



## Automated Phylogenetic Taxonomy in Fungi

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## Uses of comprehensive trees:

### Identification

Curation of public sequence databases

Identification of environmental samples

Discovery of new species

### Biogeography

Descriptive biogeography—estimation of ranges

Historical biogeography

Epidemiology, plant pathology

Conservation—phylogenetic diversity analyses

### Character evolution

Ancestral state reconstruction

Analyses of directionality

Tests of key innovation hypotheses

## Uses of classifications:

### Communication

Research

Teaching

Legislation

Representation of the history of life



- I. Progress in phylogenetic reconstruction in Fungi/Agaricomycetes
- II. Progress in classification in Agaricomycetes
- III. Automated Phylogenetic Taxonomy in Agaricomycetes
- IV. Conclusions and future directions



- I. Progress in phylogenetic reconstruction in Fungi/Agaricomycetes
- II. Progress in classification in Agaricomycetes
- III. Automated Phylogenetic Taxonomy in Agaricomycetes
- IV. Conclusions and future directions

## Fungal diversity:

Total species of Fungi	1,500,000 (Hawksworth, 1995)
Described species of Fungi	70,000-100,000 (Rossman, 1995)
Described species of Agaricomycetes	20,000 (Kirk et al. 2001)

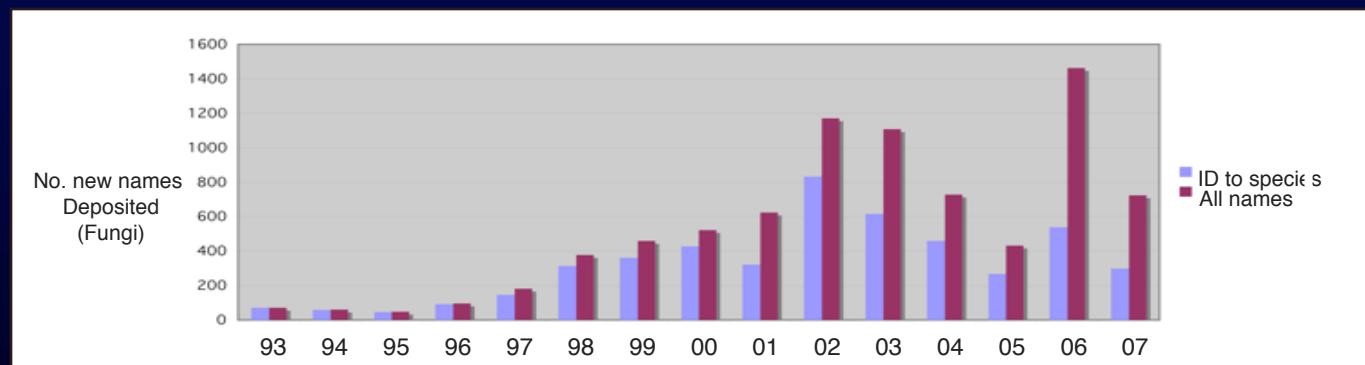
## Fungal sequence data in GenBank:

### Fungi

Core nucleotide seqs	631,464
No. unique names <i>including</i> uncultured, unspecified	32,766
No. spp. <i>excluding</i> uncultured, unspecified	17,131 (17-24% of described spp.; 1% of extant spp.)

### Agaricomycetes

Core nucleotide seqs	38,589
No. unique names <i>including</i> uncultured, unspecified	8,061
No. spp. <i>excluding</i> uncultured, unspecified	4,842 (24% of described spp.)
Nuc-lsu rDNA sequences > 800 bp	3,940
ITS rDNA sequences	13,905



# DEEP HYPHA



PROJECTS

PEOPLE

RESEARCH TOOLS

MEETINGS

JOIN

LINKS

J OBS



<http://ocid.nacse.org/research/deephypheae/>



<http://aftol.org>



## LABS/PEOPLE

5 labs (Hibbett/Clark University; Lutzoni & Vilgalys/Duke University; McLaughlin/Univ. of Minnesota; Spatafora/Oregon State Univ.  
8 post-docs  
12 Ph.D. students  
26 visiting students and scholars  
17 undergraduates

## DATA

5191 sequences, 7 genes, 2087 species  
41 subcellular characters, 30 species

## PUBLICATIONS

49 articles in print, 14 in press/in review

## INFORMATICS

WASABI: <http://www.lutzonilab.net/aftol/>

*mor*: <http://mor.clarku.edu/>

Structural and Biochemical Database: <http://aftol.umn.edu/>

## OUTREACH

Workshops for teachers

Teaching the Fungal Tree of Life website

<http://www.clarku.edu/faculty/dhibbett/TFTOL/index.html>

<http://aftol.org/>

199 Fungi  
15 non-fungi

6436 bp: *rpb1*,  
*rpb2*, *tef1-α*, nuc-  
lsu rDNA, nuc-ssu  
rDNA, nuc 5.8s  
rDNA



## ARTICLES

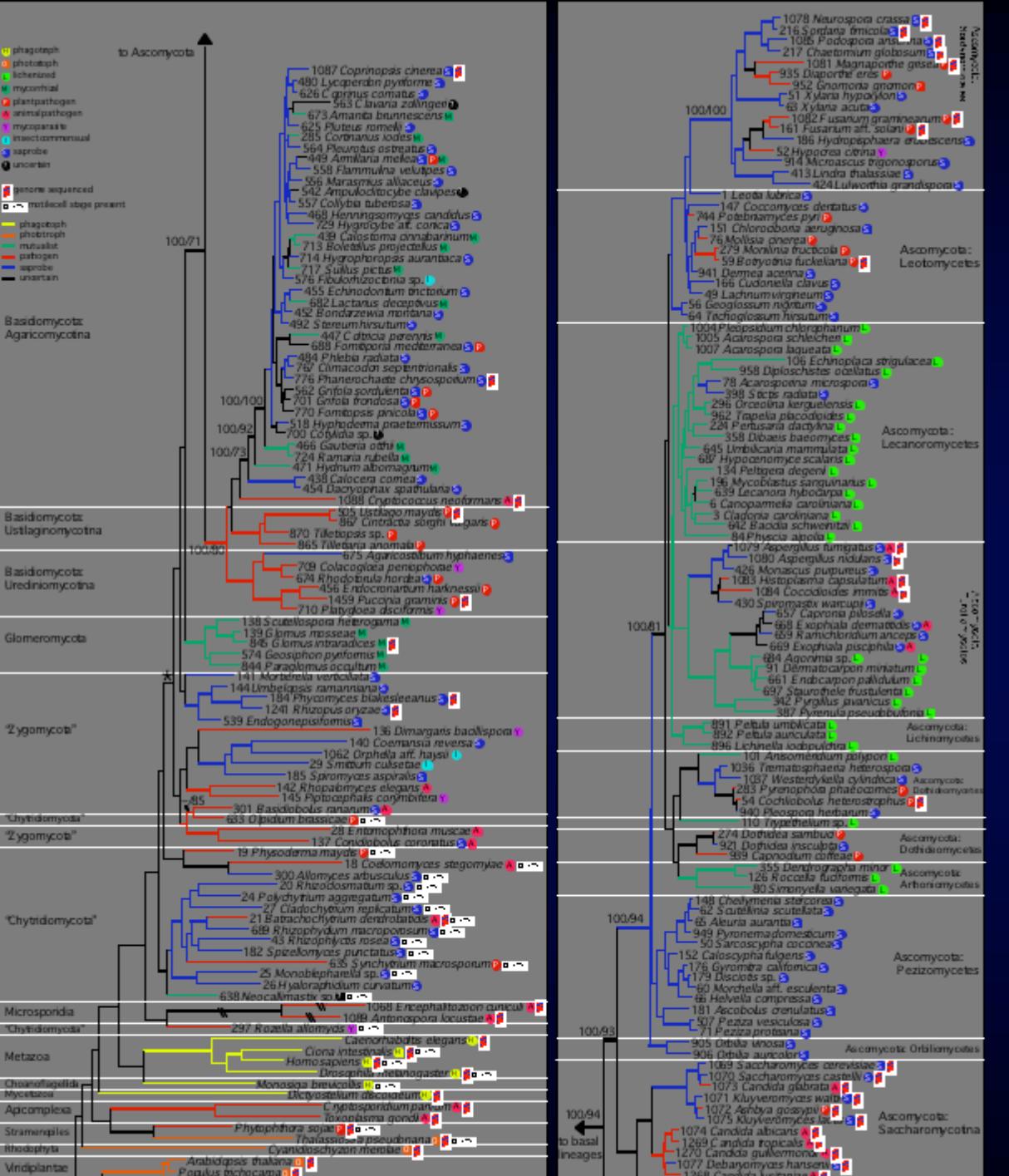
# Reconstructing the early evolution of Fungi using a six-gene phylogeny

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>

The ancestors of fungi are believed to be simple aquatic forms with flagellated spores, similar to members of the extant phylum Chytridiomycota (chytrids). Current classifications assume that chytrids form an early-diverging clade within the kingdom Fungi and imply a single loss of the spore flagellum, leading to the diversification of terrestrial fungi. Here we develop phylogenetic hypotheses for Fungi using data from six gene regions and nearly 200 species. Our results indicate that there may have been at least four independent losses of the flagellum in the kingdom Fungi. These losses of swimming spores coincided with the evolution of new mechanisms of spore dispersal, such as aerial dispersal in mycelial groups and polar tube eversion in the microsporidia (unicellular forms that lack mitochondria). The enigmatic microsporidia seem to be derived from an endoparasitic chytrid ancestor similar to *Rozella allomycis*, on the earliest diverging branch of the fungal phylogenetic tree.

# 199 Fungi 15 non-fungi

6436 bp: *rpb1*,  
*rpb2*, *tef1-α*, nuc-  
 lsu rDNA, nuc-ssu  
 rDNA, nuc 5.8s  
 rDNA

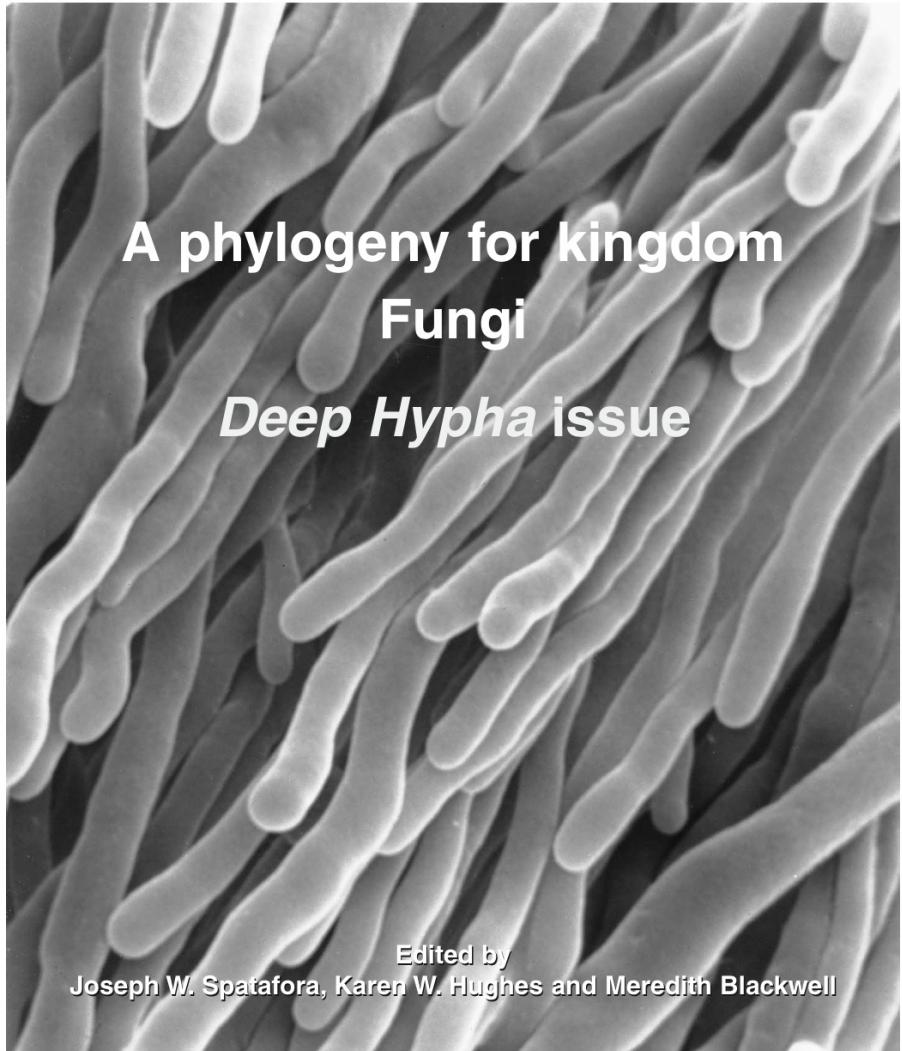


1. James et al. "Chytridiomycota"
2. White et al. "Zygomycota"
3. Redecker & Rabb Glomeromycota
4. Aime et al. Pucciniomycotina
5. Begerow et al. Ustilaginomycotina
6. Hibbett Agaricomycotina
7. Larsson et al. Hymenochaetales
8. Moncalvo et al. Cantharellales
9. Hosaka et al. Phallomycetidae
10. Miller et al. Russulales
11. Binder & Hibbett Boletales
12. Matheny et al. Agaricales
13. Sugiyama et al. Ascomycota
14. Suh et al. Saccharomycetales
15. Spatafora et al. Pezizomycotina
16. Hansen & Pfister Pezizomycetes
17. Schoch et al. Dothideomycetes
18. Geiser et al. Eurotiomycetes
19. Wang et al. Leotiomycetes
20. Zhang et al. Sordariomycetes
21. Miadlikowska et al. Lecanoromycetes

Papers citing AFTOL

MYCOLOGIA

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November December 2006



A phylogeny for kingdom  
Fungi

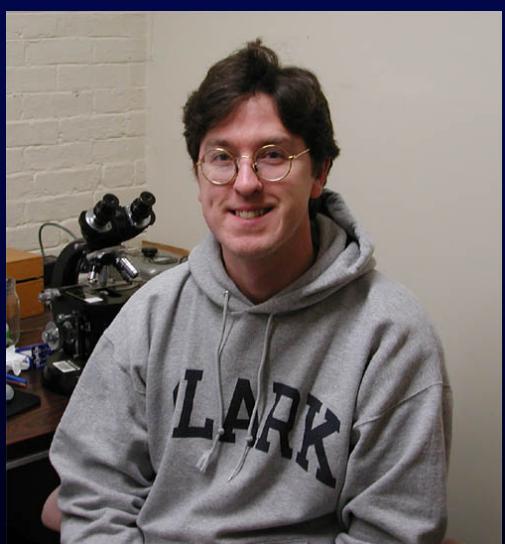
*Deep Hypha* issue

Edited by  
Joseph W. Spatafora, Karen W. Hughes and Meredith Blackwell

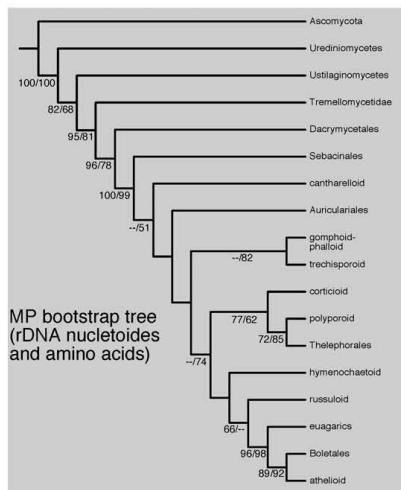
OFFICIAL BIMONTHLY PUBLICATION of the MYCOLOGICAL SOCIETY OF AMERICA

P. Matheny et al. MPE 2007.

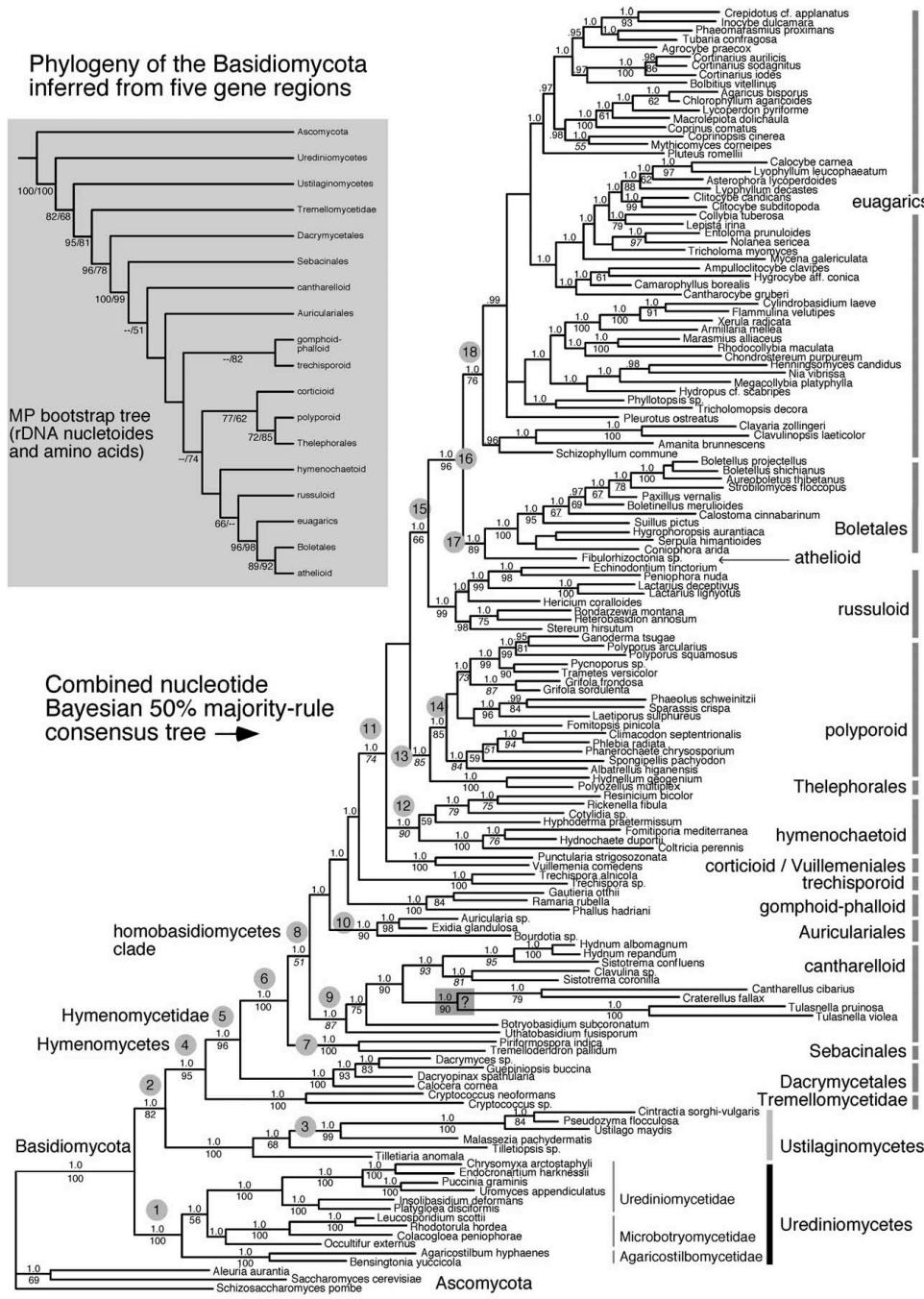
Data: 146 OTUs, five genes:  
 nuc-lsu rDNA  
 nuc-ssu rDNA  
 nuc 5.8S rDNA  
*tef1, rpb2*  
 Total: 8671 bp



### Phylogeny of the Basidiomycota inferred from five gene regions



Combined nucleotide  
Bayesian 50% majority-rule  
consensus tree →



Data: 146 OTUs, five genes:  
nuc-lsu rDNA  
nuc-ssu rDNA  
nuc 5.8S rDNA  
*tef1, rpb2*  
Total: 8671 bp

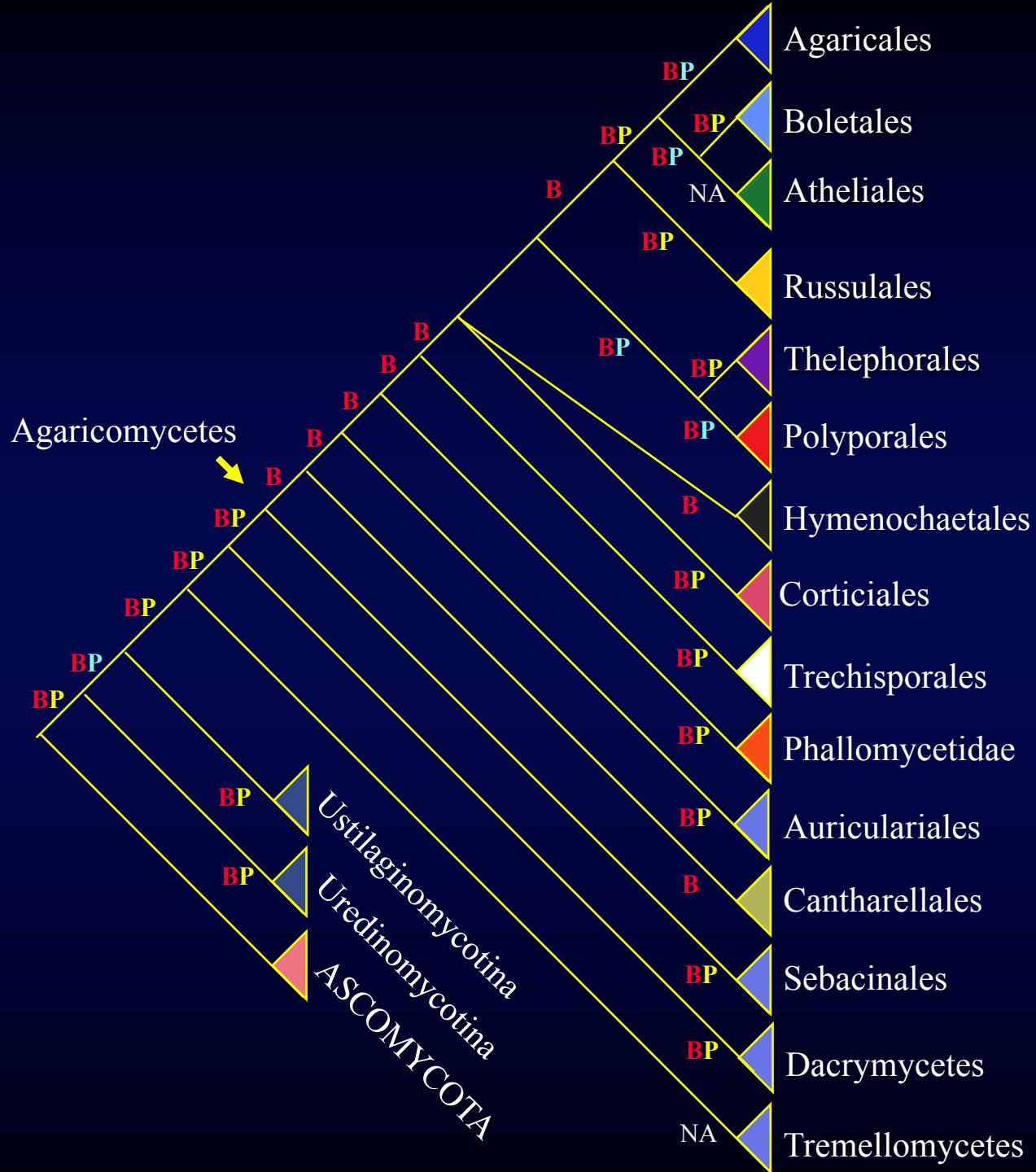
Analyses/Support:

Bayesian analysis  
of all-nucleotide dataset  
**B** = post. prob. = 1.0

Parsimony bootstrap of  
rDNA nucleotide/protein  
amino acid dataset:

**P** = 70-89%

**P** ≥ 90%



# 107 recent studies (1999-2007) on individual clades of Agaricomycetes

## **Agaricales**

Aanen et al. (2000), de Arruda et al. (2003), Binder et al. (2001), Boyle et al. (2006), Callac et al. (2005), Challen et al. (2003), Chapela and Garbelotto (2004), Coetzee et al. (2000, 2001, 2002, 2003, 2005), Dentinger et al. (2007), Drehmel et al. (1999), Frøslev et al. (2004, 2004), Garnica et al. (2003), Gulden et al. (2005), Hofstetter et al. (2002), Høiland and Holst-Jensen (2000), Hopple and Vilgalys (1999), Hughes et al. (2001), Hwang and Kim (2000), Kerrigan et al. (2005), Kirchmair et al. (2004), Krüger et al. (2001), Martin and Raccabruna (1999), Mata et al. (2001), Matheny et al. (2002), Mitchell and Bresinsky (1999), Moncalvo et al. (2000a, 2000b, 2002), Mwenje et al. (2003), Oda et al. (2004), Peintner et al. (2001, 2002, 2003, 2004), Redhead et al. (2002), Seidl (2000), Thorn et al. (2000), Vellinga (2003, 2004), Wilson et al. (2005), Yang et al. (2005)

## **Boletales**

Bakker et al. (2004), Binder and Bresinsky (2002), Bresinsky et al. (1999), Den Bakker et al. (2004), Grubisha et al. (2001, 2002), Jarosch and Besl (2001), Jarosch (2001), Kretzer and Bruns (1999), Kretzer et al. (2003), Miller (2002, 2003), Peintner et al. (2003), Reddy et al. (2005), Taylor et al. (2006), Binder and Hibbett (2007)

## **Russulales**

Henkel et al. (2000), E. Larsson et al. (2003), E. Larsson and Hallenberg (2001), Lickey et al. (2002), Miller et al. (2001, 2002), Nuytinck et al. (2004), Wu et al. (1999), Lebel et al. (2004), Miller et al. (2007)

## **Hymenochaetales**

Decock et al. (2005), Fischer and Binder (2004), Geslebin et al. (2004), Paulus et al. (2002), Redberg et al. (2003), Wagner and Fischer (2001, 2002a, 2002b), Larsson et al. (2007)

## **Polyporales**

Dai et al. (2006), De Koker et al. (2003), Desjardin et al. (2004), Hong et al. (2002), Hong and Jung (2004), Kim et al. (2005), Ko et al. (2001), Krüger (2004), Nilsson et al. (2003), Wang et al. (2004)

## **Cantharellales**

Dahlman et al. (2000), Dunham et al. (2003), Gonzalez et al. (2001), Kottke et al. (2003), Moncalvo et al. (2007)

## **Atheliales**

Eberhardt et al. (1999), Kernaghan et al. (2002), Lilleskov et al. (2002)

## **Corticiales**

DePriest et al. (2005), Diederich et al. (2003), Matsuura et al. (2000), Sikaroodi et al. (2001)

## **Thelephorales**

Köljalg et al. (2000, 2001, 2002)

## **Phallomycetidae**

Geml et al. (2005), Humpert et al. (1999), Hosaka et al. (2007)

## **Sebacinales**

Weiss et al. (2004), Selosse et al. (2002)

## **Trechisporales**

K.-H. Larsson (2001)

## Most inclusive phylogenetic analyses of Agaricomycetes

J. M. Moncalvo et al. 2002. One hundred and seventeen clades of euagarics (**Agaricales**)

Data: nuc-lsu rDNA

No. seqs. sampled	877
No. species sampled	877
Nuc-lsu rRNA > 800 bp in GenBank	2309
Species in GenBank	2429

M. Binder et al. 2005. The phylogenetic distribution of resupinate forms across the major clades of homobasidiomycetes (**Agaricomycetes**)

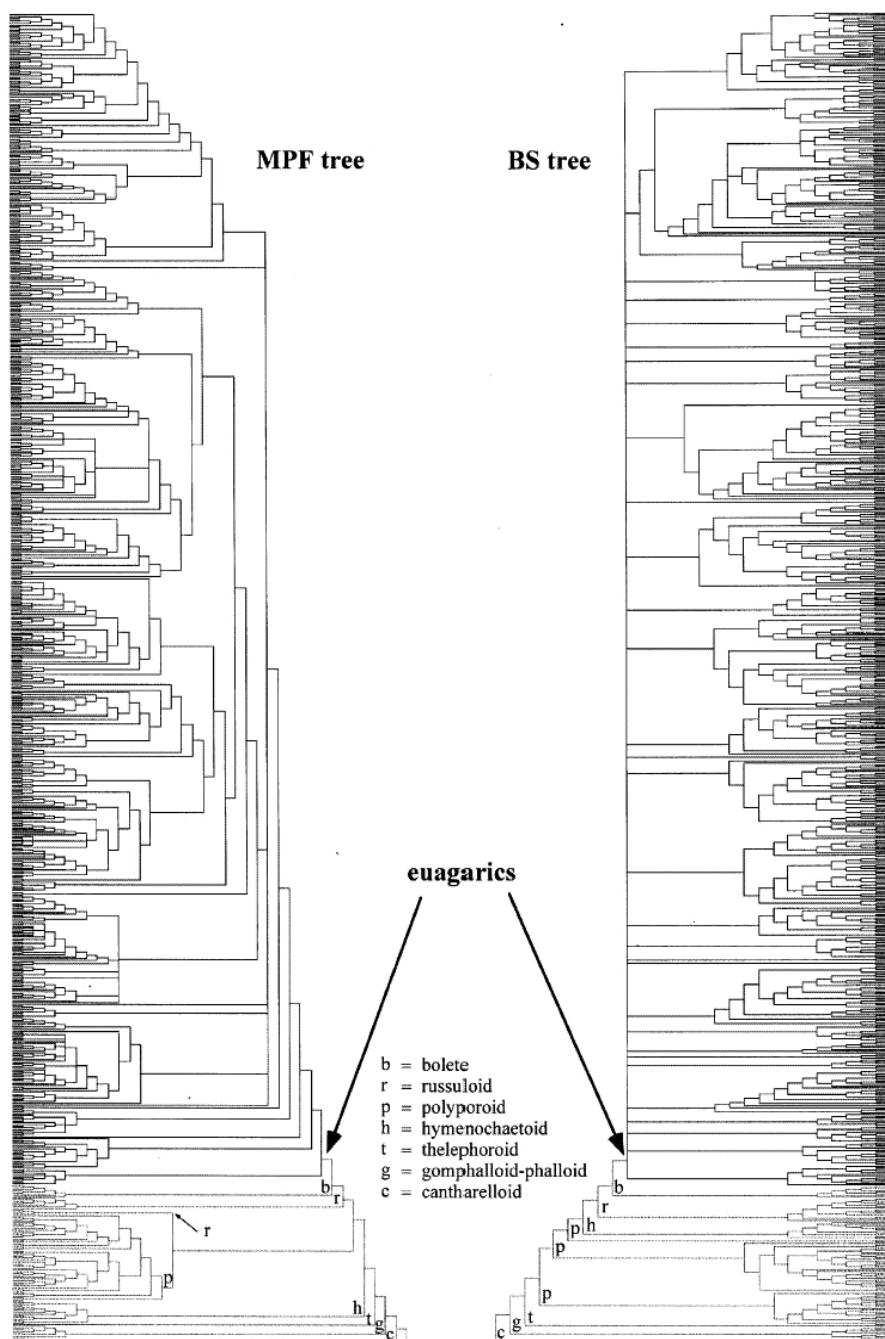
Data: mt/nuc lsu/ssu rDNA

No. seqs. sampled	656
No. species sampled	640
Nuc-lsu rRNA > 800 bp in GenBank	3940
Species in GenBank	4842

M. Binder and D. S. Hibbett. 2006. Molecular systematics and biological diversification of **Boletales**.

Data: nuc lsu rDNA

No. seqs. sampled	435
No. species sampled	301
Nuc-lsu rRNA > 800 bp in GenBank	469
Species in GenBank	442





- I. Progress in phylogenetic reconstruction in Fungi/Agaricomycetes
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**Hawsworth et al. (1995)**

Holobasidiomycetidae

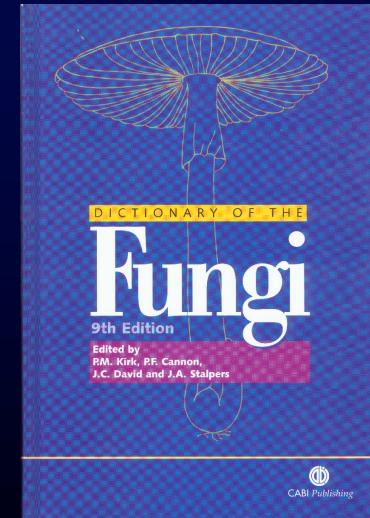
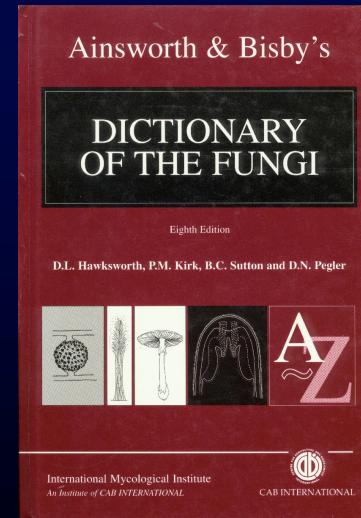
Agaricales  
Boletales  
Bondarzewiales  
Cantharellales  
Ceratobasidiales  
Cortinariales  
Dacrymycetales  
Fistulinales  
Ganodermatales  
Gautieriales  
Gomphales  
Hericiales  
Hymenochaetales  
Hymenogastrales  
Lachnocladiales  
Lycoperdales  
Melanogastrales  
Nidulariales  
Phallales  
Porales  
Russulales  
Schizophyllales  
Sclerodermatales  
Stereales  
Thelephorales  
Tulasnellales  
Tulostomatales

**Kirk et al. (2001)**

Tremellomycetidae p.p.\*  
Tulasnellales  
Agaricomycetidae\*  
Agaricales\*  
Auriculariales  
Boletales\*  
Cantharellales  
Ceratobasidiales  
Dacrymycetales\*  
Hymenochaetales  
Phallales  
Polyporales\*  
Russulales\*  
Thelephorales

\*non-monophyletic

\*not Homobasidiomycetes





# Taxonomy Browser

Entrez

PubMed

Nucleotide

Protein

Genome

Structure

PMC

Taxonomy

Books

Search for **Homobasidiomycetes**as **complete name**

lock

**Go****Clear****Display****1**levels using filter: **none**

- |   |                                  |                                       |  |                                  |                                 |
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| <input type="checkbox"/> Nucleotide     | <input type="checkbox"/> Protein | <input type="checkbox"/> Structure    | <input type="checkbox"/> Genome          | <input type="checkbox"/> Popset  | <input type="checkbox"/> SNP    |
| <input type="checkbox"/> 3D Domains     | <input type="checkbox"/> Domains | <input type="checkbox"/> GEO Datasets | <input type="checkbox"/> GEO Expressions | <input type="checkbox"/> UniGene | <input type="checkbox"/> UniSTS |
| <input type="checkbox"/> PubMed Central | <input type="checkbox"/> Gene    | <input type="checkbox"/> MapView      | <input type="checkbox"/> LinkOut         | <input type="checkbox"/> BLAST   | <input type="checkbox"/> TRACE  |

[Lineage](#) (full): root; cellular organisms; Eukaryota; Fungi/Metazoa group; Fungi; Basidiomycota; Hymenomycetes

- **Homobasidiomycetes** Click on organism name to get more information.

- [Agaricales](#) (gill mushrooms)
- [Aphylophorales](#)
- [Boletales](#)
- [Cantharellales](#)
- [Ceratobasidiales](#)
- [Echinodontiaceae](#)
- [Gautieriales](#)
- [Geastrales](#)
- [Hericiales](#)
- [Hymenochaetales](#)
- [Hymenogastrales](#)
- [Lycoperdales](#)
- [Melanogastrales](#)
- [Nidulariales](#)
- [Phallales](#)
- [Stereales](#)
- [Thelephorales](#)
- [Tulasnellales](#)
- [Tulostomatales](#)
- [unclassified Homobasidiomycetes](#)

"The NCBI taxonomy database is not a primary source for taxonomic or phylogenetic information. Furthermore, the database does not follow a single taxonomic treatise but rather attempts to incorporate phylogenetic and taxonomic knowledge from a variety of sources, including the published literature, web-based databases, and the advice of sequence submitters and outside taxonomy experts. Consequently, the NCBI taxonomy database is not a phylogenetic or taxonomic authority and should not be cited as such." <http://www.ncbi.nlm.nih.gov:80/Taxonomy/taxonomyhome.html>

**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.

**GenBank (2006)**

Homobasidiomycetes

Agaricales

Aphyllophorales

Boletales

Cantharellales

Ceratobasidiales

Echinodontiaceae

Gautieriales

Geastrales

Hericiales

Hymenochaetales

Hymenogastrales

Lycoperdales

Melanogastrales

Nidulariales

Phallales

Stereales

Thelephorales

Tulasnellales

Tulostomatales

**Kirk et al. (2001)**

Tremellomycetidae p.p.\*

Tulasnellales

Agaricomycetidae\*

Agaricales\*

Auriculariales

Boletales\*

Cantharellales

Ceratobasidiales

Dacrymycetales\*

Hymenochaetales

Phallales

Polyporales\*

Russulales\*

Thelephorales

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journal homepage: [www.elsevier.com/locate/mycres](http://www.elsevier.com/locate/mycres)

## A higher-level phylogenetic classification of the Fungi

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<sup>b</sup>National Library of Medicine, National Center for Biotechnology Information, 45 Center Drive, Bethesda, MD 20892-6510, USA

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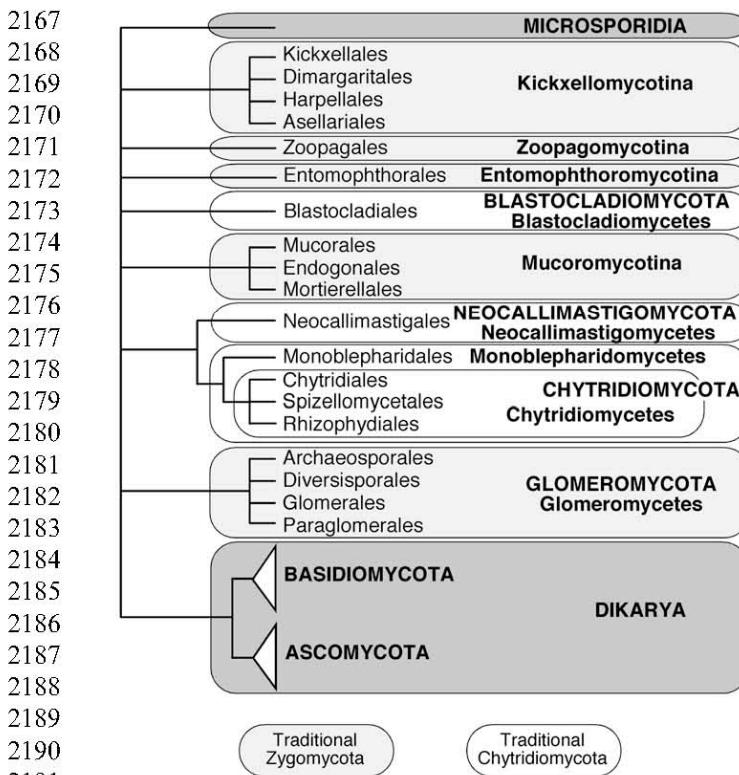
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<sup>h</sup>Department of Plant Biology, University of Minnesota, 1445 Gortner Avenue, St Paul, MN 55108-1095, USA

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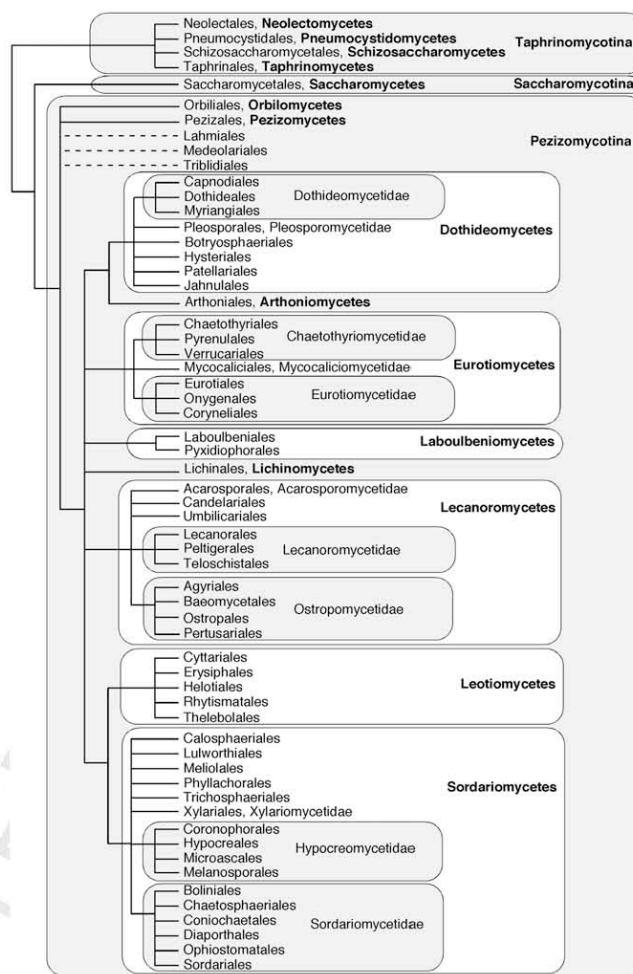
**Fig 1 – Phylogeny and classification of Fungi. Basal Fungi and Dikarya. Branch lengths are not proportional to genetic distances. See Table 1 for support values for clades.**

Order: **Rhizophydiales** Letcher, in Letcher et al., Mycol. Res. 110: 908 (2006).

Exemplar genera: *Rhizophyllum* Schenk 1858, *Kappamyces* Letcher & M.J. Powell 2005, *Terramyces* Letcher 2006, *Boothiomycetes* Letcher 2006; *Batrachochytrium* Longcore, Pessier & D.K. Nichols 1999 is on a long branch in this clade with no near relatives.

Order: **Spizellomycetales** D. J. S. Barr, Can. J. Bot. 58: 2384 (1980).

Exemplar genera: *Spizellomyces* D.J.S. Barr 1980, *Powellomyces*



**Fig 2 – Phylogeny and classification of Fungi. Ascomycota. See Table 2 for support values for clades. Dashed lines indicate taxa that are of uncertain placement.**

posteriorly uniflagellate antherozoids borne in antheridia and nonflagellate female gametes borne in oogonia.

Schaffner (1909) used the name 'Monoblepharideae' as a class but with the ending of a suborder; this must be changed with-

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459**Table 1 – Support for major groups of Fungi in selected phylogenetic studies: basal fungi and Dikarya**514  
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Rank	Taxon	Reference	Rank	Data <sup>a</sup>	OTUs <sup>b</sup>	Support <sup>c</sup>
Kingdom	FUNGI	Keeling (2003) Baldauf et al. (2000)	$\alpha$ -tub, $\beta$ -tub <i>act</i> , $\alpha$ -tub, $\beta$ -tub, <i>tef1</i>	38 12	MLBS – 98 NJBS – 94 MLBS – 85 MPBS – 95	518 519 520 521
Phylum	CHYTRIDIOMYCOTA	James et al. (2007) Seif et al. (2005)	LSU, SSU, 5.8S mt-genome	84 5	BPP $\geq$ 0.95 BPP – 1 MLBS – 100	521 522 523
Class	Chytridiomycetes	James et al. (2006) James et al. (2007)	LSU, SSU, 5.8S, <i>rpb1</i> , <i>rpb2</i> , <i>tef1</i> LSU, SSU, 5.8S	8 75	BPP $\geq$ 0.95 MLBS $\geq$ 70 BPP $\geq$ 0.95 MLBS $\geq$ 70	524 525 526 527
		Keeling (2003)	$\alpha$ -tub, $\beta$ -tub	5	MLBS – 90 NJBS – 95	528
Order	Chytridiales	James et al. (unpublished)	LSU, SSU, 5.8S, <i>rpb1</i> , <i>rpb2</i> , <i>tef1</i> , Atp6	9	MLBS – 98	529
Order	Rhizophydiales	James et al. (2006)	LSU, SSU, 5.8S, <i>rpb1</i> , <i>rpb2</i> , <i>tef1</i>	2	BPP $\geq$ 0.95 MLBS $\geq$ 70	530
		Letcher et al. (2006)	LSU, 5.8S	96	MPBS – 100 BPP – 1	531 532
Order	Spizellomycetales	James et al. (2007)	LSU, SSU, 5.8S	9	MPBS – 100	533
Class/Order	Monoblepharidomycetes, Monoblepharidales	James et al. (2007)	LSU, SSU, 5.8S	9	BPP $\geq$ 0.95 MLBS $\geq$ 70 MPBS $\geq$ 70	534 535 536
Phylum/Class/Order	NEOCALLIMASTIGOMYCOTA, Neocallimastigomycetes, Neocallimastigales	Bullerwell et al. (2003) James et al. (2007)	<i>cox</i> 1,2,3; <i>cob</i> , <i>atp6</i> , <i>nad</i> 1,2,3,4, 4L,6 LSU, SSU, 5.8S	4 6	MLBS – 100 BPP $\geq$ 0.95 MLBS $\geq$ 70 MPBS $\geq$ 70	537 538 539
Phylum/Class/Order	BLASTOCLADIOMYCOTA, Blastocladiomycetes, Blastocladiales	James et al. (2007)	LSU, SSU, 5.8S	10	BPP $\geq$ 0.95	540
		Liu et al. (2006)	<i>rpb1</i> , <i>rpb2</i>	3	BPP – 1 MPBS – 100	541 542
Phylum	MICROSPORIDIA	James et al. (2006)	LSU, SSU, 5.8S, <i>rpb1</i> , <i>rpb2</i> , <i>tef1</i>	2	BPP $\geq$ 0.95 MLBS $\geq$ 70	543 544
		Keeling (2003)	$\alpha$ -tub, $\beta$ -tub	6	MLBS – 100 NJBS – 97	545 546
Phylum/Class	GLOMEROMYCOTA, Glomeromycetes	James et al. (2006)	LSU, SSU, 5.8S, <i>rpb1</i> , <i>rpb2</i> , <i>tef1</i>	5	BPP $\geq$ 0.95 MLBS $\geq$ 70	547 548
		Schüßler et al. (2001)	<i>Ssu</i>	72	NJBS $\geq$ 90	549
Order	Archaeosporales	Schüßler et al. (2001)	<i>Ssu</i>	5	NJBS $\geq$ 95	550
Order	Diversisporales	Schüßler et al. (2001)	<i>Ssu</i>	32	NJBS $\geq$ 95	551
Order	Glomerales	Schüßler et al. (2001)	<i>Ssu</i>	32	NJBS $\geq$ 95	552
Order	Paraglomerales	Schüßler et al. (2001)	<i>Ssu</i>	3	NJBS $\geq$ 95	553
		<i>Schubunkia incepta</i> , <i>radicans</i>				

## **GenBank (2006)**

Homobasidiomycetes

Agaricales

Aphyllophorales

Boletales

Cantharellales

Ceratobasidiales

Echinodontiaceae

Gautieriales

Geastrales

Hericiales

Hymenochaetales

Hymenogastrales

Lycoperdales

Melanogastrales

Nidulariales

Phallales

Stereales

Thelephorales

Tulasnellales

Tulostomatales

## **GenBank (2007)**

Agaricomycetes

Agaricales

Atheliales

Auriculariales

Boletales

Cantharellales

Corticiales

Gloeophyllales

Hymenochaetales

Phallomycetidae

Polyporales

Russulales

Sebacinales

Thelephorales

Trechisporales

## **GenBank (2006)**

### **Homobasidiomycetes**

Agaricales  
Aphylophorales  
Boletales  
Cantharellales  
Ceratobasidiales  
Echinodontiaceae  
Gautieriales  
Geastrales  
Hericiales  
Hymenochaetales  
Hymenogastrales  
Lycoperdales  
Melanogastrales  
Nidulariales  
Phallales  
Stereales  
Thelephorales  
Tulasnellales  
Tulostomatales

## **GenBank (2007)**

### **Agaricomycetes**

Agaricales  
Atheliales  
Auriculariales  
Boletales  
Cantharellales  
Corticiales  
Gloeophyllales  
Hymenochaetales  
Phallomycetidae  
Polyporales  
Russulales  
Sebacinales  
Thelephorales  
Trechisporales

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 Genome Projects  Popset  SNP  3D Domains  Domains  GEO Datasets  GEO Expressions  
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 BLAST  TRACE  Taxonomy

**Lineage (full):** root; cellular organisms; Eukaryota; Fungi/Metazoa group; Fungi; Dikarya; Basidiomycota; Agaricomycotina

- **Agaricomycetes** Click on organism name to get more information.
  - **Agaricomycetidae**
    - [Agaricales](#) (gill mushrooms)
    - [Atheliales](#)
    - [Boletales](#)
  - **Phallomycetidae**
    - [Gastrales](#)
    - [Gomphales](#)
    - [Hysterangiales](#)
    - [Phallales](#)
  - **unclassified Agaricomycetes**
    - [homobasidiomycete sp. 4472](#)
    - [homobasidiomycete sp. A14](#)
    - [homobasidiomycete sp. BM63-1206](#)
    - [homobasidiomycete sp. DE-P2](#)
    - [homobasidiomycete sp. HK-S163](#)
    - [homobasidiomycete sp. HK-S195](#)
    - [homobasidiomycete sp. HK-S200](#)
    - [homobasidiomycete sp. WRCF-B5](#)
    - [homobasidiomycete sp. WRCF-B7](#)
    - [homobasidiomycete sp. WRCF-B9](#)
    - [homobasidiomycetes sp. DIS 181c](#)
  - **Agaricomycetes incertae sedis**
    - [Auriculariales](#)
    - [Cantharellales](#)
    - [Chondrocytaceae](#)
    - [Corticiales](#)
    - [Gloeophyllales](#)
    - [Hymenochaetales](#)
    - [Polyporales](#)
    - [Russulales](#)
    - [Sebacinales](#)
    - [Thelephorales](#)
    - [Trechisporales](#)
  - **environmental samples**
    - [uncultured ectomycorrhizal homobasidiomycete](#)
    - [uncultured homobasidiomycete](#)

→



<http://www.abc.net.au/science/scribblygum/>

## Phylogenetic relationships among coprinoid taxa and allies based on data from restriction site mapping of nuclear rDNA

John S. Hopple, Jr.  
Rytas Vilgalys

Department of Botany, Duke University, Durham, North Carolina 27708-0339

**Abstract:** Phylogenetic relationships among coprinoid and closely related taxa were studied using restriction

(May et al., 1991), the genus *Coprinus* (Pers. : Fr.) S. F. Gray has played a central role in fungal research. The genus contains some of the most commonly encountered species of mushrooms and was one of the first genera recognized by Fries as he subdivided *Agaricus* Fr. (Fries, 1836–1838). *Coprinus* has also served as the model system for the development of ideas concerning intersterility (Bensaude, 1918), the biological species

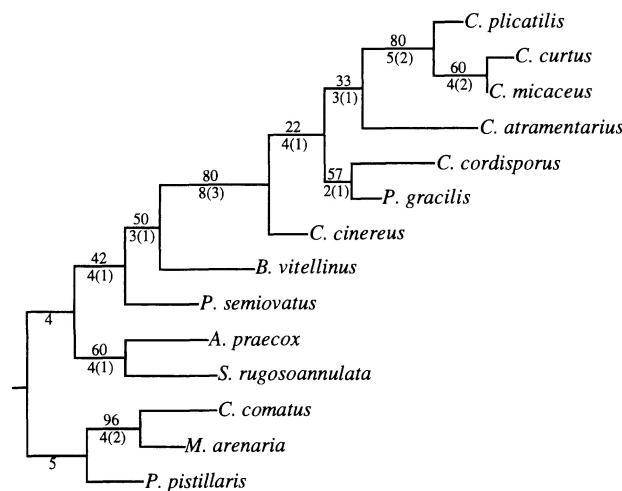


FIG. 7. Phylogram produced using stepmatrix weighting of 1.25:1 (gains : losses). Numbers above branches indicate bootstrap confidence intervals determined from 1000 rep-



***Coprinus* Pers. and the disposition of *Coprinus* species *sensu lato***

Scott A. Redhead<sup>1</sup>, Rytas Vilgalys<sup>2</sup>, Jean-Marc Moncalvo<sup>2</sup>, Jacqui Johnson<sup>3</sup> & John S. Hopple, Jr.<sup>4</sup>

**Summary**

Redhead, S. A., Vilgalys, R., Moncalvo, J.-M., Johnson, J. & Hopple, J. S., Jr.: *Coprinus* Pers. and the disposition of *Coprinus* species *sensu lato*. – Taxon 50: 203–241. 2001. – ISSN 0040-0262.

The screenshot shows the homepage of the Centraalbureau voor Schimmelcultures (CBS) Fungal Biodiversity Center. The main navigation bar includes links for Research, Databases, Ordering info, Prices, Publications, Services, and Courses. Below this, a large heading reads "Fungal nomenclature". A text block discusses the International Committee for Fungi's role in the International Botanical Congress. It lists members of the IAPT Nomenclature Committee for Fungi as of May 31, 2007, including names and contact information for various institutions like Illinois Natural History Survey, Institut de Botanique, Royal Botanic Gardens, and CABI Bioscience.

**(1486) Proposal to conserve the name *Coprinus* Pers. (*Basidiomycota*) with a conserved type**

Per M. Jørgensen<sup>1</sup>, Svengunnar Ryman<sup>2</sup>, W. Gams<sup>3</sup>, & J. A. Stalpers<sup>3</sup>

(1486) *Coprinus* Pers., Tent. disp. meth. fung. 62 (1797) [Fungi].  
Typus: *Coprinus atramentarius* (Bull. : Fr.) Fr., typ. cons. prop.

The screenshot shows the CBS homepage again, but this time it displays the results of a search for the proposal number 1486. The results are presented in a table format with columns for Proposal No., Cons., Rej., Group, Act., Author, Where, Synopsis, and Comm. The table entries correspond to the names and roles of the proposers and supporters listed in the text above. To the right of the table, a note states: "Here are the results of your query: 1486 Coprinus Fungi Cg Jørgensen, Ryman, & Stalpers Taxon 50: 909. 2001. -Taxon 54: 521. 2005. ñTaxon 55: 799. 2006. Comm. vote in 2005 6:7:1:1 was not decisive, although negative (not 60%) and is referred back." At the bottom, a URL is visible: <http://persoon.si.edu/codes/props/help.htm#props>.

### **Genera resolved as non-monophyletic in Binder et al. (2005):**

*Acanthophysium, Albatrellus, Aleurodiscus, Antrodia, Antrodiella, Athelia, Ceraceomyces, Ceriporia, Dendrothele, Fuscoporia, Gloeocystidiellum, Hericium, Hydnochaete, Hymenochaete, Hyphoderma, Hyphodontia, Hypochnicium, Kavinia, Leucogyrophana, Marchandiomyces, Oligoporus, Peniophora, Phanerochaete, Phellinus, Phlebia, Phlebiella, Physalacria, Polyporus, Polyporus, Pseudotomentella, Schizopora, Scytinostroma, Sistotrema, Stereum, Xylobolus* (34)

### **Genera resolved as non-monophyletic in Moncalvo et al. (2002):**

*Agaricus, Agrocybe, Amanita, Boletus, Clitocybe, Collybia, Coprinus, Cortinarius, Cystoderma, Cystolepiota, Entoloma, Galerina, Gerronema, Gloiocephala, Gymnopilus, Gymnopus, Hemimycena, Hohenbuehelia, Hydropus, Hypholoma, Lepiota, Lepista, Leptonia, Leucoagaricus, Leucocoprinus, Limacella, Lyophyllum, Macrolepiota, Marasmiellus, Marasmius, Montagnea, Mycena, Naucoria, Omphalina, Omphalotus, Pholiota, Poromycena, Psathyrella, Psilocybe, Resinomycena, Resupinatus, Rhodocybe, Russula, Stropharia* (44)

## **Summary: current status of homobasidiomycete systematics**

- ❖ Largely incomplete documentation of extant species
- ❖ Ca. 20% of described species represented in GenBank
- ❖ Steady accumulation of “taxonomic” sequences, accelerating accumulation of “environmental” sequences
- ❖ Higher-level analyses resolve broad outlines of Agaricomycete phylogeny
- ❖ A plethora of analyses at lower taxonomic levels
- ❖ Lack of integration of existing data
- ❖ Unacceptably slow translation of phylogenies into classifications
- ❖ A disconnect between phylogenetic reconstruction and classification, creating a (widening?) gap between taxonomy and understanding of phylogeny

## **What is needed to achieve a comprehensive, phylogenetically accurate classification of homobasidiomycetes?**

- ❖ A dramatic increase in the rate of species discovery, including sequence-based discovery and description
- ❖ Automated integration of emerging data into comprehensive trees
- ❖ Automated translation of trees into classifications



- I. Progress in phylogenetic reconstruction in Fungi/Agaricomycetes
- II. Progress in classification in Agaricomycetes
- III. Automated Phylogenetic Taxonomy in Agaricomycetes
- IV. Conclusions and future directions



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## welcome to mor

**Welcome.** *mor* is an ongoing project based in the [Hibbett lab of Clark University](#) that seeks to produce continually updated phylogenetic trees and classifications for the homobasidiomycetes (mushroom-forming fungi) on an automated basis. In brief, *mor* retrieves, screens, aligns, and analyzes nuc-lsu rDNA sequences of homobasidiomycetes from [GenBank](#), and then parses out the contents of individual clades using node-based phylogenetic taxon definitions. Thus, *mor* represents a step toward automated phylogenetic taxonomy. For more information about homobasidiomycete phylogeny, visit the [Tree of Life Web Project](#) page for [homobasidiomycetes](#).

*mor* creates two phylogenetic trees each week: an unconstrained jackknife neighbor-joining tree, and a topologically constrained consensus maximum parsimony tree. The parsimony tree is used to delimit the clades.

On the following pages, you can view the NJ and MP trees, link to GenBank, search for images of fungi on the internet, view individual clade pages, download alignments and treefiles (for the entire dataset or individual clades), post comments, and create new clade definitions. Please note that some files are quite large (about 6 MB) and can take some time to load.

## sequences in the database

View List of Current...

Accepted Sequences			Rejected Sequences			
(sorted by...)			(sorted by...)			
name	accession number	date	name	accession number	date	reason

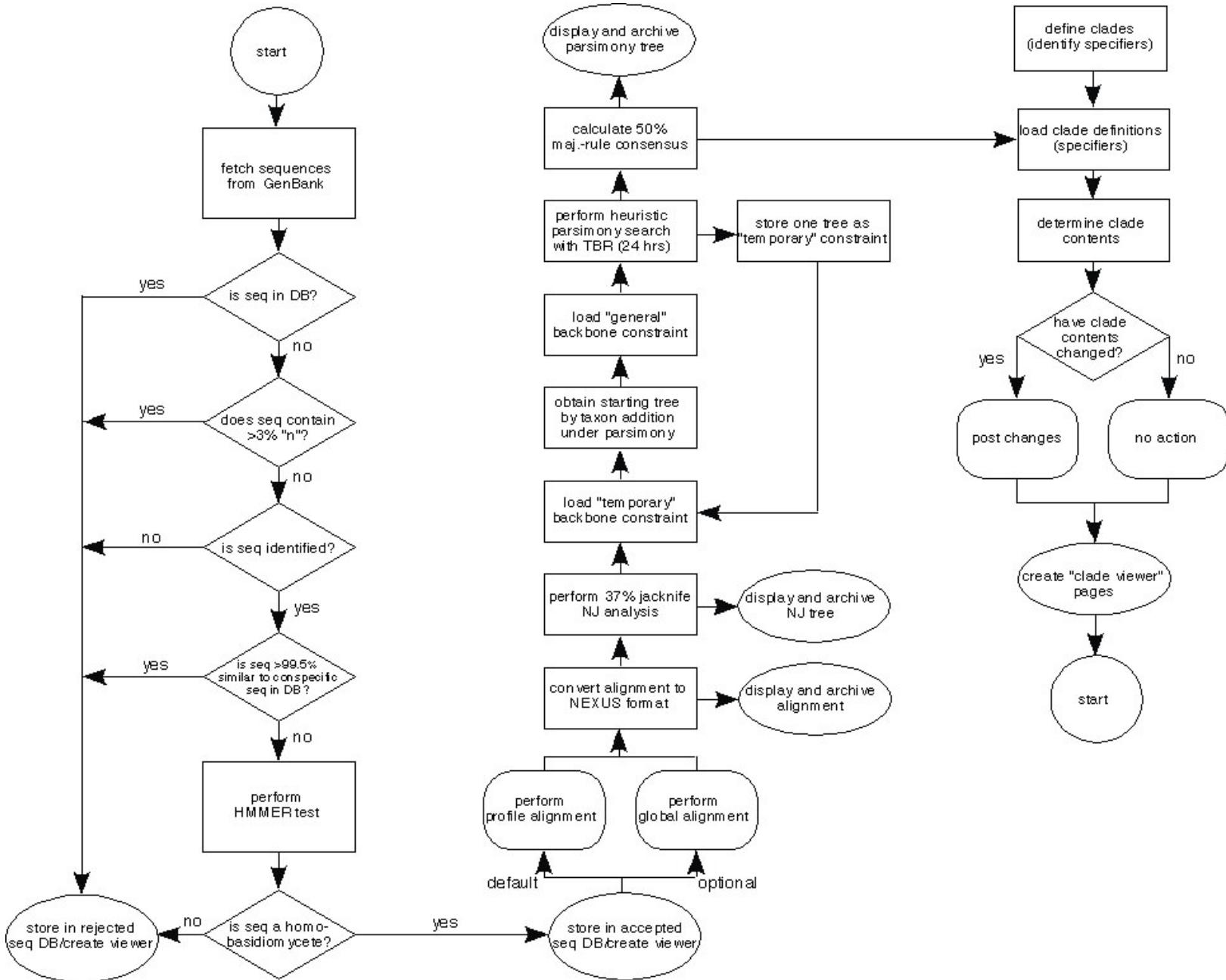
## main clades

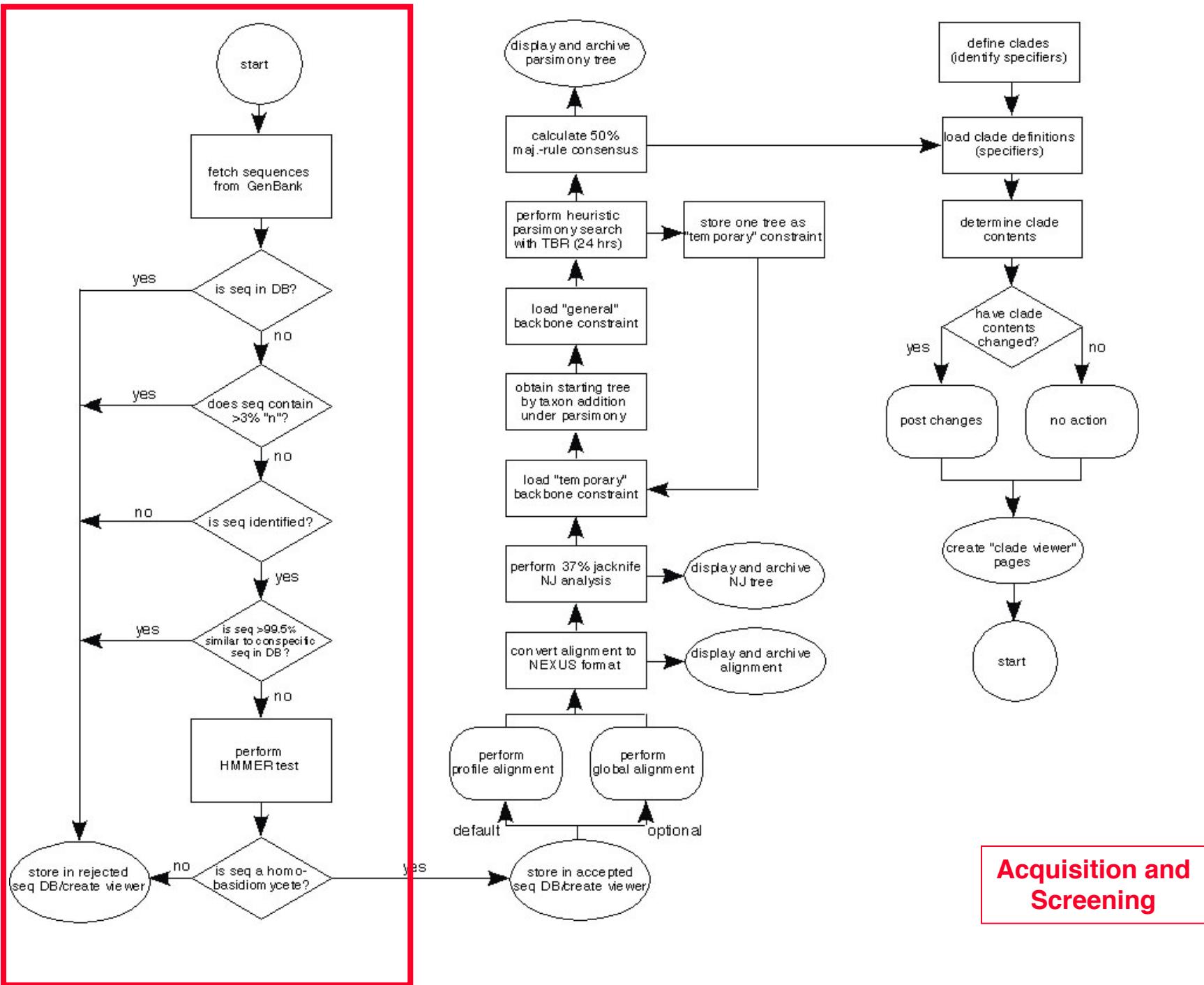
## citation

Hibbett, D. S., R. H. Nilsson, M. Snyder, M. Fonseca, J. Costanzo, and M. Shonfeld. 2005. Automated Phylogenetic Taxonomy: An Example in the Homobasidiomycetes (Mushroom-Forming Fungi). Systematic Biology 54: 660-668. [Download reprint \(PDF\)](#).

## news

Read about mor and WASABI in Science: Pennisi, E. 2005. Fungal trees grow faster with computer help. *Science* 309: 374 (meeting report). [Download PDF](#).







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## accepted sequences

**Number of OTUs in accepted table:** 3010**Number of OTUs in databases (accepted + rejected):** 4842**Number of distinct species in database:** 2144**Number of distinct genera:** 606

in alphabetical order by species name

Date of Acceptance (into mor)	Acc. #	Species Name	Length	Trimmed	Images	Available Literature	Jump to Tree
2007-04-10	AJ406527	<i>Abortiporus biennis</i>	913	0	<a href="#">Images</a>	<a href="#">Literature</a>	<a href="#">nj / parsimony</a>
2007-04-10	AF287842	<i>Abortiporus biennis</i>	882	0	<a href="#">Images</a>	<a href="#">Literature</a>	<a href="#">nj / parsimony</a>
2007-04-10	AY039328	<i>Acanthobasidium norvegicum</i>	852	0	<a href="#">Images</a>	<a href="#">Literature</a>	<a href="#">nj / parsimony</a>
2007-04-10	AY039305	<i>Acanthobasidium phragmitis</i>	854	0	<a href="#">Images</a>	<a href="#">Literature</a>	<a href="#">nj / parsimony</a>
2007-04-10	AY039333	<i>Acanthofungus rimosus</i>	882	0	<a href="#">Images</a>	<a href="#">Literature</a>	<a href="#">nj / parsimony</a>
2007-04-10	AY039318	<i>Acanthophysium bisporum</i>	952	0	<a href="#">Images</a>	<a href="#">Literature</a>	<a href="#">nj / parsimony</a>
2007-04-10	AY039327	<i>Acanthophysium bisporum</i>	883	0	<a href="#">Images</a>	<a href="#">Literature</a>	<a href="#">nj / parsimony</a>
2007-04-10	AF518595	<i>Acanthophysium cerrusatus</i>	882	0	<a href="#">Images</a>	<a href="#">Literature</a>	<a href="#">nj / parsimony</a>
2007-04-10	AY039310	<i>Acanthophysium cerussatum</i>	959	0	<a href="#">Images</a>	<a href="#">Literature</a>	<a href="#">nj / parsimony</a>
2007-04-10	AY039335	<i>Acanthophysium cerussatum</i>	887	0	<a href="#">Images</a>	<a href="#">Literature</a>	<a href="#">nj / parsimony</a>



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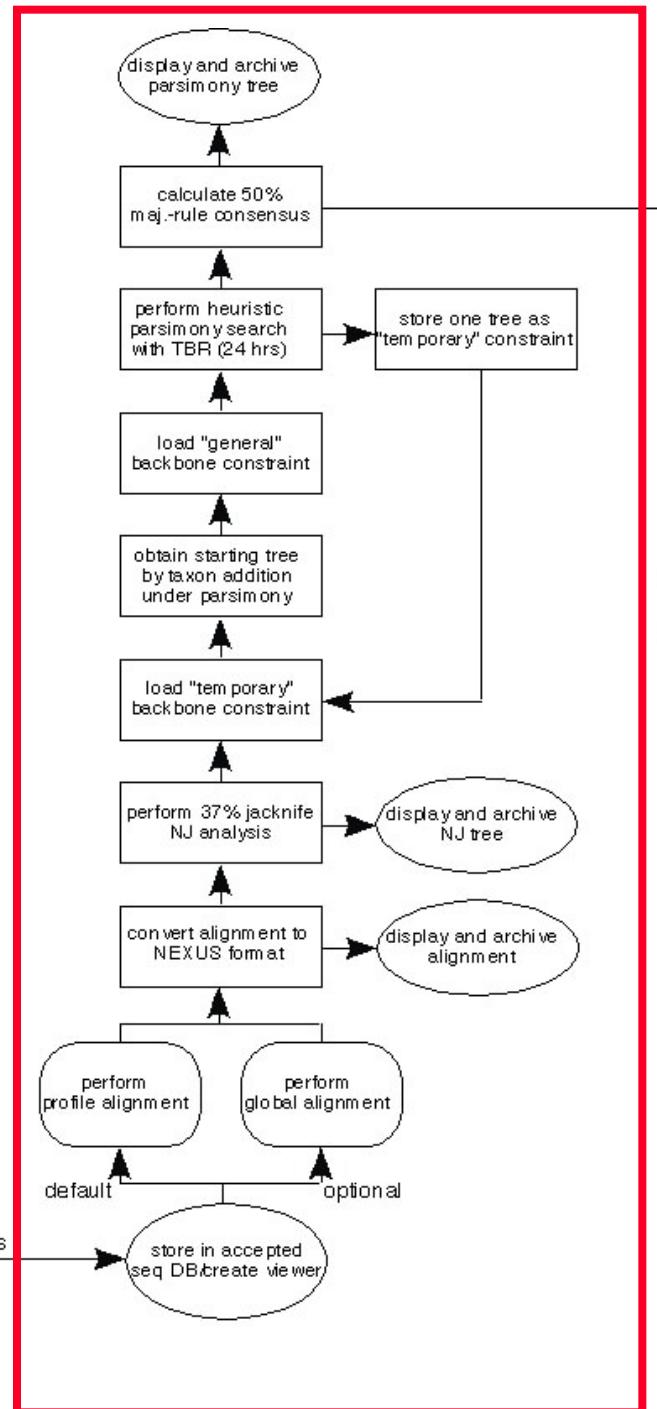
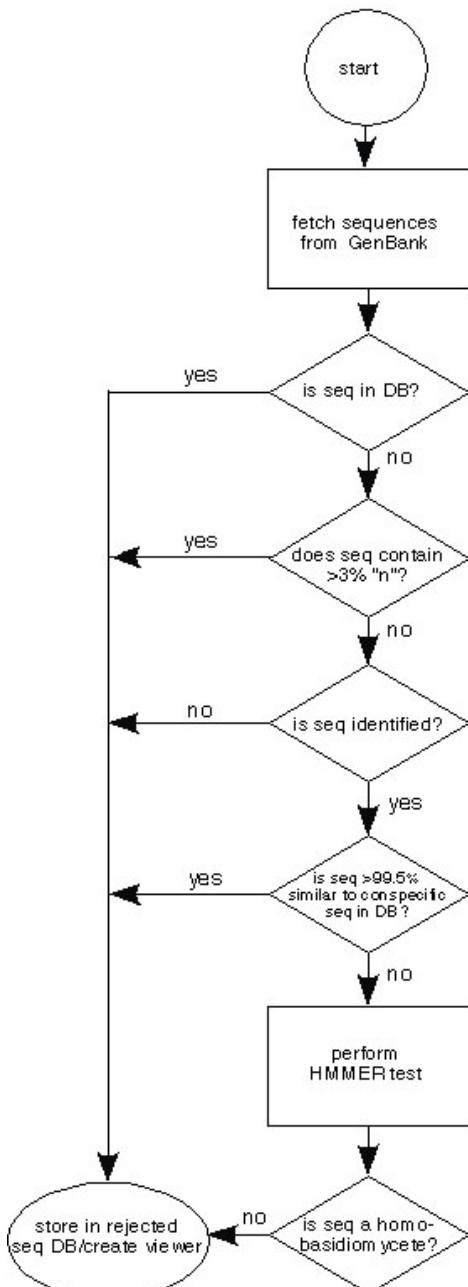
## rejected sequences

Number of OTUs in rejected table: 1832

Number of OTUs in databases (accepted + rejected): 4842

all rejected sequences ordered by accession number

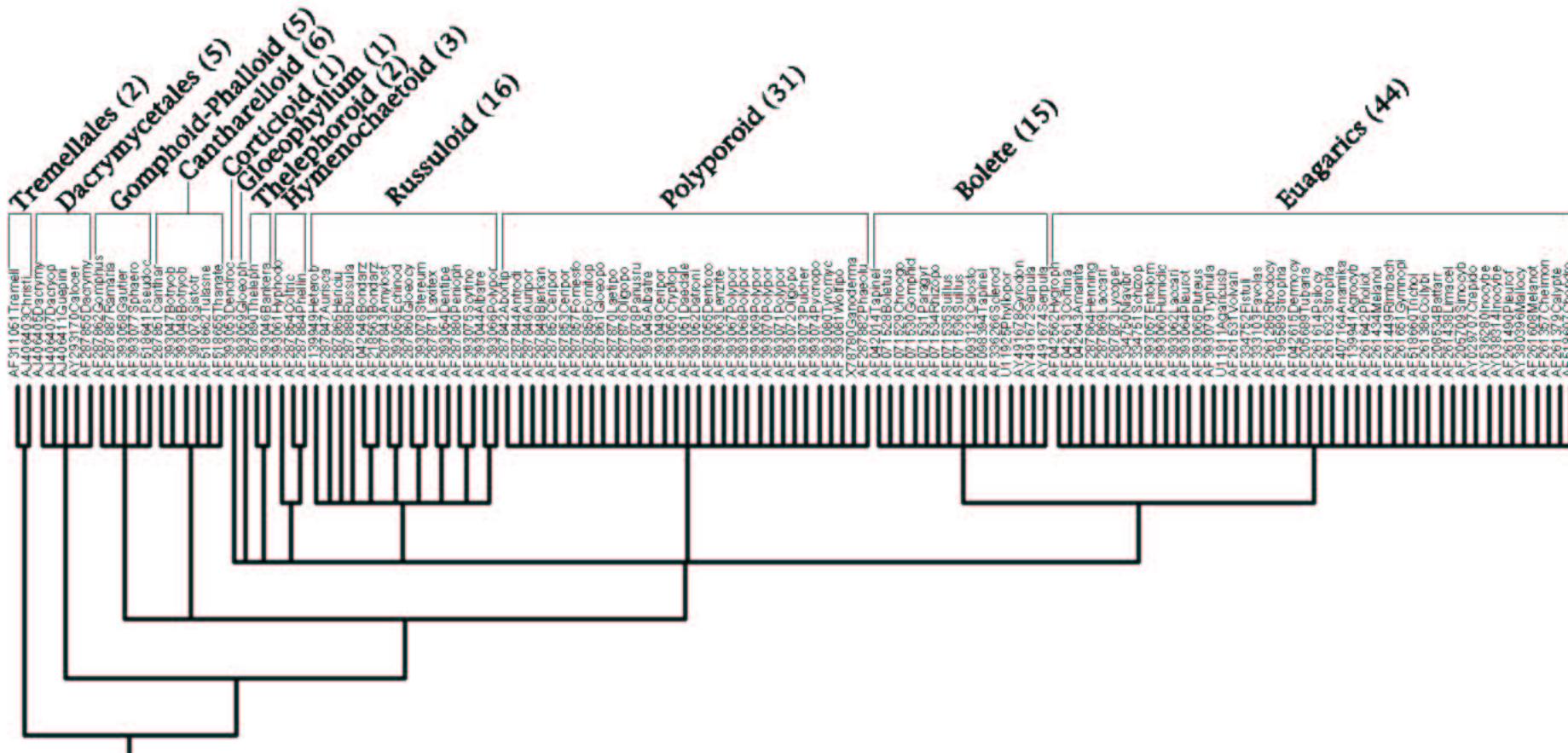
Date of Rejection	Acc. #	Species Name	Length	Trimmed	Available Literature	Reason for rejection
2007-04-10	<a href="#">AB000001</a>	Thanatephorus cucumeris	3	657	<a href="#">Literature</a>	008 Sequence too short
2007-04-10	<a href="#">AB000002</a>	Thanatephorus cucumeris	5	655	<a href="#">Literature</a>	008 Sequence too short
2007-04-10	<a href="#">AB000003</a>	Thanatephorus cucumeris	3	638	<a href="#">Literature</a>	008 Sequence too short
2007-04-10	<a href="#">AB000004</a>	Thanatephorus cucumeris	3	657	<a href="#">Literature</a>	008 Sequence too short
2007-04-10	<a href="#">AB000005</a>	Thanatephorus cucumeris	3	657	<a href="#">Literature</a>	008 Sequence too short
2007-04-10	<a href="#">AB000006</a>	Thanatephorus cucumeris	3	663	<a href="#">Literature</a>	008 Sequence too short
2007-04-10	<a href="#">AB000007</a>	Thanatephorus cucumeris	3	661	<a href="#">Literature</a>	008 Sequence too short
2007-04-10	<a href="#">AB000008</a>	Thanatephorus cucumeris	3	663	<a href="#">Literature</a>	008 Sequence too short
		Thanatephorus				008



**Alignment and Analysis**

## Backbone monophyly constraint

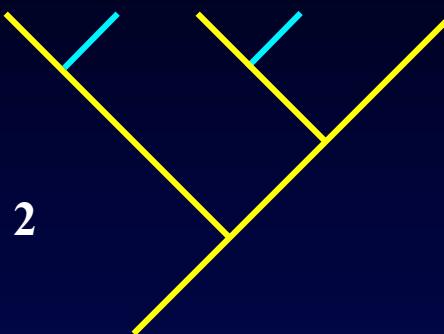
220 species, based on multi-locus analyses



## Heuristic search strategy:

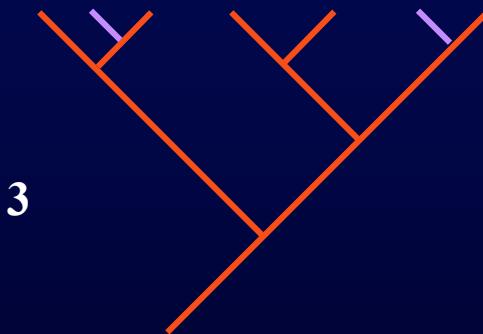


Create **General Constraint** tree (220 species, based on multilocus analyses).

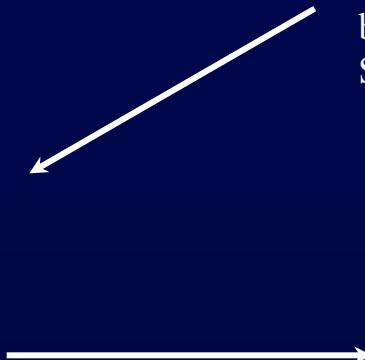


2

Load **General Constraint** as backbone monophly constraint.  
Add **new** sequences to dataset and tree and perform branch swapping (TBR, 5 hours).  
Save new tree as **Temporary Constraint**.



Load **Temporary Constraint** as backbone monophly constraint.  
Add **new** sequences to dataset and tree, but perform no swapping.  
Save new tree as **Temporary Constraint** (i.e., overwrite file).



4

Load **General Constraint** as backbone.  
Use (new) **Temporary Constraint** as a starting tree for branch swapping (TBR, 5 hours).  
Save new tree as **Temporary Constraint**.  
Go to 3.



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**Date of phylogeny:** Tue Aug 7 15:05:41 2007

**Process ID:** 12350

**New sequences since last week:** 44

**Total number of sequences:** 3009

nj/parsimony = Placement of taxon in the other main tree.

\* = Species present in constraints tree

(n) = There are n comments available for this sequence.

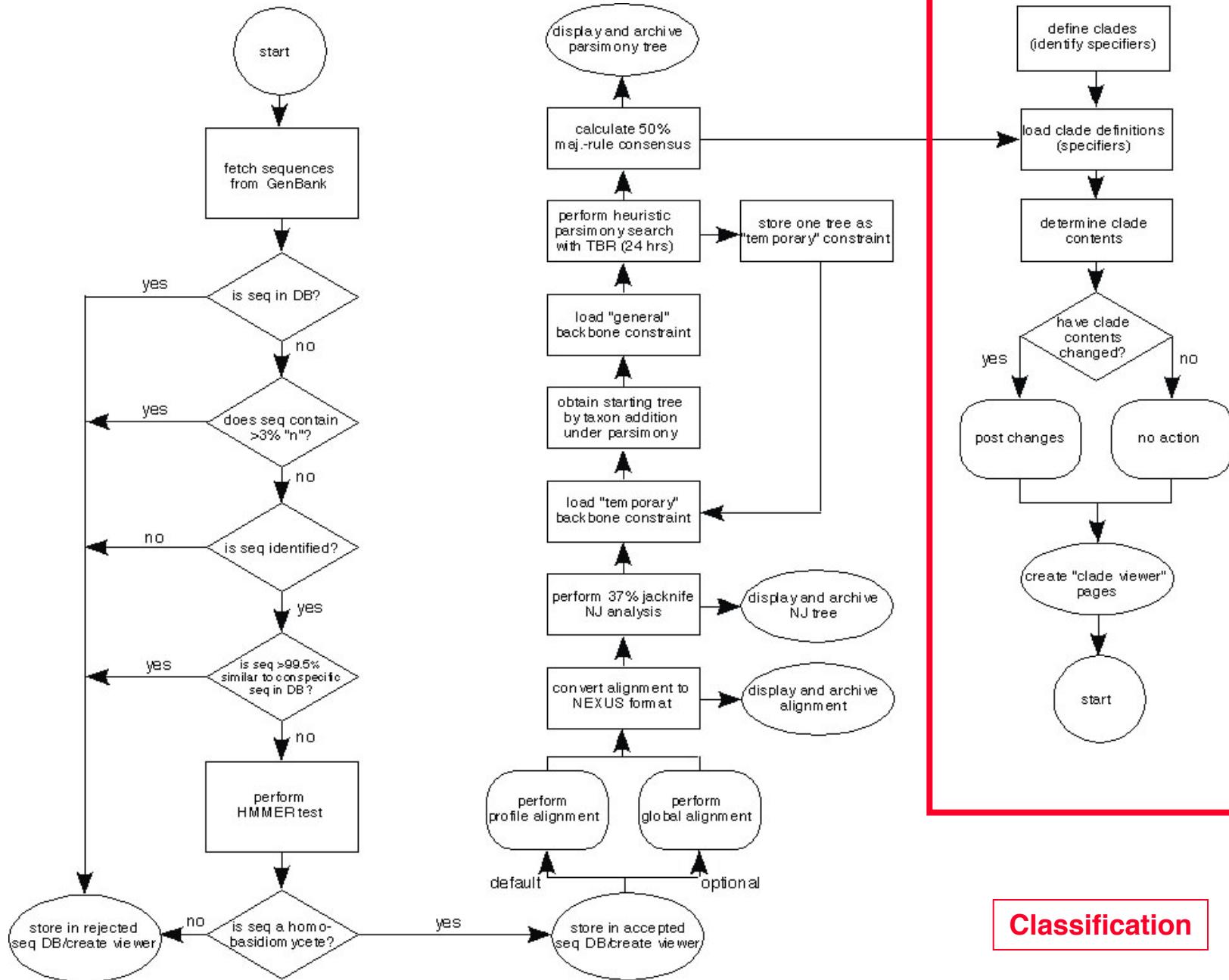
HRI = n; the H Rejection Index; n distinct Genbank sequences with the same species name have been tested and found to be over 99.5% identical to this sequence, and hence discarded.

Tree statistics (first tree)

Length: 61490 CI: 0.070467 RI: 0.842812  
RC: 0.059390 HI: 0.929533 GFIT: -356.940741

50% Majority-rule consensus of 100 trees

```
    /- Calvatia sp \(AF261482\) image? comments? ni(1)
100
   \|- Calvatia gigantea \(AF518603\) image? comments? ni(2)
100
   \|- Lycoperdon sp \(AF287873\) image? comments? ni(8)
100
   \|- Bovista sp \(AF261483\) image? comments? ni(3)
|
| /- Lycoperdon marginatum \(AF261485\) image? comments? ni(4)
-----100100
| | \|- Lycoperdon perlatum \(AJ406503\) image? comments? ni(5)
| | 100
| | \|- Lycoperdon perlatum \(AF518630\) image? comments? ni(6)
| | 100
| | \|- Lycoperdon coloratum \(AF261484\) image? comments? ni(7)
|
| /----- Stagnicola perplexa \(AF261509\) image? comments? ni(464)
|
| | \- Pluteus brunneoradiatus \(AF261567\) image? comments? ni(2622)
|
| | 100- Pluteus cervinus \(AF261570\) image? comments? ni(2623)
|
| | \|- Pluteus pallidus \(AF261569\) image? comments? ni(2624)
| | 100
| | \+- Pluteus pouzarianus \(AF261568\) image? comments? ni(2625)
```

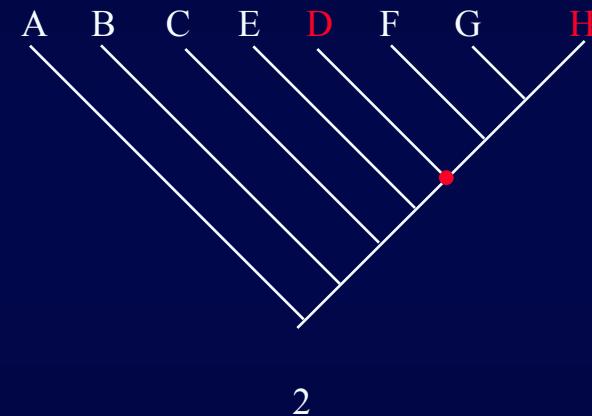
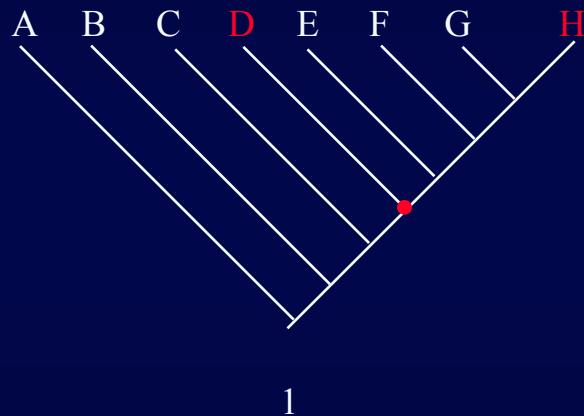


**Classification**

Parsing a node-based phylogenetic taxon definition:

“Taxon X is the least-inclusive clade that contains **D** and **H**”.

**D** and **H** are “specifiers”



Tree 1 (A(B(C(**D**(E(F(G,**HD**, E, F, G, **H**

Tree 2 (A(B(C(E(**D**(F(G,**HD**, F, G, **H**

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# The PhyloCode

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The *PhyloCode* is a formal set of rules governing phylogenetic nomenclature. It is designed to name the parts of the tree of life by explicit reference to phylogeny. The *PhyloCode* will go into operation in a few years, but the exact date has not yet been determined. It is designed so that it may be used concurrently with the existing codes based on rank-based nomenclature (*ICBN*, *ICZN*, etc.). We anticipate that many people whose research concerns phylogeny will find phylogenetic nomenclature advantageous.

**THE VERSION OF THE *PHYLOCODE* THAT IS POSTED HERE IS A DRAFT.** Some parts of it may change before the code is implemented. Comments are welcome and may be sent to [phylocode@www.ohiou.edu](mailto:phylocode@www.ohiou.edu).



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*Science* 23 March 2001:  
Vol. 291, no. 5512, pp. 2304 – 2307  
DOI: 10.1126/science.291.5512.2304

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## NEWS FOCUS

TAXONOMY:  
**Linnaeus's Last Stand?**

Elizabeth Pennisi

A fight has erupted over the best way to name and classify organisms in light of current understanding of evolution and biodiversity

These days the once-serene hallways of the world's natural history museums are anything but tranquil. A small but powerful contingent of systematists is challenging more than 2 centuries of taxonomic tradition by proposing a new system for naming and classifying life, one they say is more in line with the current understanding of evolution. Their brash proposal, which will be debated at a symposium in Washington, D.C., on 30 and 31 March, has raised the ire of the more conservative leaders in the field. The resulting controversy over the new naming system, known

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[Newsweek](#): "If more money doesn't buy more happiness, then the behavior of most Americans looks downright insane."

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Just as alien-like bacteria can "breathe" sulfur, some microbes can breathe poisonous PCB muck.

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04.28.2005

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In the South Pacific, the crew of a yacht saw new land form right beneath their boat.

## Pushing PhyloCode

**What if we decide to rename every living thing on Earth?**

by Joshua Foer, Photography by Dan Winters

Last summer on a warm Paris morning, a few dozen members of the International Society for Phylogenetic Nomenclature gathered at the National Museum of Natural History. The occasion was a talk by Jason Anderson, a professor of veterinary medicine at Western University of Health Sciences in Pomona, California. Anderson's talk—the fifth of the day—was about Lepospondyli, an extinct group of small four-limbed creatures that may be the ancestors of modern amphibians. To the uninitiated, it would have seemed deeply pedantic: The title of the talk was "Phylogenetic Taxonomy of Lepospondyli: Top-Down Versus Bottom-Up Approaches to Nomenclature in Uncertain Topologies." Yet Anderson's real subject was a revolution that could shake the foundations of how we describe life on Earth.

The 60 taxonomists from 11 countries who came to Paris for the society's inaugural meeting had a radical agenda: to overthrow the system of classifying species that has reigned for a quarter of a millennium and replace it with a new one called the PhyloCode. Proponents of the PhyloCode say the old system, originally developed by Swedish botanist Carl Linnaeus before Darwin

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## edit a clade

Name Public? 

### Creator Comments

The corticioid clade was recognized by K.-H. Larsson and colleagues (2002). All members of this small clade are resupinate. Members of this group include lignicolous taxa as well as the "red thread" pathogen of turf grasses, *Laetisaria fuciformis*, and certain lichenicolous taxa in *Marchandiomyces*. An analysis by Binder and Hibbett (2002) placed one member of the corticioid clade (*Dendrocorticium roseocarneum*) as the sister group of the rest of the homobasidiomycetes, but with weak bootstrap support. Other analyses (Vánky et al. 2002; Hibbett and Binder

## clade specifiers

Below you may add accession numbers as specifiers for your clade. Your clade will need at least two specifiers before it can be processed.

Specifier #	Species Name	Accession Number	
1	Dendrocorticium roseocarenum	AF393053	<a href="#">delete</a>
2	Punctularia strigosozonata	AF518642	<a href="#">delete</a>
3	Vulleminia comedens	AF518666	<a href="#">delete</a>
4	Cytidia salicina	U80648	<a href="#">delete</a>
5	Laetisaria fuciformis	AY293192	<a href="#">delete</a>
6	Galzinia incrustans	AF518617	<a href="#">delete</a>
7	Marchandiomyces corallinus	AY583331	<a href="#">delete</a>

Add accession number as new constraint:

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Name	created	number of specifiers	
Allsequences	2004-11-09	9	<a href="#">edit</a> <a href="#">delete</a>
Athelioid	2004-06-15	3	<a href="#">edit</a> <a href="#">delete</a>
Auriculariales1	2004-06-15	5	<a href="#">edit</a> <a href="#">delete</a>
Auriculariales2	2004-06-15	3	<a href="#">edit</a> <a href="#">delete</a>
Bolete	2004-06-15	17	<a href="#">edit</a> <a href="#">delete</a>
Cantharelloid	2004-06-15	6	<a href="#">edit</a> <a href="#">delete</a>
Corticoid	2004-06-15	7	<a href="#">edit</a> <a href="#">delete</a>
Crustoderma	2004-06-15	4	
Dacrymycetales	2004-06-15	10	<a href="#">edit</a> <a href="#">delete</a>
Euagarics	2004-06-15	20	<a href="#">edit</a> <a href="#">delete</a>
Gloeophyllum	2004-06-15	5	<a href="#">edit</a> <a href="#">delete</a>
Gomphoid-Phalloid	2004-06-15	10	<a href="#">edit</a> <a href="#">delete</a>
Hymenochaetoid	2004-06-15	13	<a href="#">edit</a> <a href="#">delete</a>
JanineTest	2004-11-04	3	
JanineTest2	2004-11-04	2	
JanineTest3	2004-11-04	2	
JanineTest4	2004-11-08	2	
Polyporoid	2004-06-15	20	<a href="#">edit</a> <a href="#">delete</a>
Russuloid	2004-06-15	16	<a href="#">edit</a> <a href="#">delete</a>
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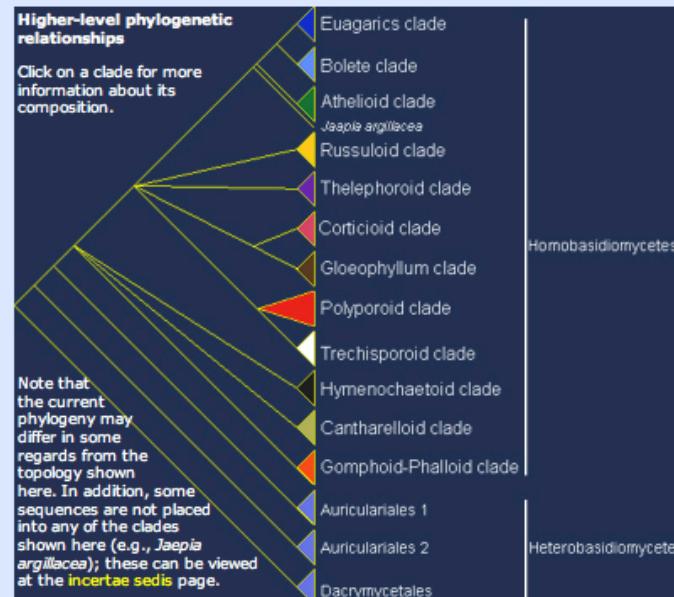
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name	accession number	date	name	accession number	date
					reason

**main clades**

Click on the clade names in the tree below to view the main clades, or view [all public clades](#).

**acknowledgements**

Development of *mor* is supported by the [National Science Foundation](#) through the "Assembling the Fungal Tree of Life (AFTOL)" project. We also

**disclaimer**

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# mor - clade details for *corticoid*

## clade administration

You are the creator of this clade. To regenerate this clade (based on the current consensus tree of all sequences) click the button below:

[generate clade](#)

## author comments

The corticioid clade was recognized by K.-H. Larsson and colleagues (2002). All members of this small clade are resupinate. Members of this group include lignicolous taxa as well as the "red thread" pathogen of turf grasses, *Laetisaria fuciformis*, and certain lichenicolous taxa in *Marchandiomyces*. An analysis by Binder and Hibbett (2002) placed one member of the corticioid clade (*Dendrocyrtium roseocarneum*) as the sister group of the rest of the homobasidiomycetes, but with weak bootstrap support. Other analyses (K.-H. Larsson et al., 2002; Hibbett and Binder 2002; Binder et al., in press) suggest that the corticioid clade is nested within the homobasidiomycetes, although its precise placement is not well resolved.

## results for clade:

- [Specifiers for clade](#)
- [Graphical Representation of clade](#)
- [Complete list of included species with literature links](#)
- [History of clade updates](#)
- [Comments for Corticioid clade](#)

## Files for this clade:

- [Aligned sequences and tree specification for this clade in nexus format](#)

## specifiers for the clade

Specifier #	Species Name	Accession Number
1	<i>Dendrocyrtium roseocarneum</i>	AF393053
2	<i>Punctularia strigosozonata</i>	AF518642
3	<i>Vuilleminia comedens</i>	AF518666
4	<i>Cyphella</i>	NC00510

### specifiers for the clade

Specifier #	Species Name	Accession Number
1	Dendrocorticium roseocarenum	AF393053
2	Punctularia strigosozonata	AF518642
3	Vuilleminia comedens	AF518666
4	Cytidia salicina	U80648
5	Laetisaria fuciformis	AY293192
6	Galzinia incrustans	AF518617
7	Marchandiomyces corallinus	AY583331

### graphical representation of tree



(The [nj](#) and [parsimony](#) links below will take you to the corresponding taxon in the main trees.)

### complete list of sequences in clade

Accession #	Species Name	Available Literature	Jump to Tree
AF393053	<a href="#">Dendrocorticium roseocarenum</a>	Literature	<a href="#">nj / parsimony</a>
AF506709	<a href="#">Corticium salmonicolor</a>	Literature	<a href="#">nj / parsimony</a>
AF518617	<a href="#">Galzinia incrustans</a>	Literature	<a href="#">nj / parsimony</a>
AF518642	<a href="#">Punctularia strigosozonata</a>	Literature	<a href="#">nj / parsimony</a>
AF518666	<a href="#">Vuilleminia comedens</a>	Literature	<a href="#">nj / parsimony</a>
AJ406531	<a href="#">Dendrocorticium polygonioides</a>	Literature	<a href="#">nj / parsimony</a>
AY293192	<a href="#">Laetisaria fuciformis</a>	Literature	<a href="#">nj / parsimony</a>

AF318000	<i>Vullemmina corredens</i>	Literature	nj / parsimony
AJ406531	<i>Dendrocorticium polygonoides</i>	Literature	nj / parsimony
AY293192	<i>Laetisaria fuciformis</i>	Literature	nj / parsimony
AY583330	<i>Marchandiomyces aurantiacus</i>	Literature	nj / parsimony
AY583331	<i>Marchandiomyces corallinus</i>	Literature	nj / parsimony
AY583332	<i>Marchandiomyces lignicola</i>	Literature	nj / parsimony
AY885164	<i>Waitea circinata</i>	Literature	nj / parsimony
U80648	<i>Cytidia salicina</i>	Literature	nj / parsimony

Total sequences included in clade: 12

#### clade update history

Accession #	Species	Status	Date
2006-11-08 12:46:47			
AY885164	<i>Waitea circinata</i>	added	2006-11-08 12:46:47

#### comments for corticioid clade

No comments posted.

#### add a comment (clade-8)

Name:

E-mail Address:

Comment:



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- I. Progress in phylogenetic reconstruction in Fungi/Agaricomycetes
- II. Progress in classification in Agaricomycetes
- III. Automated Phylogenetic Taxonomy in Agaricomycetes
- IV. Conclusions and future directions

## Conclusions

Current taxonomic and phylogenetic practices are **failing** in two key areas:

- ❖ Integration of available and emerging data
- ❖ Translation of trees into classifications

Core elements of taxonomy--tree building and translation of trees into classifications--can be automated. Phylogenetic definitions of taxa (ranked or unranked) are essential for this purpose.

But, expert user input is still required for:

- ❖ Curation of the backbone tree
- ❖ Clade definition

*mor* does not replace traditional taxonomy, produce monographs or keys

*mor* is most useful for mega-diverse, poorly-known groups, with large quantities of emerging data, including Fungi and all groups of “microbes”

## Future directions

### Enhancements:

Improvements to alignment and phylogenetic analysis routines

- ❖ RAxML, Parsimony Ratchet, TNT, DCM...

Incorporation of ITS data, including environmental sequences

- ❖ Will dramatically expand taxonomic content
- ❖ May enable sequence-based species discovery
- ❖ Will require automated supertree analyses
- ❖ Will require protocols to assign correspondence between ITS and nuc-lsu sequences

Expansion to all groups of Fungi ([AFTOL2](#))

Definition of many more clades

Integration with traditional taxonomy

- ❖ Possible because taxonomic hierarchies have an inherent tree structure
- ❖ Will require protocols for determining correspondence between sequences and names (difficult when type specimen has not been sequenced)
- ❖ Will allow automated construction of trees and classifications that approach the total knowledge of fungal diversity and phylogeny



Ryan Twomey\*, Pete Stein\*



J. P. Burke\*

Not shown: Moran Shonfeld\*, Mario Fonseca\*,

Thomas Heider\*, Daniel Menard\*

\*undergraduates



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