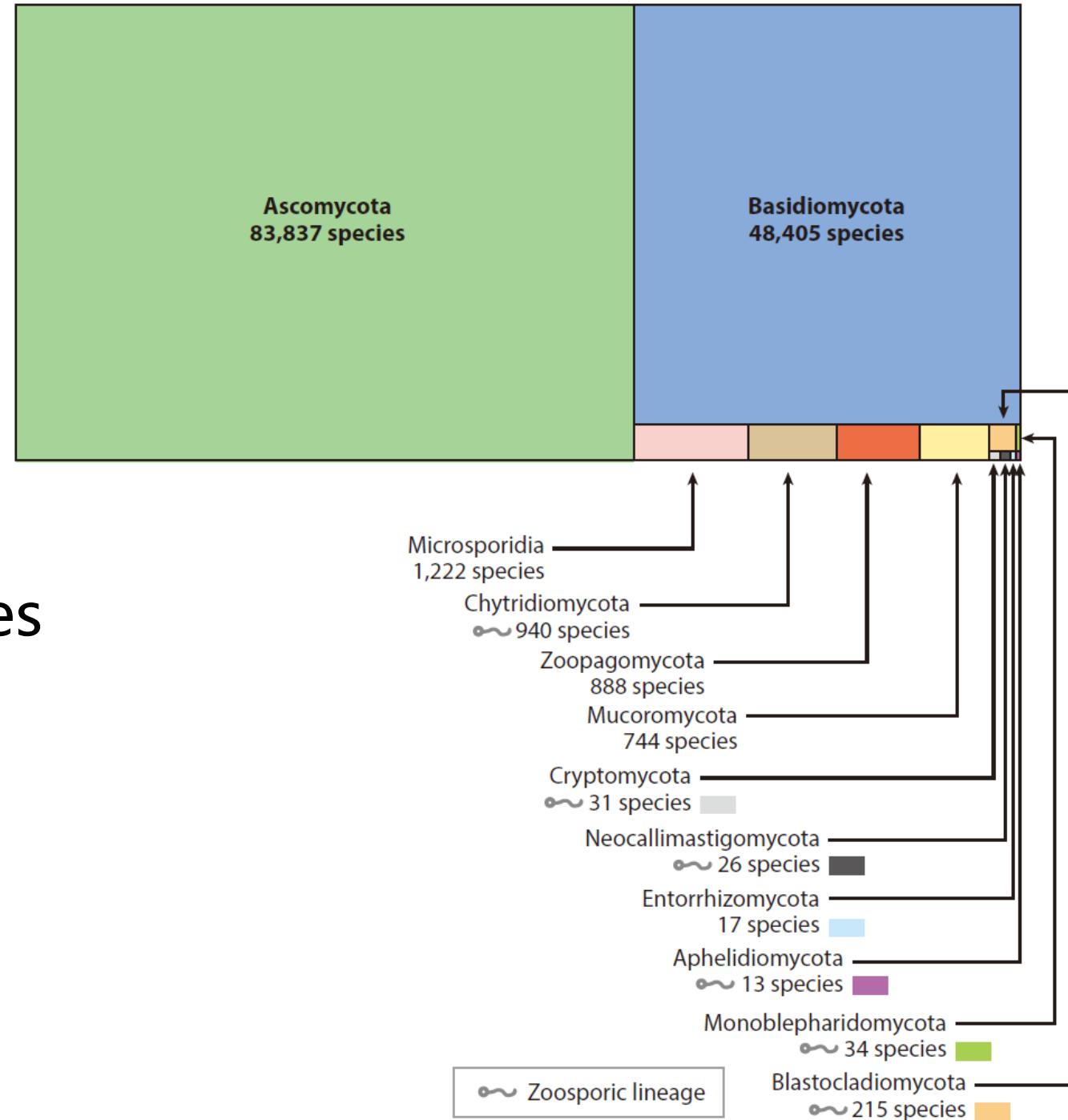
Six major groups with **12 phyla** of Fungi recognized

1. Subkingdom **Dikarya** (双核亚界), composed of **Ascomycota** (子囊菌门), **Basidiomycota** (担子菌门), and **Entorrhizomycota** (根肿黑粉菌门).
2. **Mucoromycota** (毛霉门), a clade of mostly plant-associated taxa with coenocytic hyphae and zygosporangia, is sister to the Dikarya.
3. **Zoopagomycota** (捕虫霉门), another clade of fungi primarily having coenocytic hyphae and zygosporangia, is composed of three subphyla of fungi in parasitic or predatory (sometimes saprobic) association with animals, protists, or other fungi.
4. **Blastocladiomycota** (芽枝霉门) forms a distinct clade of fungi with zoospore ultrastructure with a nuclear cap of ribosomes, and it is the only clade in Fungi with alternation of haploid/diploid generations.
5. **Chytridiomycota** (壶菌亚界) is recognized as a subkingdom comprising most zoosporic (flagellated) fungi in the phyla **Chytridiomycota** (壶菌门), **Monoblepharidomycota** (单毛壶菌门), and **Neocallimastigomycota** (新丽鞭毛菌门).
6. **Opisthosporidia** is possibly a paraphyletic group composed of **Aphelidiomycota**, **Cryptomycota** (隐菌门)/**Rozellomycota** (罗兹壶菌门), and **Microsporidia** (微孢子虫菌门). These endoparasites are the basal branch(es) of Fungi.



# Described species of fungi in each phyla

- Most of the described species (~97%) are concentrated in Ascomycota (子囊菌门) and Basidiomycota (担子菌门)



# 真菌物种鉴定通用DNA条形码

**Nuclear ribosomal internal transcribed spacer (ITS) region as a universal DNA barcode marker for *Fungi***

Conrad L. Schoch<sup>a,1</sup>, Keith A. Seifert<sup>b,1</sup>, Sabine Huhndorf<sup>c</sup>, Vincent Robert<sup>d</sup>, John L. Spouge<sup>a</sup>, C. André Levesque<sup>b</sup>, Wen Chen<sup>b</sup>, and Fungal Barcoding Consortium<sup>a,2</sup>

**Fungal Barcoding Consortium:** 共有来自全世界 74 间实验室或机构的 149 位作者，其中 8 位来自国内实验室

Bai, Feng-Yan  
Cai, Lei  
Cai, Qing  
Ge, Zai-Wei

Guo, Liang-Dong  
Wang, Qi-Ming  
Yang, Zhu L.  
Zhuang, Wen-Ying



# 常用补充DNA条形码

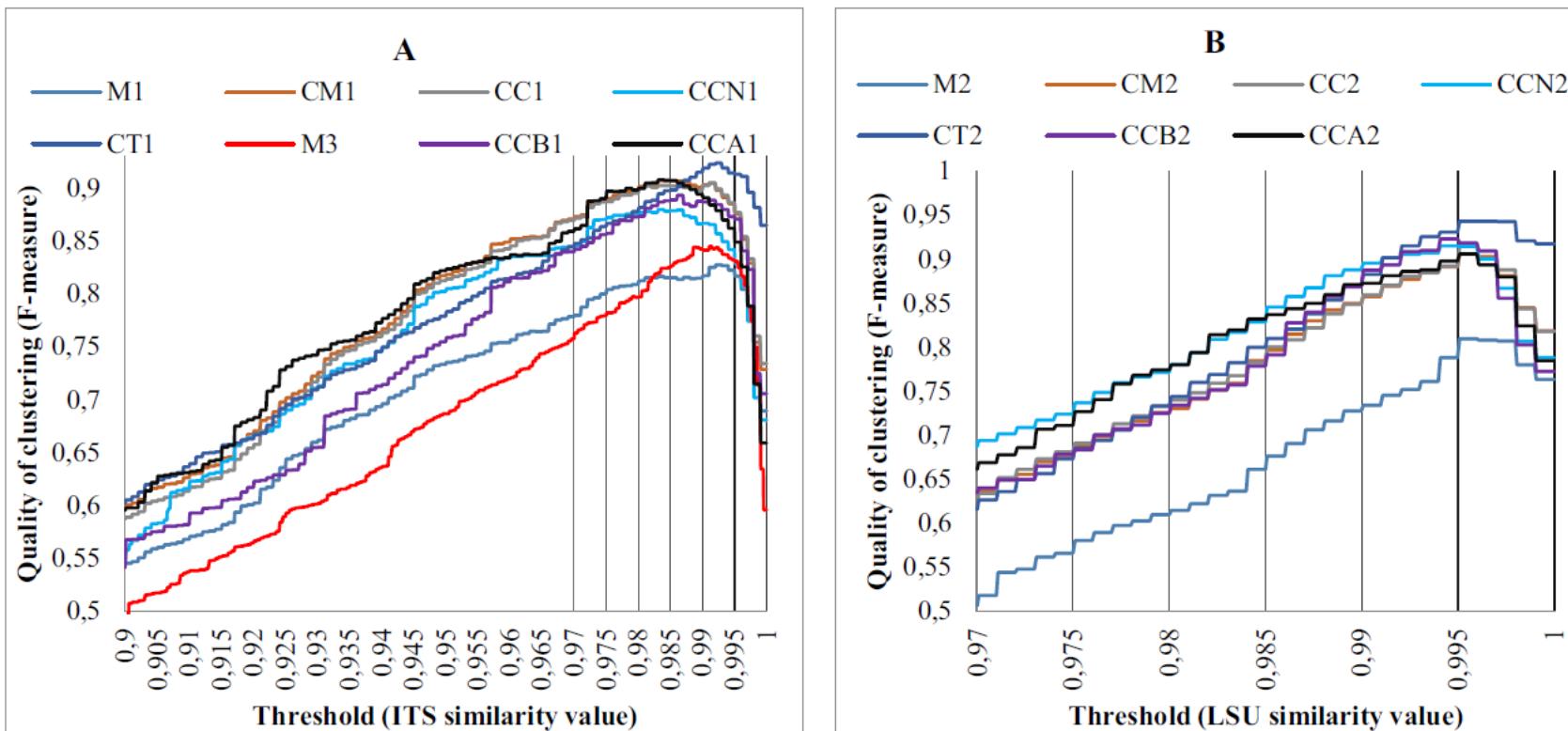
---

- LSU rDNA (D1/D2 domain)
- 单拷贝蛋白编码基因: TEF1/EF1- $\alpha$ ,  $\beta$ -tubulin, actin, RPB1, RPB2, MCM7, calmodulin等
- 不同类群常选用不同的补充条形码
  - 酵母菌: LSU D1/D2 (首选条形码)
  - 青曲霉(*Penicillium, Aspergillus*): BenA (encoding  $\beta$ -tubulin), CaM (encoding calmodulin), RPB2
  - 镰刀菌(*Fusarium*): TEF1, RPB2
  - .....

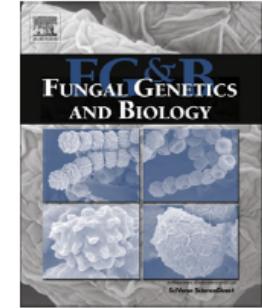


# DNA barcoding analysis of more than 9 000 yeast isolates contributes to quantitative thresholds for yeast species and genera delimitation

D. Vu<sup>1\*</sup>, M. Groenewald<sup>1</sup>, S. Szöke<sup>2</sup>, G. Cardinali<sup>3</sup>, U. Eberhardt<sup>4</sup>, B. Stielow<sup>1</sup>, M. de Vries<sup>1</sup>, G.J.M. Verkleij<sup>1</sup>, P.W. Crous<sup>1</sup>, T. Boekhout<sup>1</sup>, and V. Robert<sup>1\*</sup>



**DNA Barcoding Markers for the Yeasts: LSU D1/D2 and ITS  
Thresholds for yeast species identification: ~ 99% identity**



## Recognition of seven species in the *Cryptococcus gattii/Cryptococcus neoformans* species complex



Ferry Hagen <sup>a,b</sup>, Kantarawee Khayhan <sup>a,c</sup>, Bart Theelen <sup>a</sup>, Anna Kolecka <sup>a</sup>, Itzhack Polacheck <sup>d</sup>,  
Edward Sionov <sup>d,e</sup>, Rama Falk <sup>d,f</sup>, Sittiporn Parnmen <sup>g</sup>, H. Thorsten Lumbsch <sup>h</sup>, Teun Boekhout <sup>a,i,j,\*</sup>

<sup>a</sup> CBS-KNAW Fungal Biodiversity Centre, Basidiomycete and Yeast Research, Utrecht, The Netherlands

<sup>b</sup> Department of Medical Microbiology and Infectious Diseases, Canisius-Wilhelmina Hospital, Nijmegen, The Netherlands

<sup>c</sup> Department of Microbiology and Parasitology, Faculty of Medical Sciences, University of Phayao, Phayao, Thailand

<sup>d</sup> Department of Clinical Microbiology and Infectious Diseases, Hadassah-Hebrew University Medical Center, Ein Kerem, Jerusalem, Israel

<sup>e</sup> Department of Food Quality & Safety, Institute for Postharvest and Food Sciences, Agricultural Research Organization, The Volcani Center, Bet Dagan, Israel

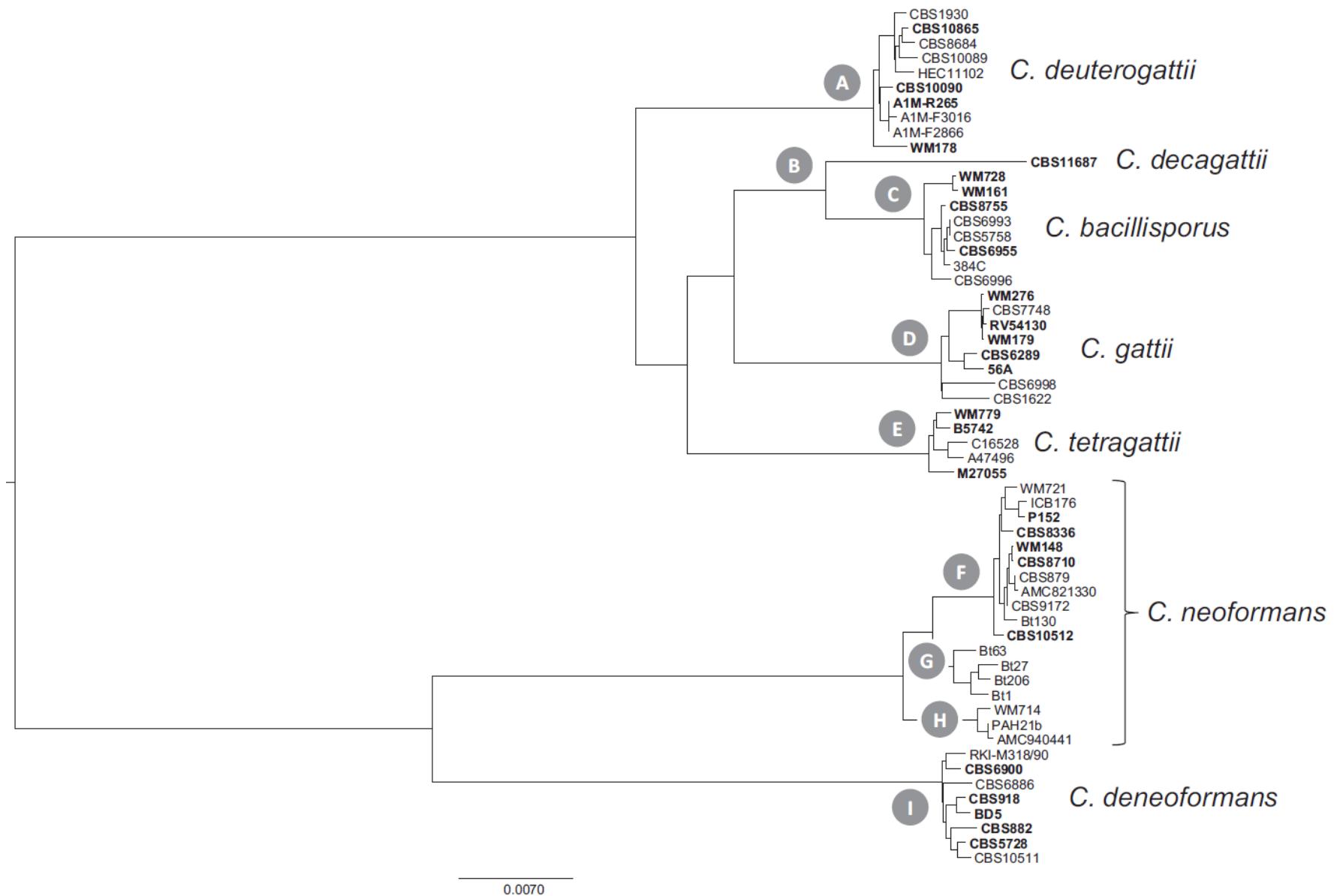
<sup>f</sup> Department of Fisheries and Aquaculture, Ministry of Agriculture and Rural Development, Nir-David, Israel

<sup>g</sup> Department of Medical Sciences, Ministry of Public Health, Nonthaburi, Thailand

<sup>h</sup> Science & Education, The Field Museum, Chicago, IL, USA

<sup>i</sup> Shanghai Key Laboratory of Molecular Medical Mycology, Changzheng Hospital, Second Military Medical University, Shanghai, China

<sup>j</sup> Institute of Microbiology, Chinese Academy of Sciences, Beijing, China



Diversity in the *C. gattii*/*C. neoformans* species complex inferred from a concatenated data set of 11 loci (Hagen et al., 2015).

# Current and proposed species in the *C. gattii/C. neoformans* species complex

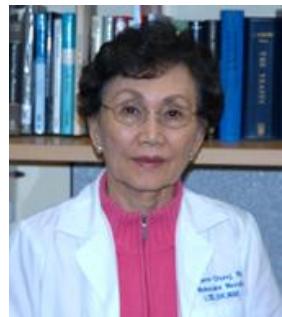
Current species name	MLST/AFLP	PCR/RFLP	Proposed species name
<i>C. neoformans</i> var. <i>grubii</i>	Clade F, AFLP1 Clade G, AFLP1A/VNB Clade H, AFLP1B	VNI VNII VNII	<i>C. neoformans</i>
<i>C. neoformans</i> var. <i>neoformans</i>	Clade I, AFLP2	VNIV	<i>C. deneoformans</i>
<i>C. neoformans</i> intervariety hybrid	AFLP3	VNIII	<i>C. neoformans</i> x <i>C. deneoformans</i> hybrid
<i>C. gattii</i>	Clade D, AFLP4 Clade C, AFLP5 Clade A, AFLP6 Clade E, AFLP7 Clade B, AFLP10	VGI VGIII VGII VGIV VGIV/VGIIIC	<i>C. gattii</i> <i>C. bacillisporus</i> <i>C. deuterogattii</i> <i>C. tetragattii</i> <i>C. decagattii</i>

Hagen et al., 2015

# The Case for Adopting the “Species Complex” Nomenclature for the Etiologic Agents of Cryptococcosis

Kyung J. Kwon-Chung,<sup>a</sup> John E. Bennett,<sup>a</sup> Brian L. Wickes,<sup>b</sup> Wieland Meyer,<sup>c,d</sup>  
 Christina A. Cuomo,<sup>e</sup> Kurt R. Wollenburg,<sup>f</sup> Tihana A. Bicanic,<sup>g</sup>

Elizabeth Castañeda,<sup>h</sup> Yun C. Chang,<sup>a</sup> Jianghan Chen,<sup>i</sup> Massimo Cogliati,<sup>j</sup>  
Françoise Dromer,<sup>k</sup> David Ellis,<sup>l</sup> Scott G. Filler,<sup>m</sup>  Matthew C. Fisher,<sup>n</sup>  
Thomas S. Harrison,<sup>o</sup> Steven M. Holland,<sup>a</sup> Shigeru Kohno,<sup>o</sup> James W. Kronstad,<sup>p</sup>  
Marcia Lazera,<sup>q</sup> Stuart M. Levitz,<sup>r</sup> Michail S. Lionakis,<sup>a</sup>  Balint C. May,<sup>s</sup>  
Popchai Ngamskulrongroj,<sup>t</sup> Peter G. Pappas,<sup>u</sup> John R. Perfect,<sup>v</sup> Volker Rickerts,<sup>w</sup>  
Tania C. Sorrell,<sup>d,x</sup> Thomas J. Walsh,<sup>y</sup> Peter R. Williamson,<sup>a</sup>  Jianping Xu,<sup>z</sup>  
Adrian M. Zelazny,<sup>aa</sup> Arturo Casadevall<sup>bb</sup>



K. J. Kwon-Chung



Wieland Meyer



Jianping Xu

## Recommending using

- *Cryptococcus neoformans* species complex and
- *Cryptococcus gattii* species complex as a practical intermediate step

## Disadvantages in adopting the new classification system:

- (i) An insufficient number of isolates was studied.
- (ii) More of the genome needs to be represented
- (iii) Models applied for species delineation may not be appropriate
- (iv) Species designations are too complex (i.e., routine identification is impractical)
- (v) Species names are confusing
- (vi) Names for hybrid and aneuploid strains are not readily accommodated

## Importance of Resolving Fungal Nomenclature: the Case of Multiple Pathogenic Species in the *Cryptococcus* Genus

✉ Ferry Hagen,<sup>a,b</sup> H. Thorsten Lumbsch,<sup>c</sup> Valentina Arsic Arsenijevic,<sup>d</sup>  
✉ Hamid Badali,<sup>e</sup> Sébastien Bertout,<sup>f</sup> R. Blake Billmyre,<sup>g</sup> M. Rosa Bragulat,<sup>h</sup>  
F. Javier Cabañes,<sup>h</sup> Mauricio Carbria,<sup>i</sup> Arunaloke Chakrabarti,<sup>j</sup>  
✉ Sudha Chaturvedi,<sup>k</sup> Vishnu Chaturvedi,<sup>k</sup> Min Chen,<sup>l,m</sup>  
✉ Anuradha Chowdhary,<sup>n</sup> Maria-Francisca Colom,<sup>o</sup> Oliver A. Cornely,<sup>p,q,r</sup>  
✉ Pedro W. Crous,<sup>s,t,u</sup> Maria S. Cuétara,<sup>v</sup> Mara R. Diaz,<sup>w,x</sup> Ana Espinel-Ingroff,<sup>y</sup>  
✉ Hamed Fakhim,<sup>z</sup> Rama Falk,<sup>aa,bb</sup> Wenjie Fang,<sup>l,m</sup> Patricia F. Herkert,<sup>a,cc</sup>  
Consuelo Ferrer Rodríguez,<sup>o</sup> James A. Fraser,<sup>dd</sup> Josepa Gené,<sup>ee</sup>  
✉ Josep Guarro,<sup>ee</sup> Alexander Idnurm,<sup>ff</sup> María-Teresa Illnait-Zaragoza,<sup>gg</sup>  
Ziauddin Khan,<sup>hh</sup> Kantarawee Khayhan,<sup>ii,jj</sup> Anna Kolecka,<sup>jj</sup>  
Cletus P. Kurtzman,<sup>ll</sup> Katrien Lagrou,<sup>kk,ll</sup> Wanqing Liao,<sup>l,m</sup> Carlos Linares,<sup>o</sup>  
✉ Jacques F. Meis,<sup>a,b</sup> Kirsten Nielsen,<sup>mm</sup> Tinashe K. Nyazika,<sup>nn,oo,pp</sup>  
Weihua Pan,<sup>l,m</sup> Marina Pekmezovic,<sup>qq</sup> Itzhack Polacheck,<sup>aa</sup>  
✉ Brunella Posteraro,<sup>rr</sup> Flávio de Queiroz Telles Filho,<sup>ss</sup> Orazio Romeo,<sup>tt,uu</sup>  
Manuel Sánchez,<sup>o</sup> Ana Sampaio,<sup>vv</sup> Maurizio Sanguinetti,<sup>ww</sup> Pojana Sriburee,<sup>xx</sup>  
Takashi Sugita,<sup>yy</sup> Saad J. Taj-Aldeen,<sup>zz</sup> Masako Takashima,<sup>aaa</sup> John W. Taylor,<sup>bbb</sup>  
Bart Theelen,<sup>jj</sup> Rok Tomazin,<sup>ccc</sup> Paul E. Verweij,<sup>b,ddd</sup> Retno Wahyuningsih,<sup>eee,fff</sup>  
✉ Ping Wang,<sup>ggg,hhh</sup> Teun Boekhout<sup>ii,jj</sup>

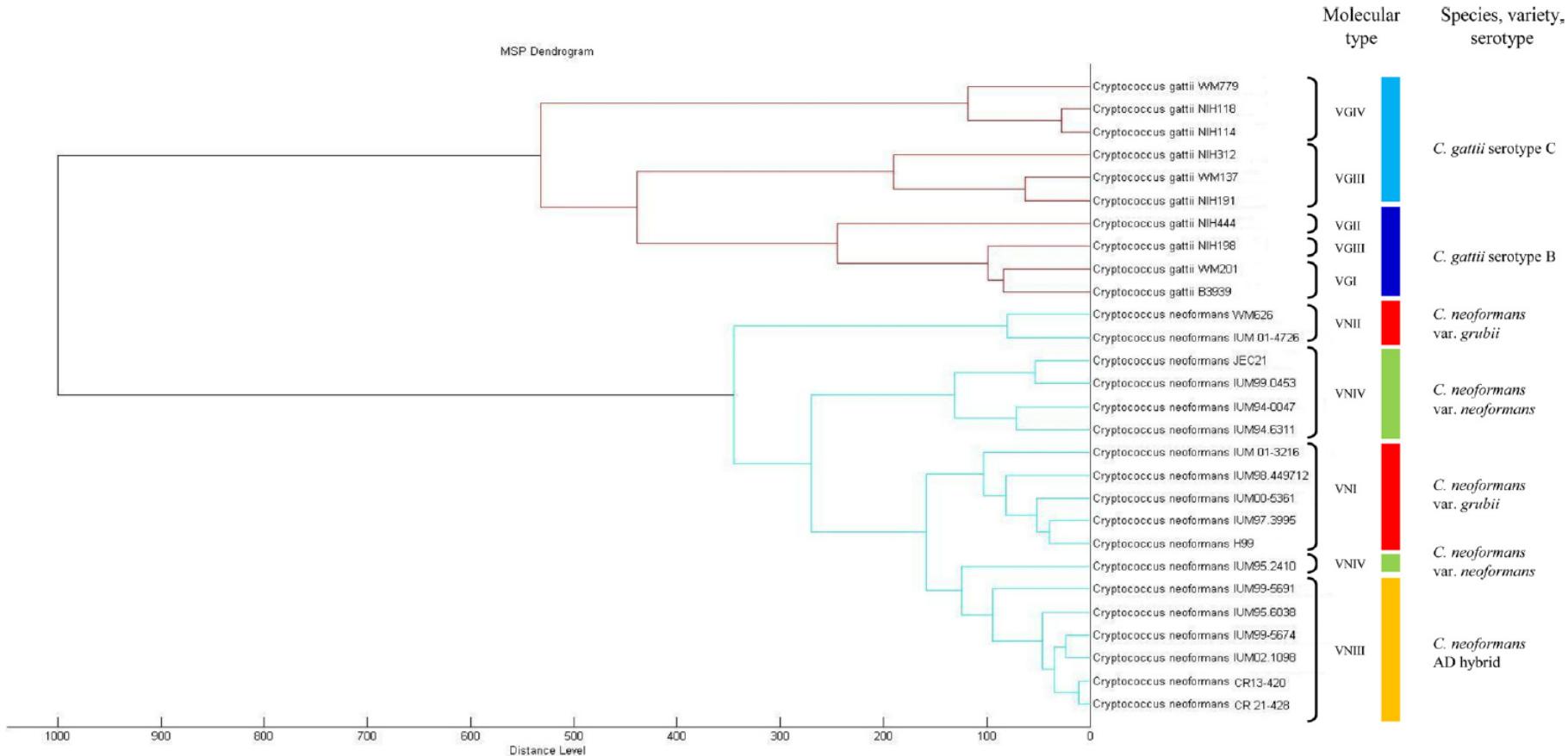
(co-authors: 60)



### Advantages of the seven species system:

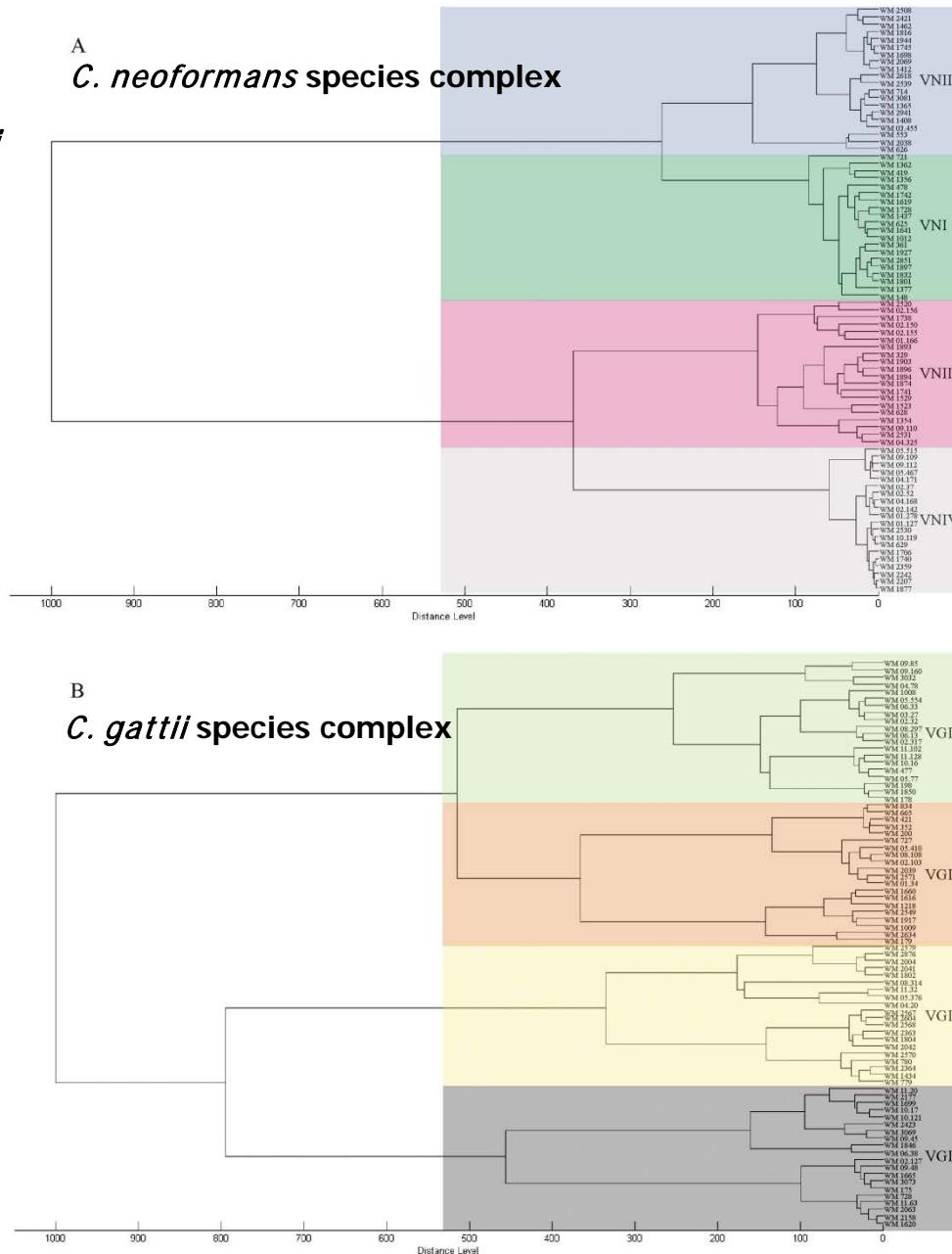
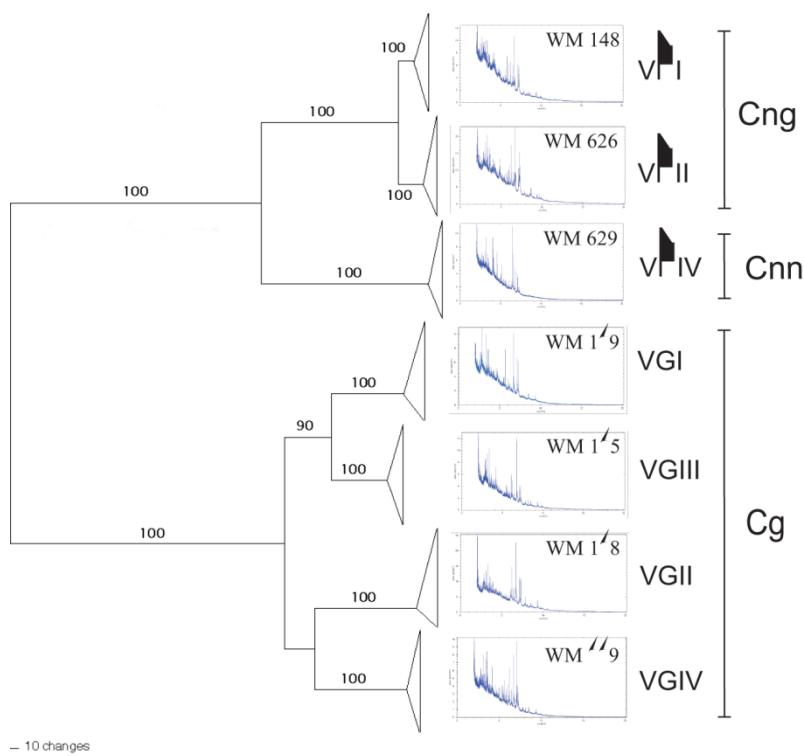
- Stimulating search for further phenotypic and genetic differences and similarities between the recognized species, yielding new features, including differences in drug susceptibility.
- The species can be identified using molecular diagnostics and MALDI-TOF MS.
- Ignoring the species impedes deciphering the differences among them, which may delay future clinical advances.
- More species seem to occur within *Cryptococcus*.

# Discrimination between Molecular Types of *Cryptococcus neoformans* and *Cryptococcus gattii* using MALDI-TOF MS



Cluster analysis of MALDI-TOF MS spectra of *C. neoformans* and *C. gattii* isolates (Posteraro et al., 2012, J. Clin. Microbiol)

**MALDI-TOF MS Enables the Rapid Identification of the Major Molecular Types within the *Cryptococcus neoformans/C. gattii* Species Complex** (Firacave et al., 2012. PLoS One 7:e37566)

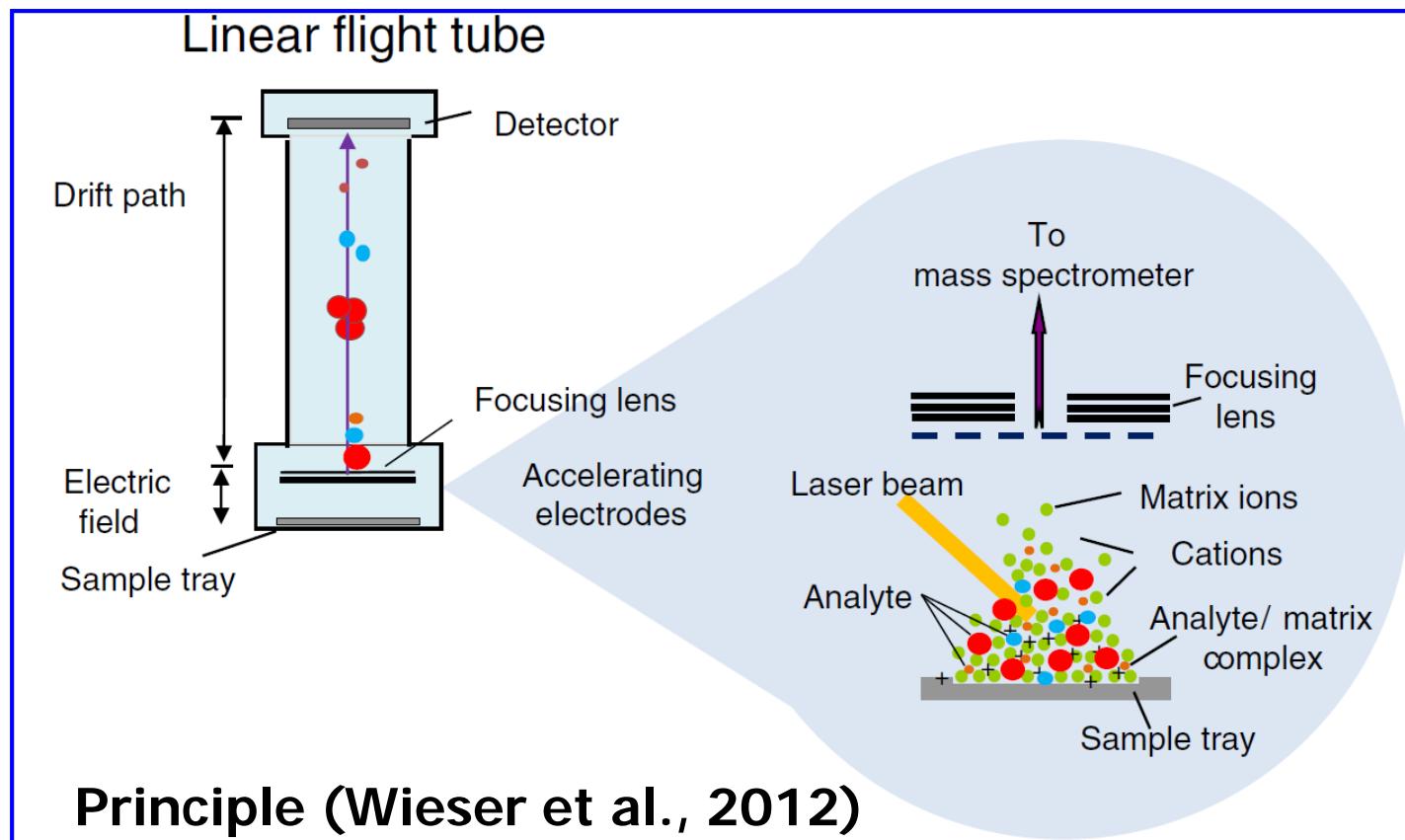


# MALDI-TOF MS 指纹图谱分析

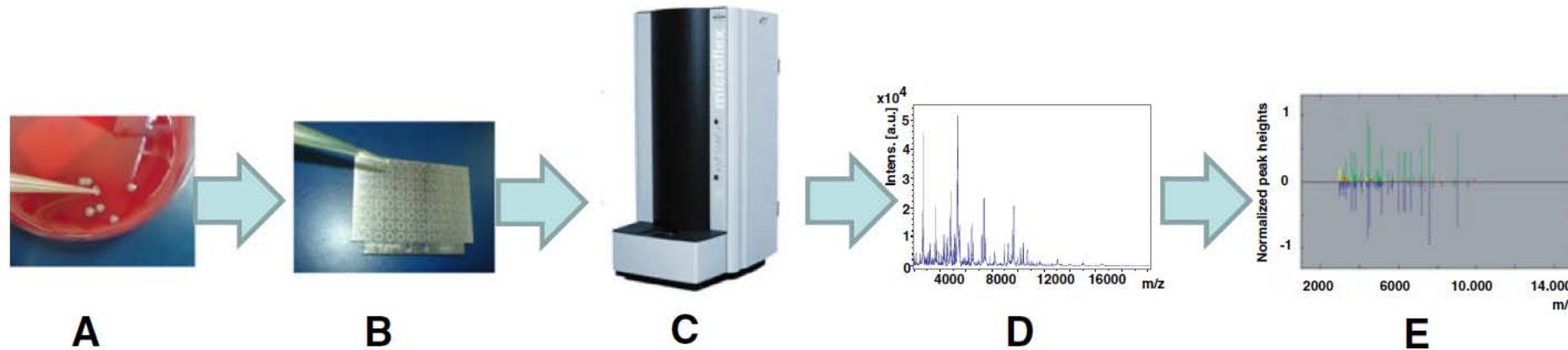
Matrix-Assisted Laser Desorption/Ionization

Time of Flight Mass Spectrometry

基质辅助激光解吸电离飞行时间质谱



# MALDI-TOF MS 微生物鉴定流程



采集 2 - 20 kDa 范围内的信号，主要由核糖体蛋白  
(ribosomal proteins)产生，因此稳定且不受培养条  
件影响

# MALDI-TOF MS 技术与其他方法比较

方法	用时	成本(元/个)	操作复杂程度	通量
传统方法	表型鉴定法	7-14 天	200	操作复杂, 需专业人员 低
	rDNA 鉴定法	1-2 天	80	操作复杂, 需专业人员 低
	DNA-DNA 杂交法	1-2 天	1000	操作复杂, 需专业人员 5个/天
	脂肪酸组分分析法	1-2 小时	1000	需专业人员 10个/天
MALDI-TOF MS 技术	3-5分钟	4	操作简单, 自动化处理	400个/天

**优势：耗时短、成本低、通量高**

**劣势：仪器昂贵，依赖已知种标准菌株数据库**

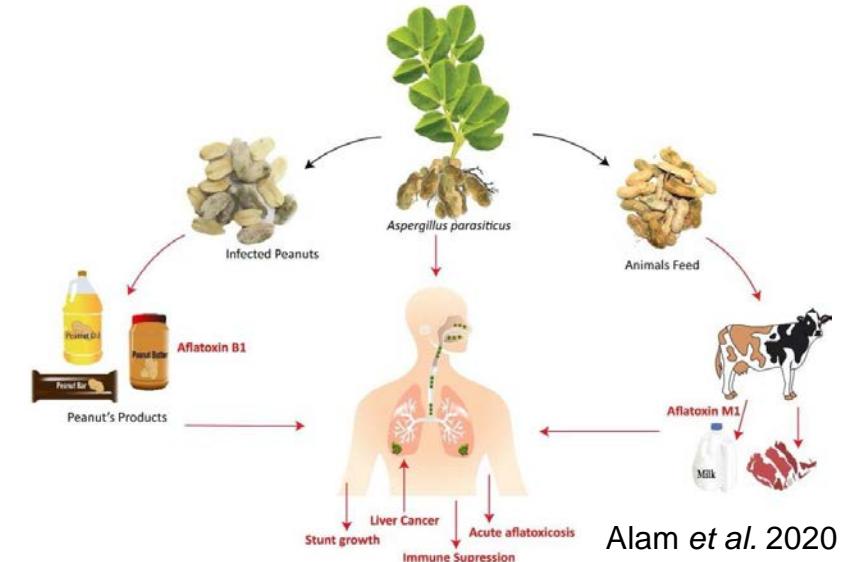
# 黄曲霉与米曲霉的分类学问题



# 黄曲霉与米曲霉：魔鬼与天使

## 黄曲霉 *Aspergillus flavus*

- 最臭名昭著的黄曲霉毒素产生真菌
- 人类高致死率曲霉病的常见病原菌



## 米曲霉 *Aspergillus oryzae*

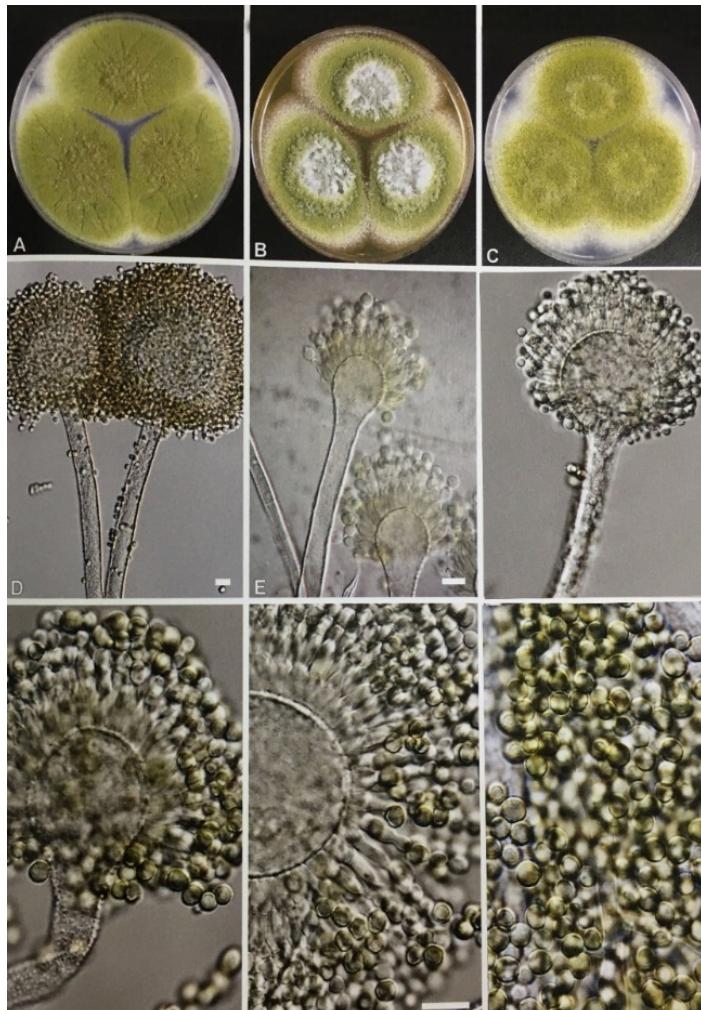
- 传统发酵食品 (>3000年历史)：
  - 中国：黄酒、酱油、醋、豆瓣酱、豆豉、白酒(大曲) 等
  - 日本：国菌 *Koji* (曲)，清酒、味增、酱油、醋等
- 美国FDA认定：Generally Recognized as Safe (GRAS)
- 研究工具和细胞工厂：高效外源基因表达、翻译后修饰、酶分泌系统，高效遗传操作系統



# 黃曲霉

***Aspergillus flavus***

Link, 1809



# 米曲霉

***Aspergillus oryzae***

(Ahlb.) Cohn, 1884



# *A. flavus*

DTO 258-C9

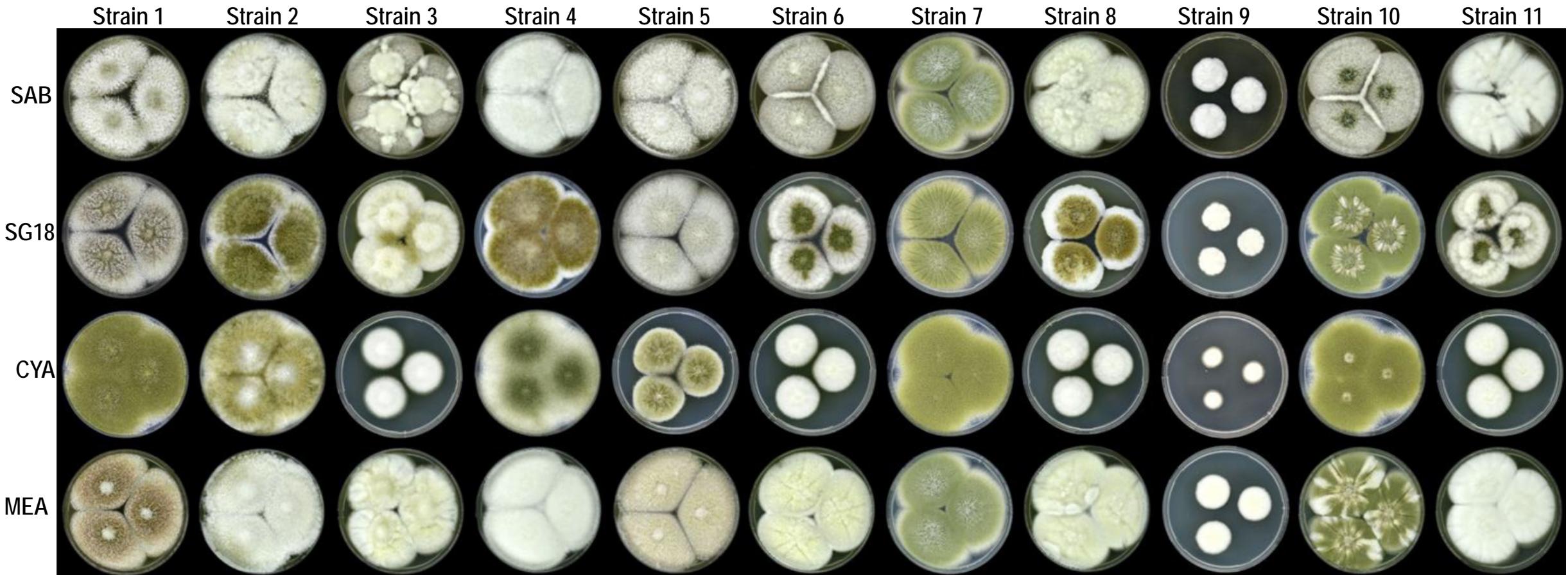
# *A. oryzae*

CBS 100925T

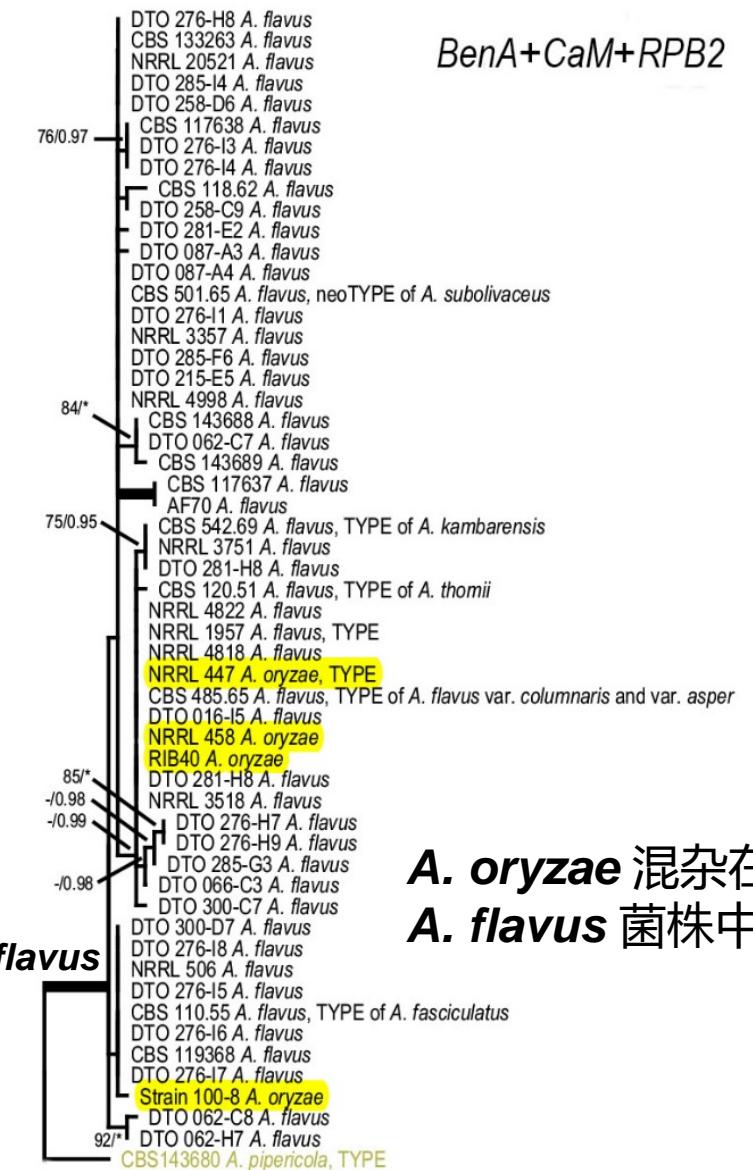
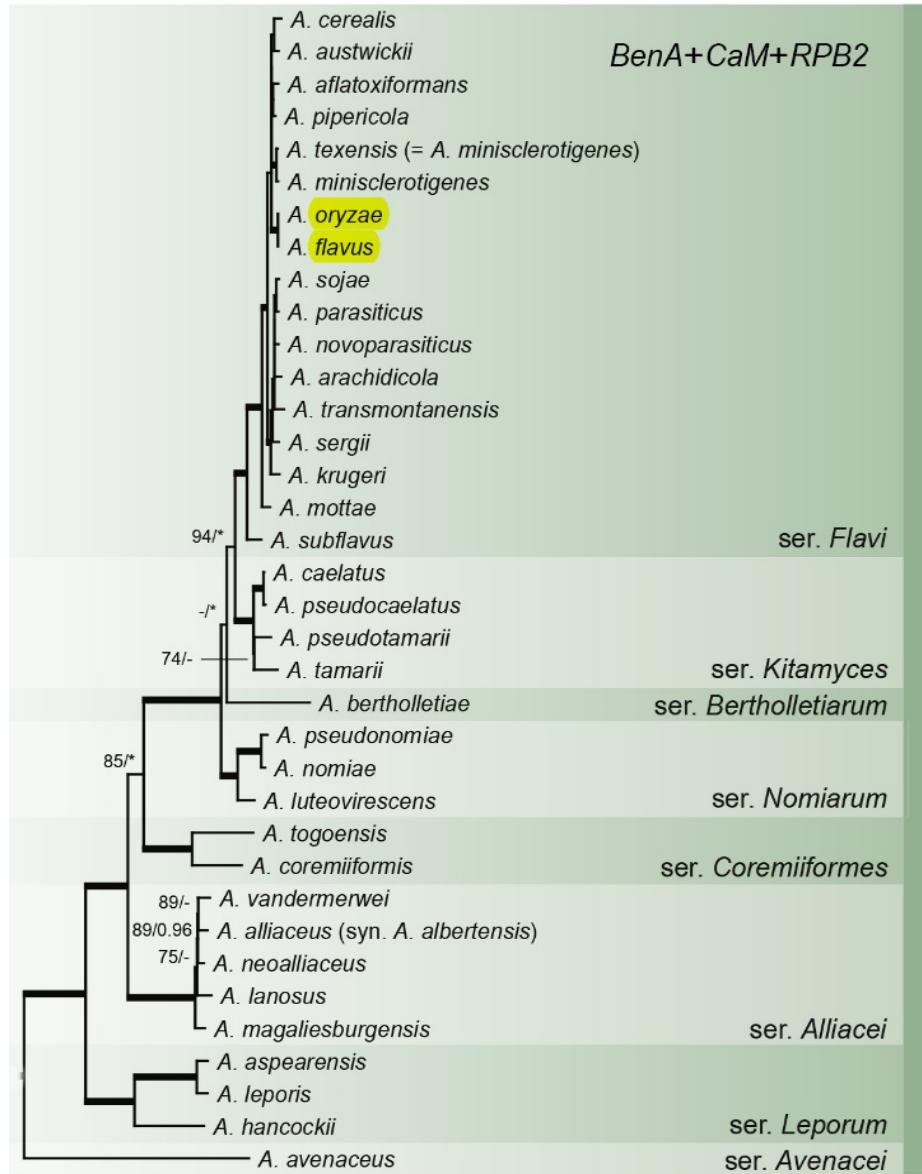
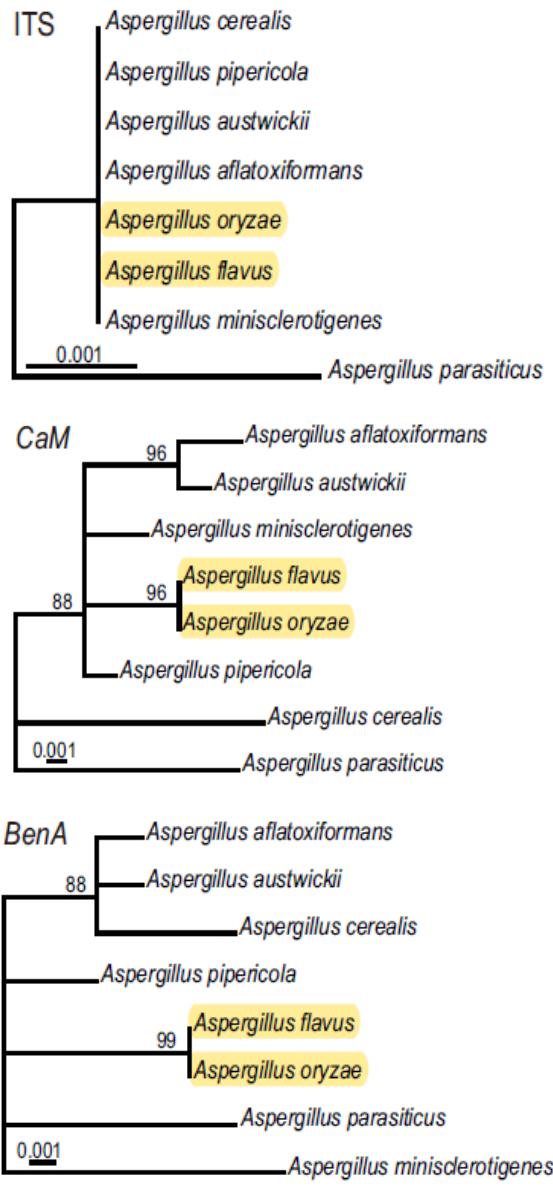


# 形态特征难以区分 *A. flavus* 和 *A. oryzae*

*A. flavus* 菌株具有高度形态多样性

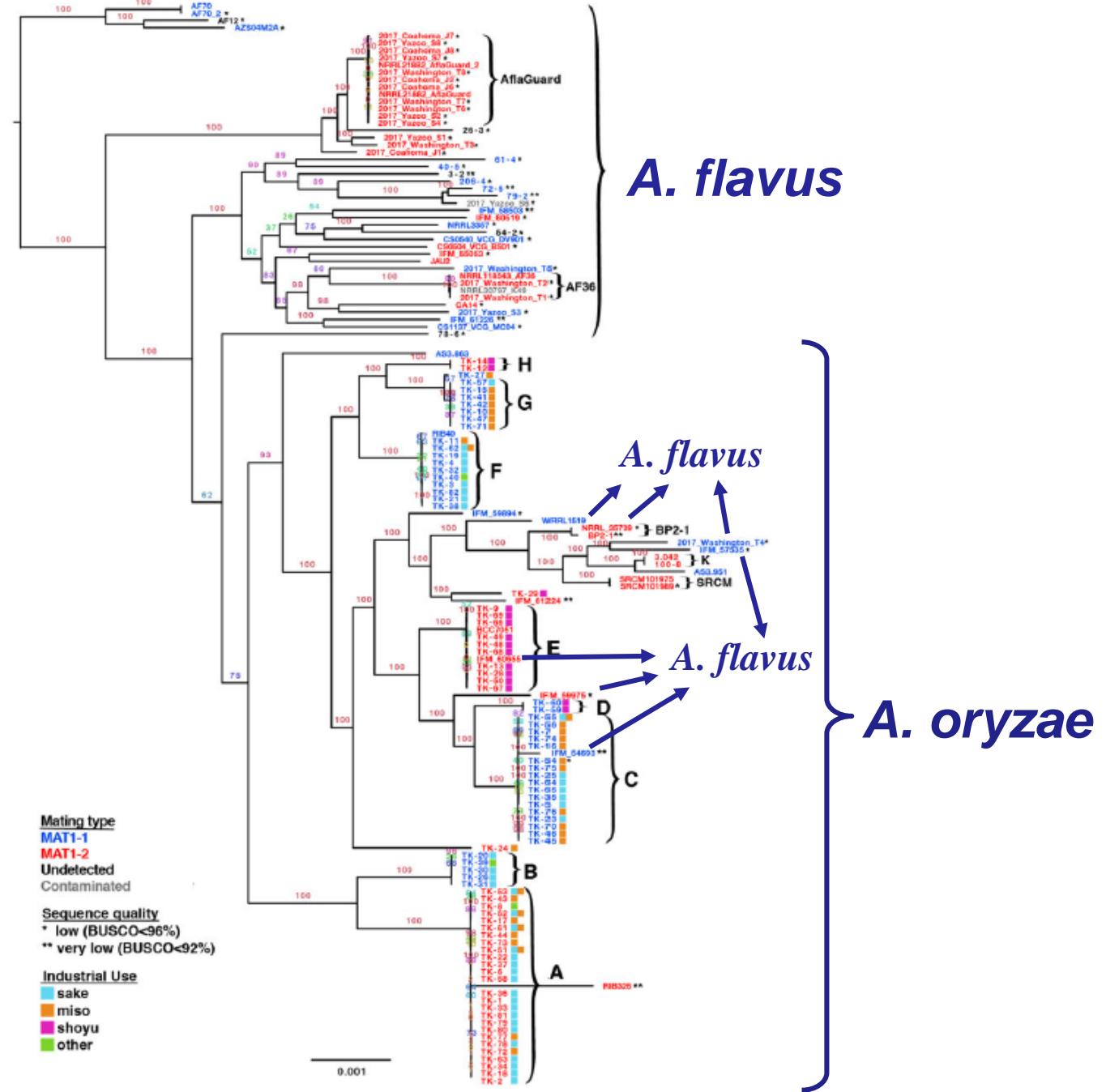


# 常用DNA条形码难以区分 *A. flavus* 和 *A. oryzae*



# *A. flavus*/*A. oryzae* 系统发育基因组分析

- 82株来自日本5个制曲企业的*A. oryzae* 形成一个单系分枝，支持其为*A. flavus* 驯养群体的观点
- 但一些原鉴定为*A. flavus*的菌株，聚在了*A. oryzae* 分枝内，这些菌株如何定名？



# *Aspergillus oryzae* 的定义

现代青曲霉分类系统承认 *A. oryzae*

附加条件：

① 来自发酵或工业环境，

② 不产毒素

(Frisvad *et al.* 2019, Houbraken *et al.* 2020)

争议：人为性，缺乏充分的科学依据



<http://www.indexfungorum.org>

**Index Fungorum**

**Record Details:**

[\*Aspergillus oryzae\* \(Ahlb.\) Cohn, Jber. schles. Ges. vaterl. Kultur](#) **61**: 227 (1884) [1883]

**Basionym:**

[\*Eurotium oryzae\* Ahlb.](#) 1878

**Citations in published lists or literature:**

Saccardo's Syll. fung. XI: 592; XII: 38; XIX: 121; XXII: 1257 [Page Image for Protologue](#)

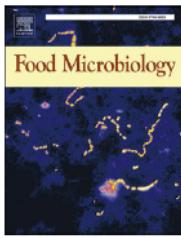
**Position in classification:**

Aspergillaceae, Eurotiales, Eurotiomycetidae, Eurotiomycetes, Pezizomycotina, Ascomycota, Fungi

**Species Fungorum current name:**

[\*Aspergillus flavus\* Link](#) 1809

认为 *A. oryzae* 是 *A. flavus* 的异名

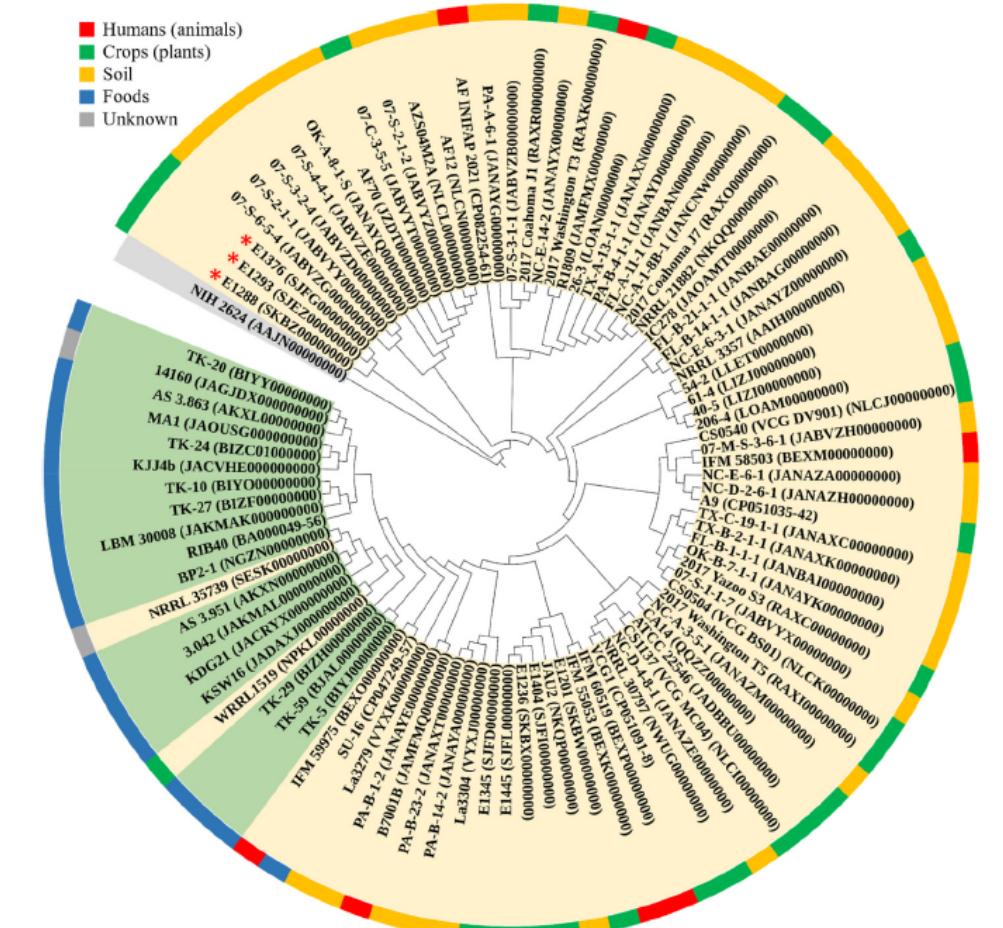


# Comparative pangenome analysis of *Aspergillus flavus* and *Aspergillus oryzae* reveals their phylogenetic, genomic, and metabolic homogeneity

Dong Min Han, Ju Hye Baek, Dae Gyu Choi, Min-Seung Jeon, Seong-il Eyun, Che Ok Jeon \*

*Department of Life Science, Chung-Ang University, Seoul 06974, Republic of Korea*

“Collectively, these findings challenge the conventional differentiation of *A. flavus* and *A. oryzae* as distinct species and highlight their phylogenetic, genomic, and metabolic homogeneity, potentially indicating that they may indeed belong to the same species.”



# 真菌命名法规的最新变化

以前复型真菌的双重或多重命名现象

- ◆ **Holomorph** 全型
- ◆ **Teleomorph** 有性型
- ◆ **Anamorph** 无性型
- ◆ **Synanamorph** 共无性型
- ◆ **Ana-holomorph** 无性全型

# 无性型-有性型 Anamorph-Teleomorph Connections

无性型 Anamorph	有性型 Teleomorph
<i>Candida guilliermondii</i>	<i>Pichia guilliermondii</i> <i>Meyerozyma guilliermondii</i>
<i>Candida krusei</i>	<i>Issatchenka orientalis</i> <i>Pichia kudriavzevii</i>
<i>Candida lusitaniae</i>	<i>Clavispora lusitaniae</i>
<i>Cryptococcus neoformans</i>	<i>Filobasidiella neoformans</i>
<i>Cryptococcus gattii</i>	<i>Filobasidiella bacillispora</i>

同一行内种名虽不一样，却属于同一个种

真菌这种特殊的双重命名系统给非分类学领域在真菌种名的应用或判断方面带来困难、误解或混乱

表 3-2 葡萄酒相关酵母菌的 ATB ID 32C 自动化系统鉴定结果

Table 3-2 Morphological characteristics of yeast strains present on wine grapes

形态类群	ATB ID 32C 鉴定结果	相似率 (%)	分子生物学鉴定结果
M1	酿酒酵母 <i>Saccharomyces cerevisiae</i>	99.9	酿酒酵母 <i>Saccharomyces cerevisiae</i>
M2	日本克勒克酵母 <i>Koekera japonica</i>	92.7	葡萄有孢汉逊酵母 <i>Hanseniaspora uvarum</i>
M3	铁红假丝酵母 <i>Candida pulcherrima</i>	99.8	美极梅奇酵母 <i>Metschnikowia pulcherrima</i>
M4	圆球形假丝酵母 <i>Candida sphaerica</i>	99.4	发酵接合酵母 <i>Zygasaccharomyces fermentati</i>
M5	罗伦隐球酵母 <i>Cryptococcus laurentii</i>	99.9	浅黄隐球酵母 <i>Cryptococcus flavescens</i>
M6	克柔假丝酵母 <i>Candida krusei</i>	98.3	发酵毕赤酵母 <i>Pichia fermentans</i>
M7	浅白隐球酵母 <i>Cryptococcus albidus</i>	98.7	橡树假丝酵母 <i>Candida quercitrusa</i>
M8	霍尔姆假丝酵母 <i>Candida holmii</i>	84.3	<i>Candida zemplinina</i>
M9	粗状假丝酵母 <i>Candida valida</i>	66.3	挪威毕赤酵母 <i>Pichia norvegensis</i>
M10	浅白隐球酵母 <i>Cryptococcus albidus</i>	99.9	浅白隐球酵母 <i>Cryptococcus albidus</i>
M12	克柔假丝酵母 <i>Candida krusei</i>	97.9	东方伊萨酵母 <i>Issatchenka orientalis</i>
M16	木兰假丝酵母 <i>Candida magnoliae</i>	96.7	熊蜂假丝酵母 <i>Candida bombi</i>

- 红筐里两对种名不一致，所以作者认为是不同的种
- 实际上它们是同一种的无性型和有性型名称

## The Amsterdam Declaration on Fungal Nomenclature

David L. Hawksworth<sup>1</sup>, Pedro W. Crous<sup>2</sup>, Scott A. Redhead<sup>3</sup>, Don R. Reynolds<sup>4</sup>, Robert A. Samson<sup>2</sup>, Keith A. Seifert<sup>3</sup>, John W. Taylor<sup>5</sup>, Michael J. Wingfield<sup>6</sup> \*, Özlem Abaci<sup>7</sup>, Catherine Aime<sup>8</sup>, Ahmet Asan<sup>9</sup>, Feng-Yan Bai<sup>10</sup>, Z. Wilhelm de Beer<sup>6</sup>, Dominik Begerow<sup>11</sup>, Derya Berikten<sup>12</sup>, Teun Boekhout<sup>2</sup>, Peter K. Buchanan<sup>13</sup>, Treena Burgess<sup>14</sup>, Walter Buzina<sup>15</sup>, Lei Cai<sup>16</sup>, Paul F. Cannon<sup>17</sup>, J. Leland Crane<sup>38</sup>, Ulrike Damm<sup>2</sup>, Heide-Marie Daniel<sup>18</sup>, Anne D. van Diepeningen<sup>2</sup>, Irina Druzhinina<sup>19</sup>, Paul S. Dyer<sup>20</sup>, Ursula Eberhardt<sup>2</sup>, Jack W. Fell<sup>21</sup>, Jens C. Frisvad<sup>22</sup>, David M. Geiser<sup>23</sup>, József Geml<sup>24</sup>, Chirlei Glienke<sup>25</sup>, Tom Gräfenhan<sup>26</sup>, Johannes Z. Groenewald<sup>2</sup>, Marizeth Groenewald<sup>2</sup>, Johannes de Gruyter<sup>27</sup>, Eveline Guého-Kellermann<sup>28</sup>, Liang-Dong Guo<sup>10</sup>, David S. Hibbett<sup>29</sup>, Seung-Beom Hong<sup>30</sup>, G. Sybren de Hoog<sup>2</sup>, Jos Houbraken<sup>2</sup>, Sabine M. Huhndorf<sup>31</sup>, Kevin D. Hyde<sup>32</sup>, Ahmed Ismail<sup>2</sup>, Peter R. Johnston<sup>13</sup>, Duygu G. Kadaifciler<sup>33</sup>, Paul M. Kirk<sup>34</sup>, Urmas Kõljalg<sup>35</sup>, Cletus P. Kurtzman<sup>36</sup>, Paul-Emile Lagneau<sup>37</sup>, C. André Lévesque<sup>3</sup>, Xingzhong Liu<sup>10</sup>, Lorenzo Lombard<sup>2</sup>, Wieland Meyer<sup>38</sup>, Andrew Miller<sup>39</sup>, David W. Minter<sup>40</sup>, Mohammad Javad Najafzadeh<sup>41</sup>, Lorelei Norvell<sup>42</sup>, Svetlana M. Ozerskaya<sup>43</sup>, Rasime Öziç<sup>44</sup>, Shaun R. Pennycook<sup>13</sup>, Stephen W. Peterson<sup>36</sup>, Olga V. Pettersson<sup>45</sup>, William Quaedvlieg<sup>2</sup>, Vincent A. Robert<sup>2</sup>, Constantino Ruibal<sup>1</sup>, Johan Schnürer<sup>45</sup>, Hans-Josef Schroers<sup>46</sup>, Roger Shivas<sup>47</sup>, Bernard Slippers<sup>6</sup>, Henk Spierenburg<sup>2</sup>, Masako Takashima<sup>48</sup>, Evrim Taşkın<sup>49</sup>, Marco Thines<sup>50</sup>, Ulf Thrane<sup>22</sup>, Alev Haliki Uztan<sup>51</sup>, Marcel van Raak<sup>27</sup>, János Varga<sup>52</sup>, Aida Vasco<sup>53</sup>, Gerard Verkley<sup>2</sup>, Sandra I.R. Videira<sup>2</sup>, Ronald P. de Vries<sup>2</sup>, Bevan S. Weir<sup>13</sup>, Neriman Yilmaz<sup>2</sup>, Andrey Yurkov<sup>54</sup>, and Ning Zhang<sup>55</sup>

88 位署名者  
4 位来自国内



# MYCOTAXON

Volume 116, pp. 501–512

April–June 2011

DOI: 10.5248/116.501

## Fungal nomenclature 3. A critical response to the 'Amsterdam Declaration'

WALTER GAMS\*, WALTER JAKLITSCH  
& 77 SIGNATORIES\*

- 共 79 位属名者
- 中国 8 位：
  - 其中大陆 2 位, 台湾 6 位



Secretary of the Special  
Committee for Fungi, ICBN  
Chairperson of the MSA  
Nomenclature Committee



# 涉及真菌的命名法规 关键修订

澳大利亚 墨尔本, 2011. 7. 23-30

- ◆ **The title of the Code will be changed**
  - New title: the International Code of Nomenclature for algae, fungi, and plants (ICN)
- ◆ **Electronic publication of new names will be permitted**
  - Publication online in PDF in a electronic publication with an ISSN or ISBN is permitted on or after 1 January 2012.
- ◆ **Latin descriptions no longer required**
  - Either a Latin **or an English** description or diagnosis on or after 1 January 2012 is required
- ◆ **One fungus, one name**
  - Article 59 will be changed, so that different names applying to asexual and sexual morphs of the same fungus compete for priority in the same manner.
    - An additional new set of rules will allow lists of widely used names to be protected.
- ◆ **Registration of fungal names will be required**
  - Publication of a new fungal name must include a citation of “an identifier issued by a recognized repository”, at present the MycoBank number, in order to be validly published

# 因命名法规改变引起的种名改变问题

- ◆ 1F = 1N 新规则的实施将引起大量种名的变动
- ◆ 虽然常用名称将尽量被保留，但因属的重新划分而引起的名称变动将难以避免
  - ◆ 种名 = 属名 (*Candida*) + 种加词 (*albicans*)
  - ◆ Species name = Genus name + Specific epithet

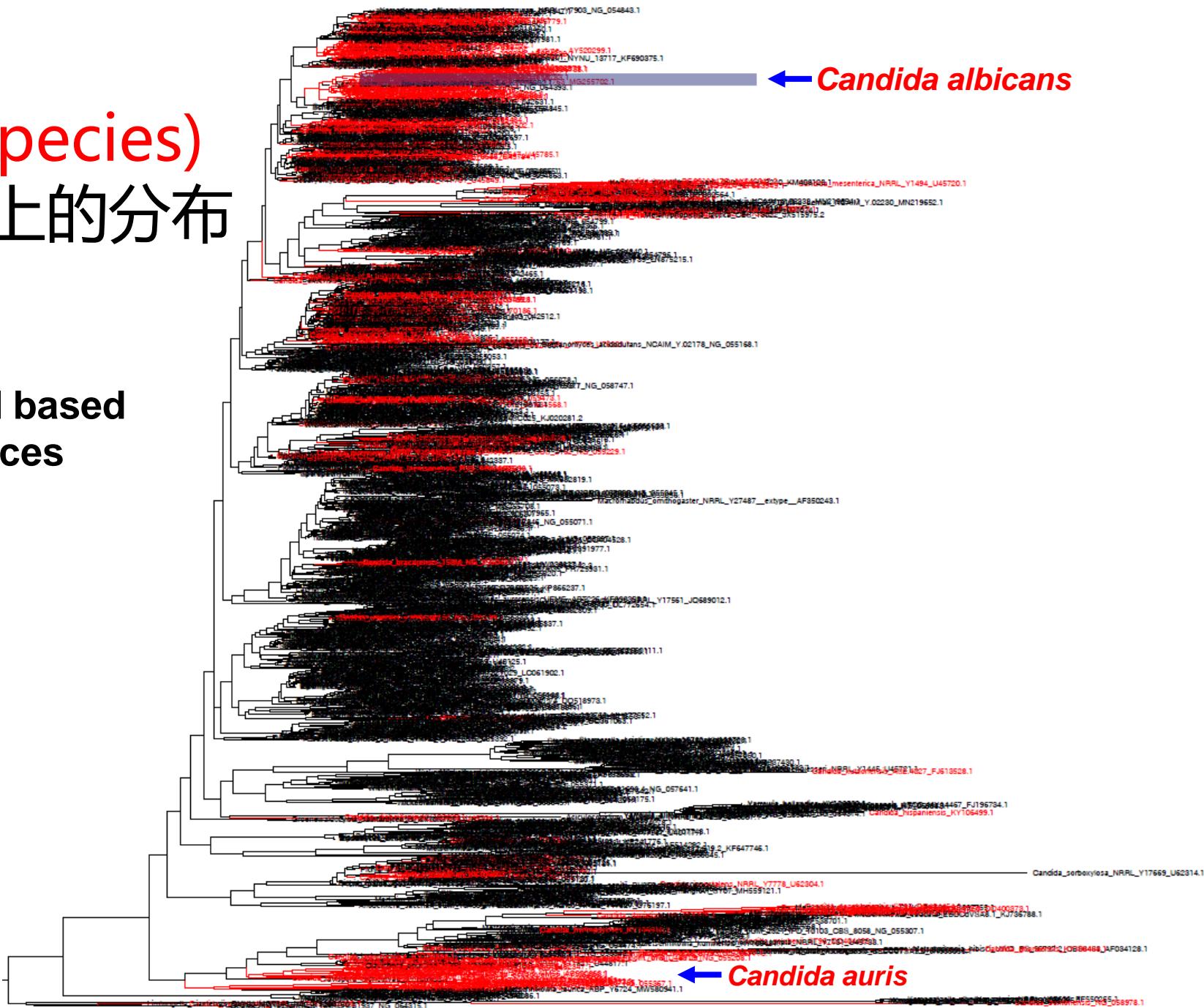
# The heterogeneous nature of *Candida*

Saccharomycetales	<i>Candida</i> spp.
1 Ascoideaceae	
2 Cephaloascaceae	
3 Debaryomycetaceae	
4 Dipodascaceae	
5 Endomycetaceae	
6 Lipomycetaceae	
7 Metschnikowiaceae	
8 Phaffomycetaceae	
9 Pichiaceae	
10 Saccharomycetaceae	
11 Saccharomycodaceae	
12 Saccharomycopsidaceae	
13 Trichomonascaceae	
14 Wickerhamomycetaceae	
	<i>incertae sedis</i>

- >400 *Candida* species scatter in ~15 clades covering at least 9 families of the Saccharomycetales
- In medical mycology, *Candida* is the synonym of pathogenic yeast
- Only ~20 *Candida* species are opportunistic pathogens
- Many other *Candida* species are of industrial significance; but a name bearing *Candida* may be a obstacle for the application and commercialization of the products of the species
- Reclassification of *Candida* would be welcome from applied fields

# 念珠菌种(*Candida* species) 在子囊菌酵母系统树上的分布

# **Phylogenetic tree constructed based on LSU D1/D2 domain sequences**



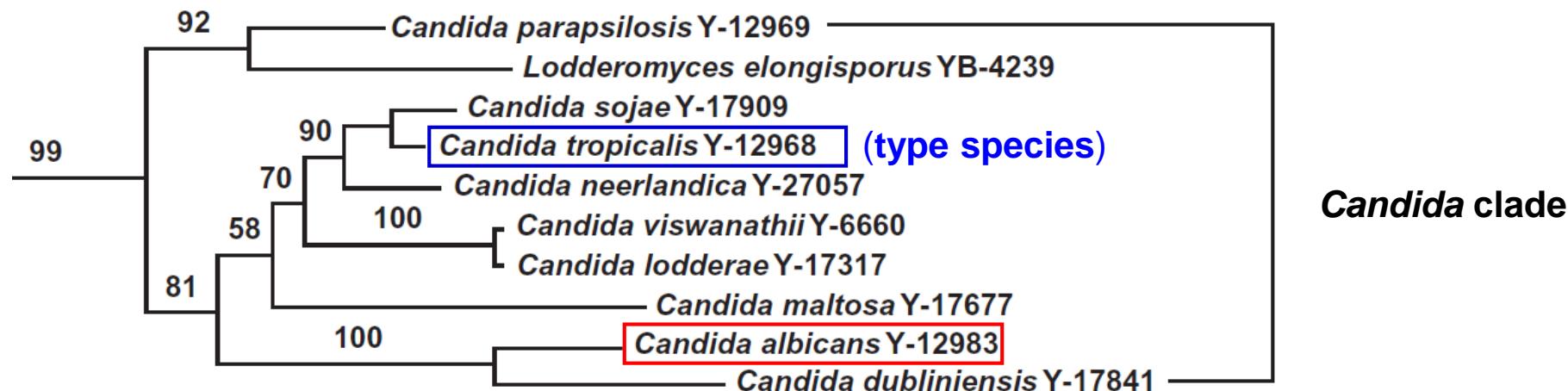
# *Candida* (念珠菌屬):

the most polyphyletic genus of ascomycetous yeasts

434 species in 15 clades covering >10 families.

*Candida* clade: 30 *Candida* species.

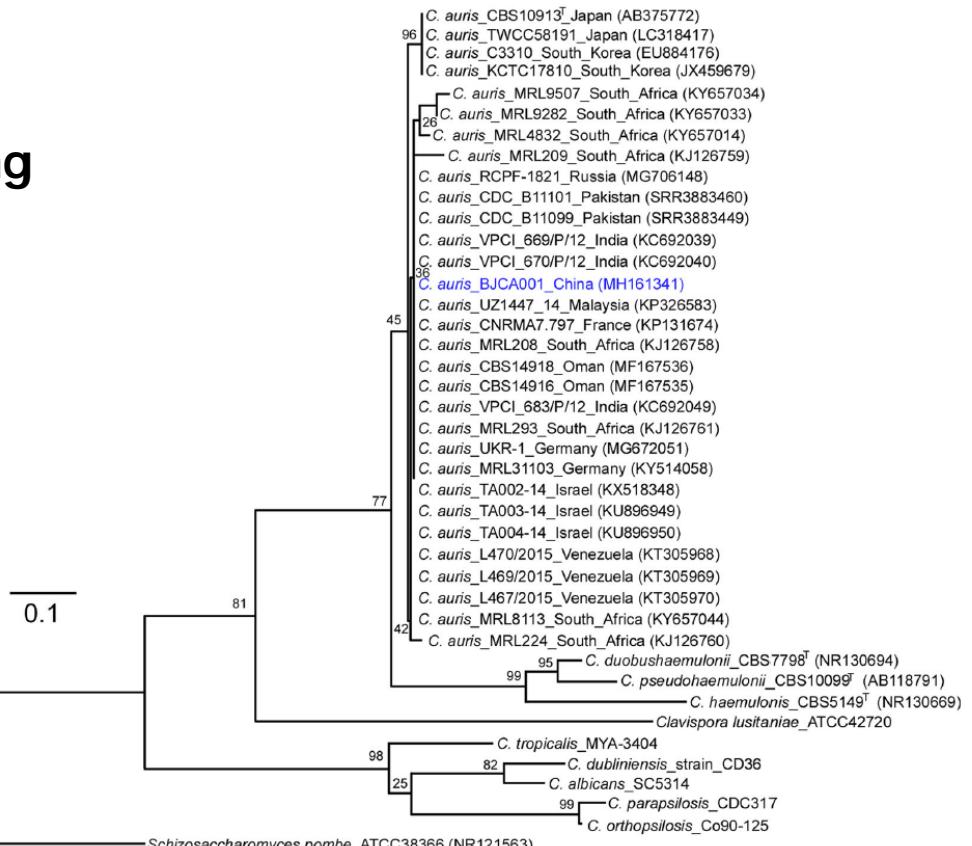
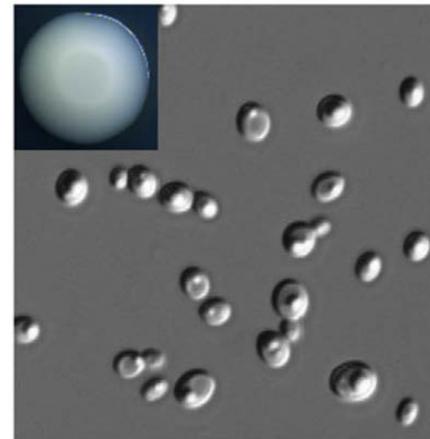
The other 400+ *Candida* species must be re-named.



(Also see Daniel et al., 2014, Antonie van Leeuwenhoek 106:67–84)

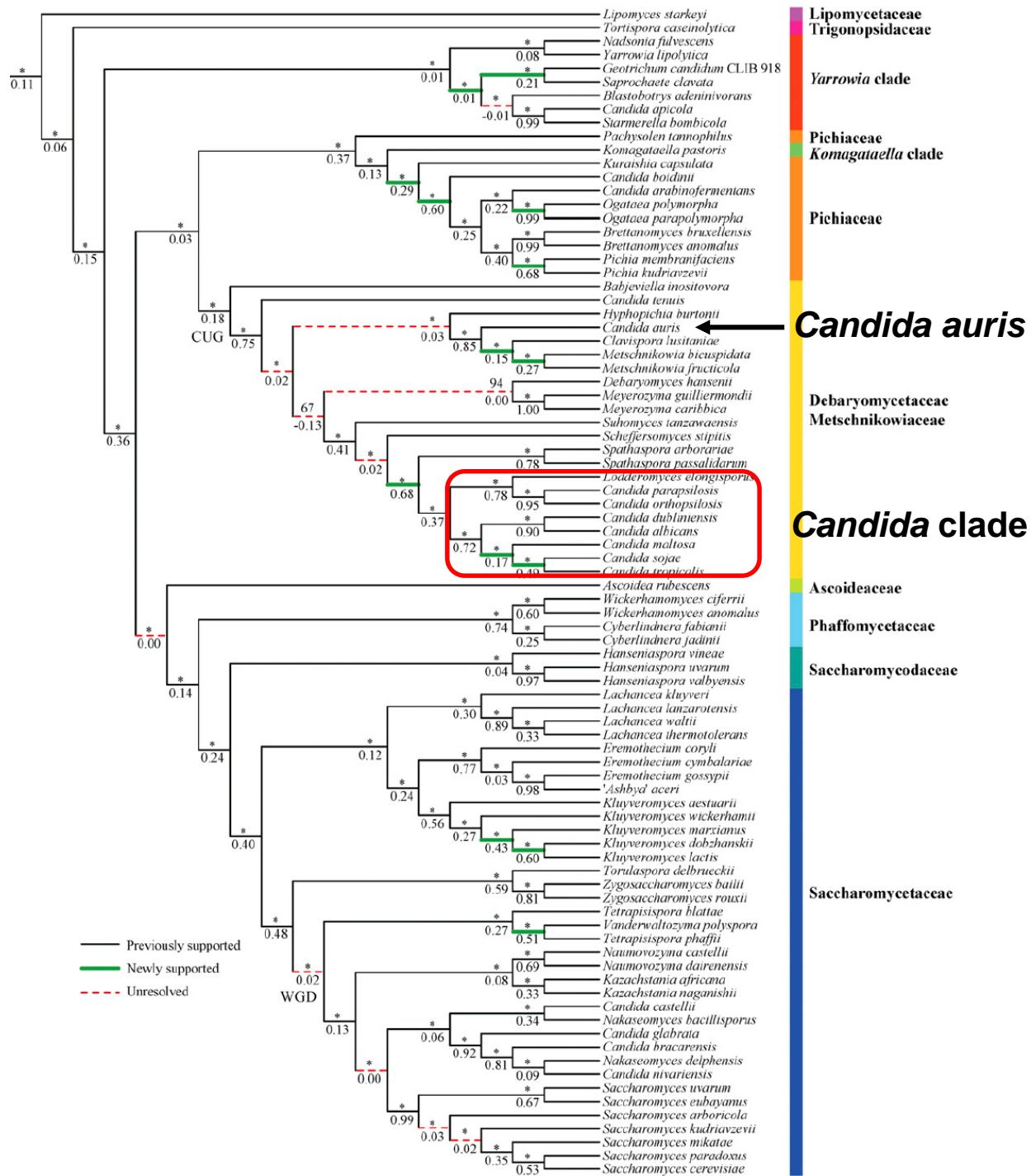
# 耳念珠菌 *Candida auris*

- First described from a patient in Japan in 2009 (Satoh et al., 2009)
- Resistance to FLU and variable susceptibility to other azoles, AMB, and echinocandins
- Emerging as a global nosocomial pathogen, causing healthcare-associated invasive infections
- Reported in 27+ countries on five continents, including China
- Often misidentified as *C. haemulonii* and *Rhodotorula glutinis* by VITEK and API-20C AUX, respectively
- Robust identification methods:
  - 26S rDNA D1/D2 or ITS sequencing
  - MALDI-TOF MS
- Phylogenetically not belonging to the *Candida* clade, implying its name will inevitable be changed



# Backbone of the Saccharomycotina Yeast Phylogeny Based on Genome-Scale Data

(Shen et al., 2016)

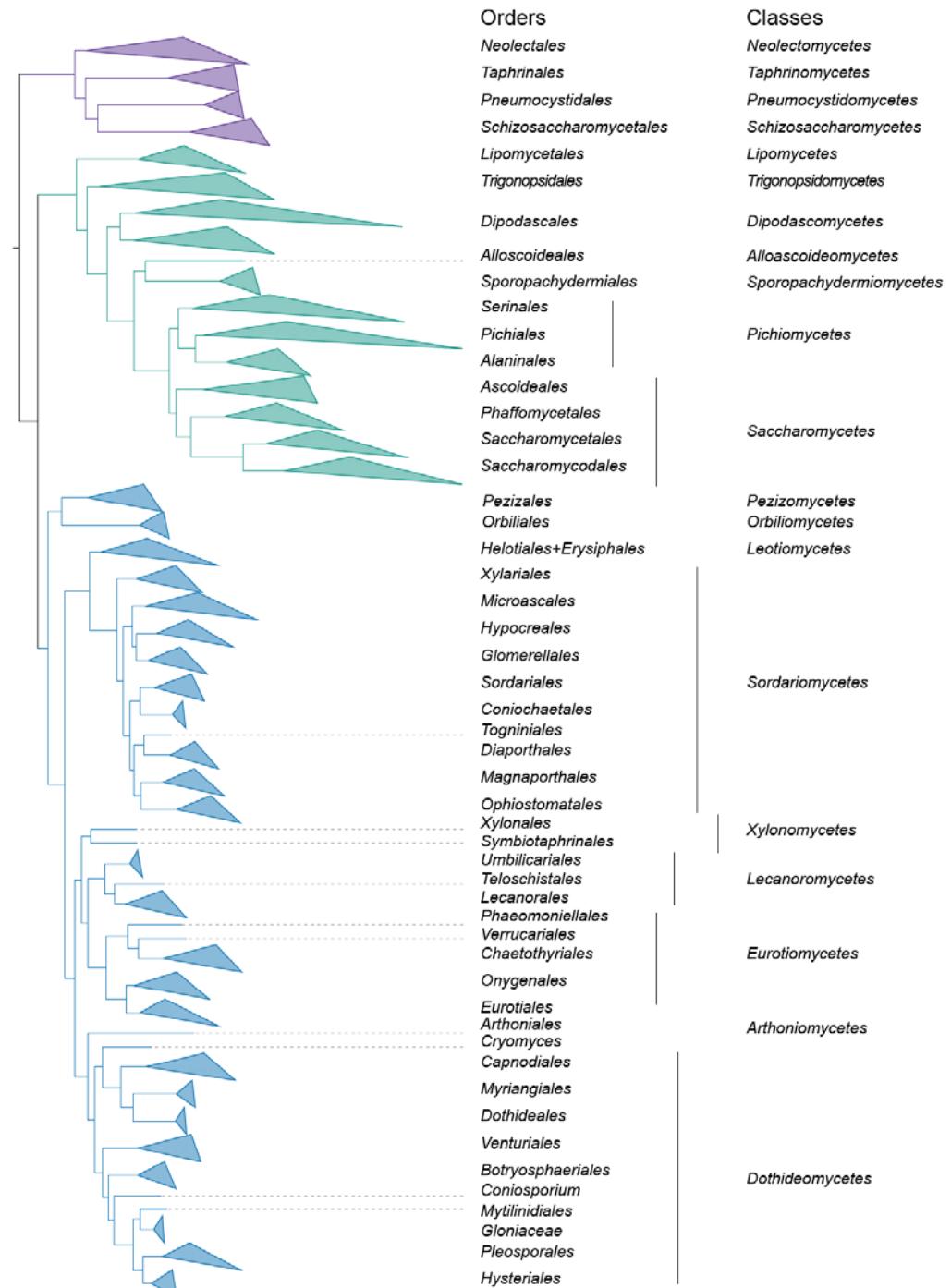


## A genome-informed higher rank classification of the biotechnologically important fungal subphylum *Saccharomycotina*

M. Groenewald<sup>1\*</sup>, C.T. Hittinger<sup>2</sup>, K. Bensch<sup>1</sup>, D.A. Opulente<sup>2,3</sup>, X.-X. Shen<sup>4</sup>, Y. Li<sup>5</sup>, C. Liu<sup>4</sup>, A.L. LaBella<sup>6</sup>, X. Zhou<sup>7</sup>, S. Limtong<sup>8</sup>, S. Jindamorakot<sup>9</sup>, P. Gonçalves<sup>10,11</sup>, V. Robert<sup>1</sup>, K.H. Wolfe<sup>12</sup>, C.A. Rosa<sup>13</sup>, T. Boekhout<sup>14</sup>, N. Čadež<sup>15</sup>, G. Péter<sup>16</sup>, J.P. Sampaio<sup>17</sup>, M.-A. Lachance<sup>18</sup>, A.M. Yurkov<sup>19</sup>, H.-M. Daniel<sup>20</sup>, M. Takashima<sup>21</sup>, K. Boundy-Mills<sup>22</sup>, D. Libkind<sup>23</sup>, K. Aoki<sup>21</sup>, T. Sugita<sup>24</sup>, A. Rokas<sup>25</sup>

**The *Saccharomycotina* consist of more than 1 200 known species which were previously divided into 1 class and 1 order.**

**Using genome-scale phylogenetic analyses analyses in combination with relative evolutionary divergence and genome content analyses, an updated classification for the *Saccharomycotina*, including 7 classes and 12 orders is proposed.**





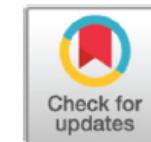
## Brewers lost in wild yeast nomenclature

(酿造者迷失在野生酵母的命名里)

Lucie Kyselová, Katarína Hanzalíková, Dagmar Matoušková, Petra Kubizniaková\*

Research Institute of Brewing and Malting, Lípová 511/15,  
120 00 Prague, Czech Republic

corresponding author: [kubizniakova@beerresearch.cz](mailto:kubizniakova@beerresearch.cz)



8 | Human Microbiome | Commentary

# A conceptual framework for nomenclatural stability and validity of medically important fungi: a proposed global consensus guideline for fungal name changes supported by ABP, ASM, CLSI, ECMM, ESCMID-EFISG, EUCAST-AFST, FDLC, IDSA, ISHAM, MMSA, and MSGERC

Sybren de Hoog,<sup>1,2,3,4,5,6</sup> Thomas J. Walsh,<sup>6,7,8,9,10,11,12,13,14,15</sup> Sarah A. Ahmed,<sup>1,2,6</sup> Ana Alastruey-Izquierdo,<sup>6,16,17</sup> Barbara D. Alexander,<sup>10,18</sup> Maiken Cavling Arendrup,<sup>19,20</sup> Esther Babady,<sup>10,21</sup> Feng-Yan Bai,<sup>22,23,24,25,26,27</sup> Joan-Miquel Balada-Llasat,<sup>10,28</sup> Andrew Borman,<sup>29</sup> Anuradha Chowdhary,<sup>17,30</sup> Andrew Clark,<sup>10,31</sup> Robert C. Colgrove,<sup>32,33</sup> Oliver A. Cornely,<sup>12,17,34,35</sup> Tanis C. Dingle,<sup>10,13,36</sup> Philippe J. Dufresne,<sup>10,13,37</sup> Jeff Fuller,<sup>10,38</sup> Jean-Pierre Gangneux,<sup>12,39</sup> Connie Gibas,<sup>40</sup> Heather Glasgow,<sup>10,41</sup> Yvonne Gräser,<sup>42</sup> Jacques Guillot,<sup>26,43</sup> Andreas H. Groll,<sup>17,44</sup> Gerhard Haase,<sup>45</sup> Kimberly Hanson,<sup>10,46</sup> Amanda Harrington,<sup>10,47</sup> David L. Hawksworth,<sup>48,49,50,51,52,53</sup> Randall T. Hayden,<sup>10,13,41</sup> Martin Hoenigl,<sup>11,12,54,55,56</sup> Vit Hubka,<sup>57</sup> Kristie Johnson,<sup>10,58</sup> Julianne V. Kus,<sup>10,59,60</sup> Ruoyu Li,<sup>3,5,15,17,20,24</sup> Jacques F. Meis,<sup>1,15,34,35</sup> Michaela Lackner,<sup>6,61</sup> Fanny Lanternier,<sup>62</sup> Sixto M. Leal Jr.,<sup>10,11,13,63</sup> Francesca Lee,<sup>10,31</sup> Shawn R. Lockhart,<sup>10,64</sup> Paul Luethy,<sup>10,58</sup> Isabella Martin,<sup>10,65</sup> Kyung J. Kwon-Chung,<sup>66</sup> Wieland Meyer,<sup>9,67</sup> M. Hong Nguyen,<sup>10,11,14,68</sup> Luis Ostrosky-Zeichner,<sup>11,69</sup> Elizabeth Palavecino,<sup>10,70</sup> Preeti Pancholi,<sup>10,28</sup> Peter G. Pappas,<sup>11,63</sup> Gary W. Procop,<sup>10,13,71,72</sup> Scott A. Redhead,<sup>9,73</sup> Daniel D. Rhoads,<sup>74,75,76</sup> Stefan Riedel,<sup>10,77</sup> Bryan Stevens,<sup>10,68</sup> Kaede Ota Sullivan,<sup>10,78</sup> Paschalis Vergidis,<sup>10,79</sup> Emmanuel Roilides,<sup>6,12,17,80</sup> Amir Seyedmousavi,<sup>10,17,26,81</sup> Lili Tao,<sup>10,82</sup> Vania A. Vicente,<sup>4</sup> Roxana G. Vitale,<sup>83,84</sup> Qi-Ming Wang,<sup>85</sup> Nancy L. Wengenack,<sup>10,79</sup> Lars Westblade,<sup>10,86</sup> Nathan Wiederhold,<sup>10,11,13,14,40</sup> Lewis White,<sup>87</sup> Christina M. Wojewoda,<sup>88</sup> Sean X. Zhang<sup>6,10,89</sup>

# Recommended names of partial pathogenic yeasts for clinical use

Classical name	Alternative name	Recommended name
<i>Candida albicans</i>		<i>Candida albicans</i>
<i>Candida auris</i>		<i>Candida auris</i>
<i>Candida glabrata</i>	<i>Torulopsis glabrata</i> , <i>Nakaseomyces glabratus</i>	<i>Candida glabrata</i> or <i>Nakaseomyces glabratus</i>
<i>Candida guilliermondii</i>	<i>Pichia guilliermondii</i> , <i>Meyerozyma guilliermondii</i>	<i>Candida guilliermondii</i> or <i>Meyerozyma guilliermondii</i>
<i>Candida haemulonis</i> (?)	<i>Torulopsis haemulonis</i> , <i>Candida haemuloni</i> , <i>Candida haemuli</i>	<i>Candida haemuli</i> (member of <i>C. haemuli</i> complex)
<i>Candida krusei</i>	<i>Issatchenkia orientalis</i> , <i>Pichia kudriavzevii</i>	<i>Candida krusei</i> or <i>Pichia kudriavzevii</i>
<i>Candida lusitaniae</i>	<i>Clavispora lusitaniae</i>	<i>Candida lusitaniae</i> or <i>Clavispora lusitaniae</i>
<i>Candida parapsilosis</i>		<i>Candida parapsilosis</i>
<i>Candida rugosa</i>	<i>Diutina rugosa</i>	<i>Candida rugosa</i> or <i>Diutina rugosa</i>
<i>Candida tropicalis</i>		<i>Candida tropicalis</i>
<i>Cryptococcus gattii</i>		<i>Cryptococcus gattii</i>
<i>Cryptococcus neoformans</i>		<i>Cryptococcus neoformans</i>
<i>Trichosporon asahii</i>		<i>Trichosporon asahii</i>
<i>Trichosporon dermatis</i>	<i>Cutaneotrichosporon dermatis</i>	<i>Trichosporon dermatis</i> or <i>Cutaneotrichosporon dermatis</i>

**Response to “A conceptual framework for nomenclatural stability and validity of  
medically important fungi: a proposed global consensus guideline for fungal name  
changes supported by ABP, ASM, CLSI, ECMM, ESCMID-EFISG, EUCAST-AFST, FDLC, IDSA,  
ISHAM, MMSA, and MSGERC”**

Sarah E. Kidd,<sup>1,2</sup> Ferry Hagen,<sup>3,4,5</sup> Catriona L. Halliday,<sup>6</sup> Alireza Abdolrasouli,<sup>7,8</sup> Teun Boekhout,<sup>9</sup> Pedro W. Crous,<sup>3,10,11</sup> David H. Ellis,<sup>2</sup> Juliet Elvy,<sup>12</sup> Graeme N. Forrest,<sup>13</sup> Marizeth Groenewald,<sup>3</sup> Rosane C. Hahn,<sup>14,15</sup> Jos Houbraken<sup>3</sup>, Anderson M. Rodrigues,<sup>16</sup> James Scott,<sup>17,18</sup> Tania C. Sorrell,<sup>19</sup> Richard C. Summerbell,<sup>17,18</sup> Clement K.M. Tsui,<sup>20,21</sup> Andrey Yurkov,<sup>22</sup> Sharon C.-A. Chen<sup>6</sup>

## 1 Answer to Kidd et al.

2

3 We would like to thank Kidd et al. for their thoughtful comments on our manuscript about a proposed  
 4 global consensus guideline for fungal name changes published in the *Journal of Clinical Microbiology*. We  
 5 would also like to take this opportunity to further explain our position and clarify the intent of this work.  
 6 The proposed International Nomenclature Committee for Clinical Fungi neither wishes to impede name  
 7 changes, nor prescribe or arbitrate nomenclatural questions.

8 Our main goal is to achieve broad acceptance of changes that are beneficial to science and patient care.  
 9 We strongly believe that the best means to achieve this important objective is to involve the clinical user  
 10 part of the process, providing understanding of the reasons for the change, and how this could improve  
 11 clinical management. In particular, the needs of clinical laboratories, which are important stakeholder  
 12 dealing with the consequences of fungal name changes on a daily basis, have been largely neglected to  
 13 date. Early and collaborative involvement leads to faster acceptance, while sudden and unexplained  
 14 name changes, even when necessary, lead to reluctance and clinical risk. We acknowledge different  
 15 viewpoints toward fungal nomenclature and taxonomy. This underlines the proposal to form an open,  
 16 international nomenclatural Working Group / Committee for clinical fungi which will provide the clinical  
 17 user with the rationale for name changes and their relevance to patient care.

18 The nomenclatural database is made with the same intention. Existing databases such as MycoBank,  
 19 Species Fungorum, and Index Fungorum cover the entire fungal Kingdom, and follow the latest  
 20 taxonomic literature. The clinical database was founded to bring taxonomy closer to clinical needs, which  
 21 may occasionally deviate from existing databases. An illustrative example is *Trichophyton indotinea* (1).  
 22 From a strictly phylogenetic perspective, this is a member of the *Trichophyton mentagrophytes* complex.  
 23 Complexes, as used in clinical routine practice, are composed of sibling lineages with identical biology,  
 24 having epidemiological rather than clinical significance. *Trichophyton indotinea*, although just a few  
 25 barcode SNPs remote from other *Trichophyton mentagrophytes* lineages, is clinically different due to its  
 26 high virulence and a high degree of antifungal resistance, and is phenotypically often urease negative. It  
 27 is therefore recommended to be identified as an individual species. This certainly is a dilemma, and the  
 28 decision of Tang et al. (2022) may be debatable; we are open to anyone's opinion.

29 We respectfully disagree with the statement from Kidd et al that includes "continue using prior (now  
 30 obsolete) *Candida* names". These new names, while may be valid, do not make old names obsolete,  
 31 particularly within a clinical context where antifungal susceptibility testing and treatment guidelines  
 32 maintain the continuity of patient care. Another misunderstanding concerns the statement about  
 33 "recommending two names is against established One Fungus One Name rule". The "one fungus one  
 34 name" concept addresses unification of the anamorph and teleomorph phase of a fungus. Our proposal  
 35 of reporting both old and new names (irrespective of life phase) will simply enable the smooth transition  
 36 and connection of knowledge affiliated with the old and new names. Furthermore, the statement about  
 37 "affiliation with the International Mycological Association Nomenclature Committee for Fungi" is not  
 38 accurate. The Nomenclature Committee for Fungi is not part of the International Mycology Associations  
 39 (IMA).

40 Our proposed global consensus guideline for fungal name changes is endorsed by 11 professional  
 41 societies that are involved in medical mycology, laboratory diagnosis, and fungal diseases. The

42 endorsement was achieved through a rigorous review process by representatives from each society. The  
 43 upcoming International Nomenclature Committee for Clinical Fungi ([https://www.isham.org/working-](https://www.isham.org/working-groups/nomenclature-clinical-fungi)  
 44 groups/nomenclature-clinical-fungi)

45 includes taxonomists, medical mycologists, clinical microbiologists,  
 46 infectious disease physicians, pharmacists, pathologists, and veterinary mycologists, representing 18  
 47 professional societies as well as industry partners who provide fungal databases for identification  
 48 through their commercial platforms. Therefore, this committee is thus far the most internationally  
 49 inclusive committee that represents global efforts to address name changes in clinical fungi. In fact, we  
 50 note that several lead authors from the letter from Kidd et al. are already members of this committee,  
 51 and thus we anticipate that the different viewpoints on fungal nomenclature and taxonomy will be  
 52 robustly discussed within the committee. Moreover, development of evidence-based multifactorial  
 53 criteria to guide the discussion and determination of fungal name changes for clinical usage is in process  
 54 and will be reviewed and commented by all committee members.

55 In summary, we hope that the different disciplines involved in medical mycology will come together in an  
 56 atmosphere of open discussion. We remain aware that any recommendation made by the committee  
 57 will continue to evolve as new data or viewpoints become available.

58

## 59 Reference

- 60 1. Tang C, Ahmed SA, Deng S, et al. Detection of emerging genotypes in *Trichophyton mentagrophytes*  
 61 species complex: A proposal for handling biodiversity in dermatophytes. *Front Microbiol.*  
 2022;13:960190. doi:10.3389/fmicb.2022.960190.

# How to find or verify the current scientific name of a fungus

---

Simply enter a name or synonym in one of the databases:

- **MycoBank**
  - <https://www.mycobank.org/page/Basic%20names%20search>
- **NCBI Taxonomy**
  - <https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi>
- **Species Fungorum**
  - <http://www.speciesfungorum.org/Names/Names.asp>
- **The Yeasts**
  - <https://theyeasts.org/>

Taxonomy browser (Meyerozyma) +

https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi

NCBI Entrez PubMed Nucleotide Protein Genome Structure PMC Taxonomy BioCollections

Search for **Candida guilliermondii** as complete name  lock Go Clear

Display 3 levels using filter: none

Nucleotide  Protein  Structure  Genome  Popset  SNP  Conserved Domains  GEO Datasets  PubMed Central  
 Gene  HomoloGene  SRA Experiments  LinkOut  BLAST  GEO Profiles  Protein Clusters  Identical Protein Groups  BioProject  
 BioSample  Assembly  dbVar  Genetic Testing Registry  Host  Viral Host  PubChem BioAssay

**Lineage** (full): [cellular organisms](#); [Eukaryota](#); [Opisthokonta](#); [Fungi](#); [Dikarya](#); [Ascomycota](#); [saccharomyceta](#); [Saccharomycotina](#); [Saccharomycetes](#); [Saccharomycetales](#); [CUG-Ser1 clade](#); [Debaryomycetaceae](#); [Meyerozyma](#)

◦ **[Meyerozyma guilliermondii](#)** [LinkOut](#) [BLAST page](#) Click on organism name to get more information.  
▪ **[Meyerozyma guilliermondii ATCC 6260](#)** [LinkOut](#)

**Disclaimer:** The NCBI taxonomy database is not an authoritative source for nomenclature or classification - please consult the relevant scientific literature for the most reliable information.

**Reference:** How to cite this resource - Schoch CL, et al. NCBI Taxonomy: a comprehensive update on curation, resources and tools. Database (Oxford). 2020; [baaa062](#). PubMed: [32761142](#) PMC: [PMC7408187](#).

Fungi (真菌界); Dikarya (双核亚界); Ascomycota (子囊菌门); Saccharomycotina (酵母亚门); Saccharomycetes (酵母纲); Saccharomycetales (酵母目); Debaryomycetaceae (德巴利酵母科); Meyerozyma (梅耶酵母属)

**Thank You!**