



One hundred and seventeen clades of euagarics

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Abstract

This study provides a first broad systematic treatment of the euagarics as they have recently emerged in phylogenetic systematics. The sample consists of 877 homobasidiomycete taxa and includes approximately one tenth (ca. 700 species) of the known number of species of gilled mushrooms that were traditionally classified in the order Agaricales. About 1000 nucleotide sequences at the 5' end of the nuclear large ribosomal subunit gene (nLSU) were produced for each taxon. Phylogenetic analyses of nucleotide sequence data employed unequally weighted parsimony and bootstrap methods. Clades revealed by the analyses support the recognition of eight major groups of homobasidiomycetes that cut across traditional lines of classification, in agreement with other recent phylogenetic studies. Gilled fungi comprise the majority of species in the euagarics clade. However, the recognition of a monophyletic euagarics results in the exclusion from the clade of several groups of gilled fungi that have been traditionally classified in the Agaricales and necessitates the inclusion of several clavarioid, poroid, secotioid, gasteroid, and reduced forms that were traditionally classified in other basidiomycete orders. A total of 117 monophyletic groups (clades) of euagarics can be recognized on the basis on nLSU phylogeny. Though many clades correspond to traditional taxonomic groups, many do not. Newly discovered phylogenetic affinities include for instance relationships of the true puffballs (Lycoperdales) with Agaricaceae, of *Panellus* and the poroid fungi *Dictyopanus* and *Favolaschia* with *Mycena*, and of the reduced fungus *Caripia* with *Gymnopus*. Several clades are best supported by ecological, biochemical, or trophic habits rather than by morphological similarities. © 2002 Elsevier Science (USA). All rights reserved.

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“As soon as it will be possible to delimit ‘mixed groups’ of this order, we shall see the Agaricales fall apart [and it will be] extremely difficult to define the

limits of the groups obtained” (Singer, 1951, pp. 127–128, footnote 51).

The rapid development of DNA sequencing techniques, phylogenetic theory, and bioinformatics has enabled systematists to envision a phylogenetic classification of all the branches of the tree of life. Notable examples include the recently published phylogenies of vascular plants (Chase et al., 1993; Qiu et al., 1999; Soltis et al., 1997, 1998, 1999; Savolainen et al., 2000)

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and the “Deep Green” land plant phylogeny study (summarized in Brown, 1999). In fungi, the pace of discovery about natural relationships has also been greatly accelerated by new evidence from molecular systematics, mostly using ribosomal DNA sequence data. Based on molecular evidence, it is now believed that the Chytridiomycetes, Zygomycetes, Glomales, Ascomycetes, and Basidiomycetes form a monophyletic group sister to the Animals, whereas the myxomycetes and oomycetes, sometimes considered to be Fungi, should be classified outside the fungal kingdom (Bruns et al., 1992; Bowman et al., 1992; Wainright et al., 1993; Spiegel et al., 1995; Lipscomb et al., 1998; Tehler et al., 2000; James et al., 2000).

rDNA phylogenies support monophyly of many traditional basidiomycete taxa, but have also demonstrated the existence of several clades composed of members of disparate traditional groups (Swann and Taylor, 1993, 1995; Hibbett et al., 1997; Begerow et al., 1997; Bruns et al., 1998). In the homobasidiomycetes, gilled mushrooms appear to have evolved multiple times from morphologically diverse ancestors (Hibbett et al., 1997; Thorn et al., 2000; Hibbett and Thorn, 2000), making the Agaricales polyphyletic. It has also been demonstrated that gasteromycetes (e.g., puffballs and sequestrate or secotioid fungi) have evolved several times from gilled or poroid ancestors (Baura et al., 1992; Bruns et al., 1989; Kretzer and Bruns, 1997; Hibbett et al., 1997; Peintner et al., 2001). These and other findings open the way to deconstruct artificial taxa (e.g., the Gasteromycetes) and redefine others in a phylogenetic context. In a preliminary outline for a major revision of the classification of the homobasidiomycetes based on phylogenetic principles, Hibbett and Thorn (2000) recognized eight major clades. The largest of these (with ca. 8400 known species), the euagarics clade, is the focus of this study.

The core group of the euagarics clade is composed of gilled mushrooms. It corresponds largely to the Agaricineae of Singer (1986), but also includes taxa that were traditionally classified in the Aphyllorphorales (e.g., *Clavaria*, *Typhula*, *Fistulina*, *Schizophyllum*, etc.) and several orders of Gasteromycetes (e.g., Hymenogastrales, Lycoperdales, Nidulariales). Phylogenetic relationships within the euagarics are still poorly known. However, an earlier molecular phylogenetic study that sampled rDNA sequences from 152 diverse agaricoid taxa showed that many families and genera of the Agaricales (e.g., Kühner, 1980; Singer, 1986) do not correspond to natural groups (Moncalvo et al., 2000).

In this study we expand our previous sampling (Moncalvo et al., 2000) for the nuclear large ribosomal subunit gene (nLSU; or 25–28S rDNA) to include about one tenth of the total number of known species of euagarics. The nLSU region has been shown to be

most useful to infer phylogenetic relationships in basidiomycetous fungi and allies at genus and family levels (Moncalvo et al., 2000; Fell et al., 2000; Weiss and Oberwinkler, 2001). Representatives of each of the eight major clades of homobasidiomycetes (as defined by Hibbett and Thorn, 2000) were also included in the analyses. The purpose of this large-scale analysis is to identify monophyletic groups (clades) of euagarics.

1. Materials and methods

1.1. Sampling of nucleotide sequences

We sampled molecular data for 877 taxa representing 126 of the 192 Agaricineae genera recognized in Singer (1986) and members of each clade of homobasidiomycetes as defined in Hibbett and Thorn (2000). Nucleotide sequences produced in this study consist of about 1000 bp located at the 5' end of the nuclear large ribosomal subunit gene, which encompass divergent domains D1–D3 (Michot et al., 1984). Sequences were produced in different laboratories using a variety of standard molecular methods. A total of 491 new sequences were produced for this study and were combined into a single data set with previously published sequences (Vilgalys and Sun, 1994; Chapela et al., 1994; Lutzoni, 1997; Binder et al., 1997; Pegler et al., 1998; Johnson and Vilgalys, 1998; Drehmel et al., 1999; Hopple and Vilgalys, 1999; Larsson and Larsson, 1998; Mitchell and Bresinsky, 1999; Thorn et al., 2000; Hwang and Kim, 2000; Moncalvo et al., 2000). The data matrix employed in Moncalvo et al. (2000) was used as a template for manual alignment of the other sequences. A small number of sequences were recoded to fit the template alignment (these sequences are labeled with an asterisk in the data matrix, which is available at http://www.biology.duke.edu/fungi/mycolab/agaricphylogeny_start.html). Recoding generally consisted in the removal of autapomorphic inserts located in otherwise highly conserved regions (these were phylogenetically uninformative, and some may also possibly be PCR-sequencing or editing errors). A sequence from the heterobasidiomycete *Auricularia polytricha* was used to root the homobasidiomycete phylogeny, as suggested in Hibbett et al. (1997).

Collection data and GenBank accession numbers of the material used in this study are given in the Appendix. Authority names of the species used in this work can be found in the CABI Bioscience Database of Fungal Name (<http://194.131.255.3/cabipages/Names/NAMES.ASP>). Although a single sequence per species was used in the final analyses, taxonomic and sequence accuracy for several taxa were evaluated by sampling multiple collections from different sources. These taxa are identified in the Appendix A.

1.2. Phylogenetic analyses

The 877 sequences sampled in this study were aligned in approximately 1000 positions. Hypervariable, indel-rich regions with problematic alignment were excluded from the analyses. Unambiguously aligned gaps were treated as missing data. Phylogenetic analyses were conducted in PAUP* (Swofford, 1998) with Power Macintosh computers using maximum-parsimony as the optimality criterion. Unequally weighted parsimony was employed to account for biases in base composition and nucleotide substitution rates, using a stepmatrix estimated from a smaller, but similar data set (Moncalvo et al., 2000). It has been shown that unequally weighted parsimony can recover correct phylogenies with fewer characters than required by equally weighted parsimony (Hillis et al., 1994).

Parsimony analyses of large data sets with high taxa/characters ratio are impractical, and most parsimonious trees are not likely to be found (Rice et al., 1997). Therefore, only suboptimal searches could be conducted in this study. We performed an initial analysis using 100 heuristic searches of random addition sequence with TBR branch-swapping, MULPARS on, and MAXTREES set to 10, saving all trees in each replicate (the other settings in PAUP* were as follows: multistate taxa were interpreted as uncertainty, the steepest descent option was not in effect, and branches were collapsed if minimum branch length was zero). The shortest trees found in the initial searches were used as starting trees for a recurrent search with TBR branch-swapping and MAXTREES set to 5000. The Templeton (1983) test was used to evaluate whether the trees found in the initial and final searches differed statistically. Branch robustness was evaluated using 100 bootstrap (BS) replicates (Felsenstein, 1985) with TBR branch-swapping and MULPARS off. Fast bootstrap searches have been shown to reveal robust branches in large-scale phylogenies within a reasonable amount of computation time (Moncalvo et al., 2000). Several other searches using smaller data sets were also conducted for empirical examination of the sensitivity of the tree topologies in relation to taxon sampling, to test the robustness of certain clades.

2. Results

2.1. Phylogenetic analyses

After removal of 123 redundant sequences (representing taxonomic duplicates) and regions with ambiguous nucleotide sequence alignment, the final data matrix was composed of 754 sequences and 781 characters: 211 characters were constant, 125 variable characters were parsimony uninformative, and 445 variable

characters were parsimony informative. The initial search produced 1000 trees ranging in size from 43988.7 to 44185.9. These trees were not significantly different from each other ($P > 0.05$, Templeton test). When the shortest trees from the initial search were used as starting trees for TBR branch-swapping with MAXTREES set to 5000, the analysis yielded 5000 equally parsimonious trees of score 43985.2 (consistency index = 0.1064, retention index = 0.6611). To facilitate the discussion, we will refer to the strict consensus tree of the 5000 equally parsimonious trees found in the final analysis as the most parsimonious trees found (MPF tree). The MPF tree was carefully compared with the bootstrap tree and with slightly longer (but statistically not significantly different) trees produced in the initial searches to identify branches that were consistently recovered by maximum-parsimony and branches that were not.

2.2. Phylogenetic relationships

Homobasidiomycetes clade. Both the MPF tree and the bootstrap tree support monophyly of six of the eight homobasidiomycetes clades recognized in Hibbett and Thorn (2000) and Binder and Hibbett (2002), i.e. (1) the euagarics clade, (2) the bolete clade, (3) the hymenochaetoid clade, (4) the theleporoid clade, (5) the gomphoid-phalloid clade, and (6) the cantharelloid clade. The russuloid clade is recovered in the bootstrap tree (58% BS), but not in the MPF tree, whereas the polyporoid clade is recovered only in the MPF tree. A possible sister group relationship between the euagarics and the bolete clades (< 40% BS) and a basal position of the cantharelloid clade (< 41% BS) are also supported. Within the polyporoid clade, reciprocal monophyly of the polyporaceae and corticioid clades is supported in both the MPF and the bootstrap trees. These results are summarized in Figs. 1 and 2.

Euagarics clade. Basal relationships within the euagarics clade were poorly resolved and several taxa remained as “orphans” (*incertae sedis*). Many branches present in the MPF tree collapsed in the bootstrap trees (Fig. 1). These branches were also generally not supported in trees slightly longer than the MPF tree (data not shown). Conversely, some branches recovered in the bootstrap tree were absent from the MPF tree but these branches generally had low statistical support (<40%; data not shown). For instance, the placement of the *Amanita* clade was inconsistent between different analyses: it is nested in a derived position of the Agaricaceae clade in the MPF tree and as sister group to *Limacella* in both the bootstrap tree and most of the suboptimal trees examined. To best summarize the results of the diverse analyses, we have edited the tree depicted in Fig. 2, as follows: branches that were not present in both the MPF tree and the bootstrap tree were collapsed, with the exception of some branches

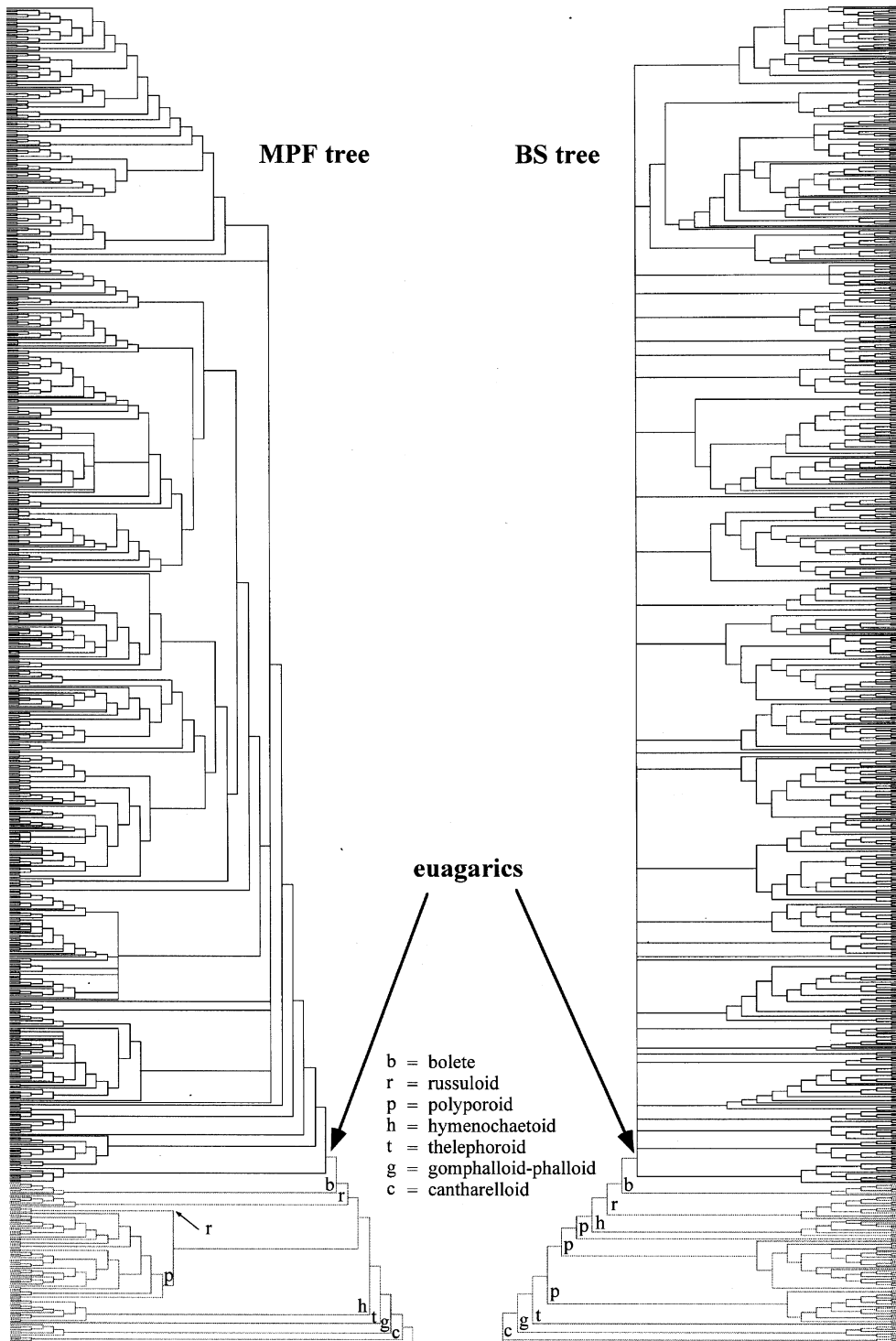


Fig. 1. Overall topologies of the strict consensus tree of 5000 equally most parsimonious trees found from heuristic searches (MPF tree) and the bootstrap 50% majority-rule consensus tree (BS tree). The placement in both trees of the eight major homobasidiomycetes groups (as defined in Hibbett and Thorn, 2000) is indicated by letters above corresponding branches. Trees are rooted with a sequence from the heterobasidiomycete *Auricularia polytricha*.

that were present in either tree (as indicated in Fig. 2) which are useful for discussion.

Within the euagarics, at least 117 clades revealed in the MPF tree (and generally also in slightly longer trees)

have a bootstrap support >40% (Fig. 2) and/or are consistent with traditional groups based on morphology. Smaller clades often correspond to traditional genera (or part of them in cases of polyphyletic genera),

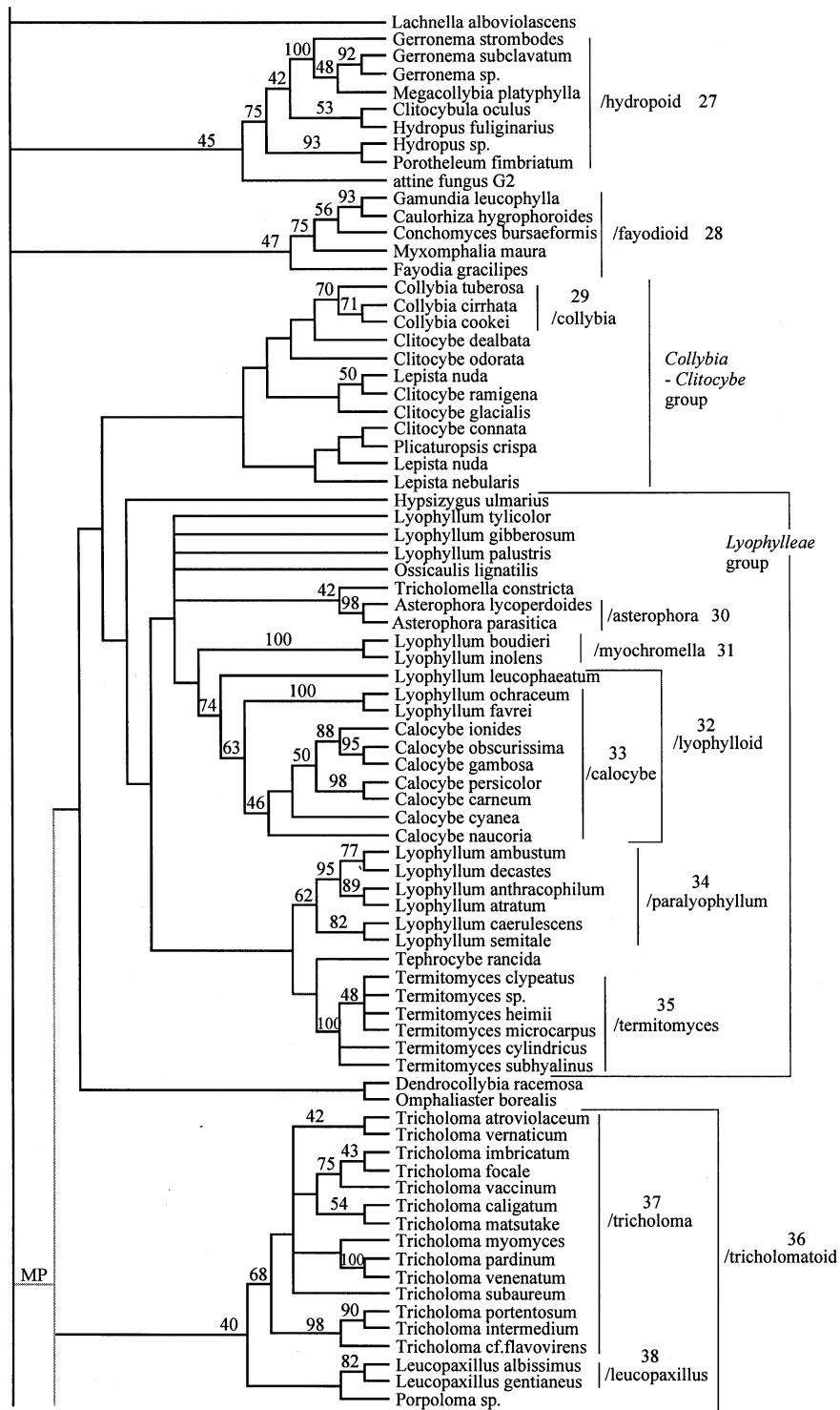


Fig. 2. (continued).

3. Discussion

This study is the first broad systematic treatment of the “euagarics” as they have recently emerged in phylogenetic systematics (summarized in Hibbett and Thorn, 2000). For the first time, this work presents the unambiguous

systematic placement among the euagarics of many Gasteromycetes (Table 1) and reduced forms (Table 2) and reveals natural relationships of several taxa for which taxonomic position has been controversial in the past. Some clades revealed in this work correspond in full or in part with taxonomic groups recognized in the last century

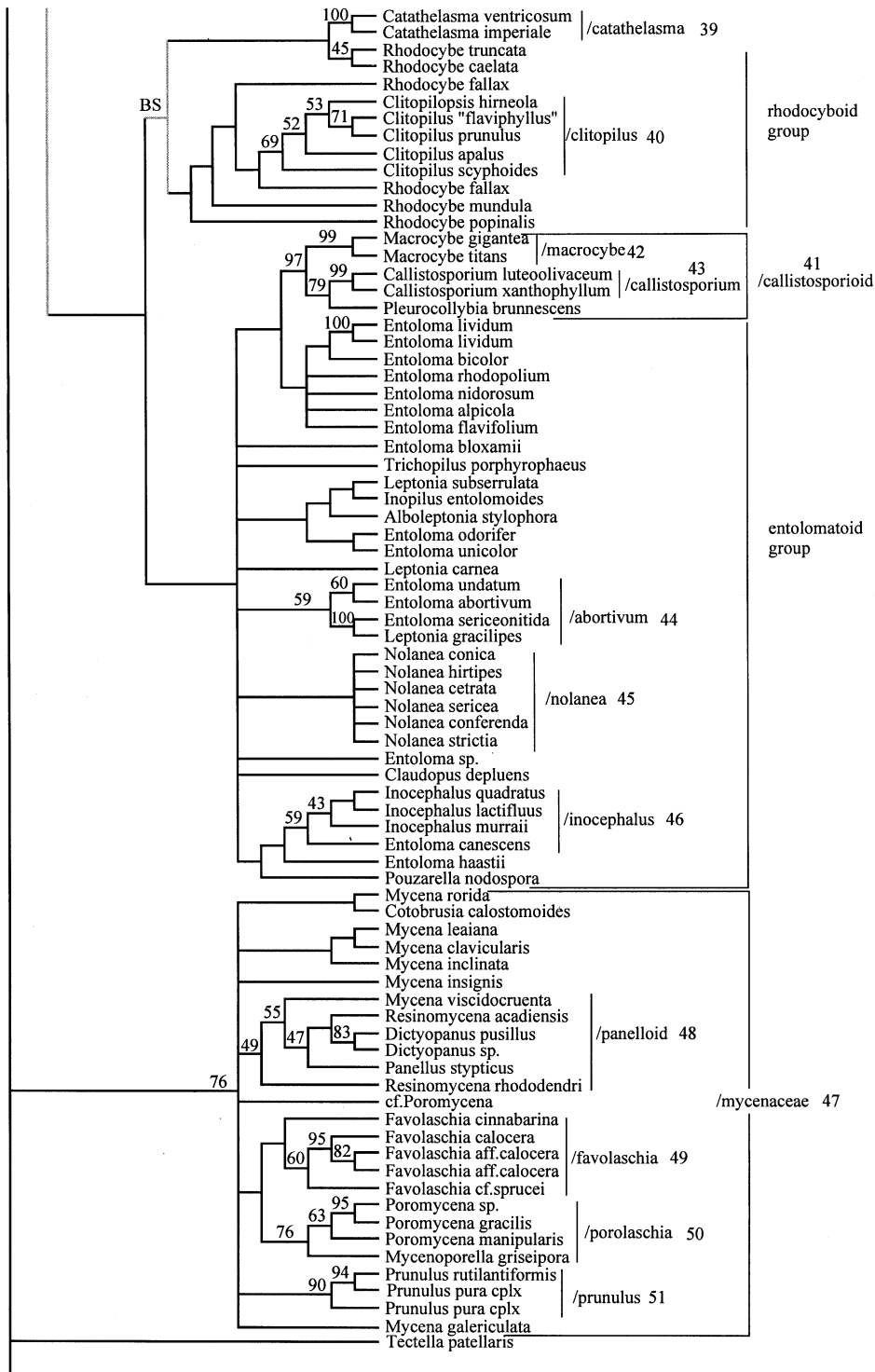


Fig. 2. (continued).

(e.g., in Kühner, 1980; Singer, 1986; Pegler, 1983; Bas et al., 1988; Jülich, 1981); however, many do not. The global taxonomic sampling of this study has allowed the identification of many distinct natural groups from which exemplar taxa could be selected to best represent both the euagarics and the homobasidiomycetes diversity in future

phylogenetic studies. Data from other genes are still necessary both to examine to what extent the nLSU phylogeny shown in Figs. 1 and 2 does reflect organismal phylogeny (Doyle, 1992; Maddison, 1997) and to better resolve phylogenetic relationships both among and within clades. By sampling about one tenth of the total number

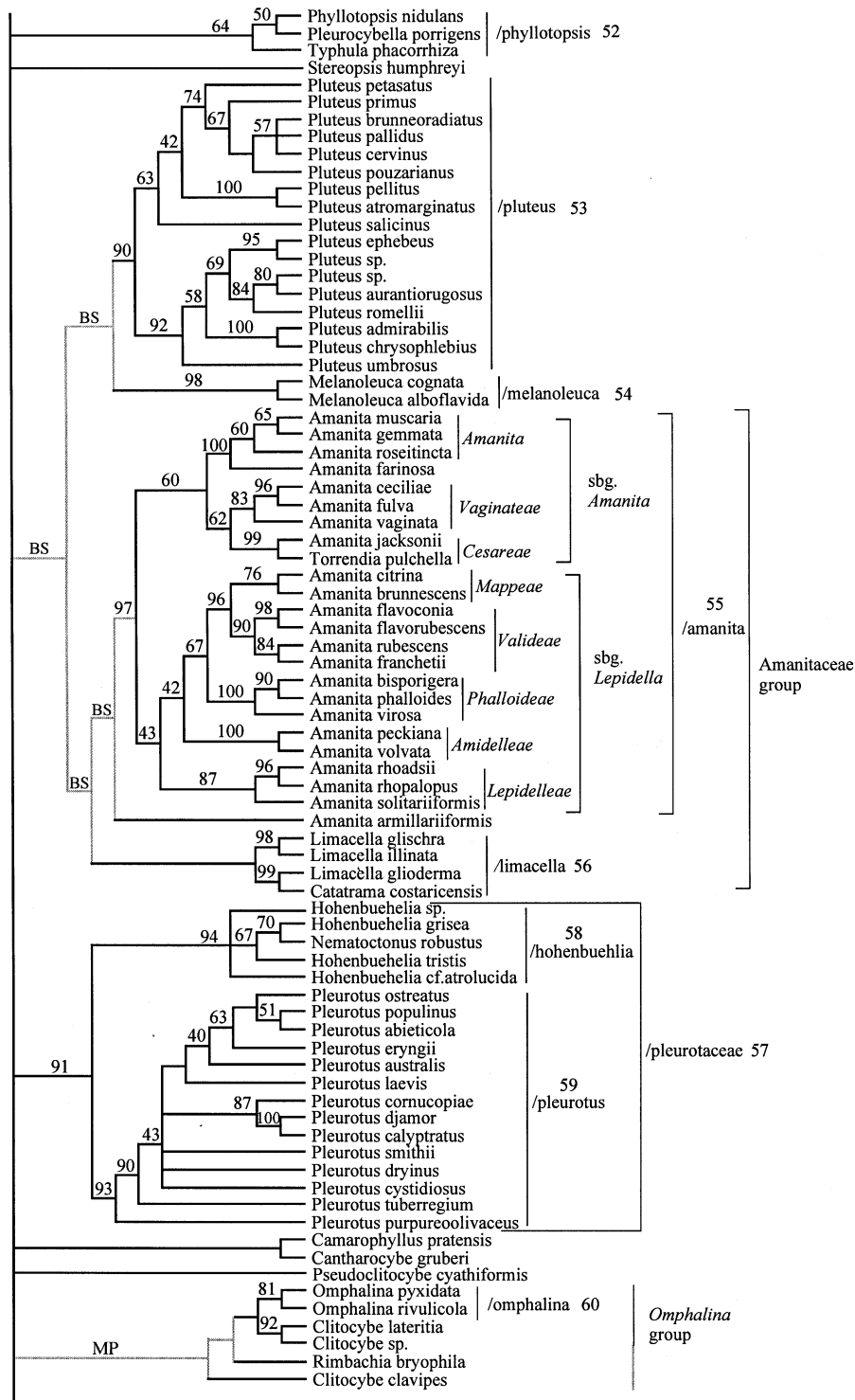


Fig. 2. (continued).

of known species of euagarics (Hawksworth et al., 1995; Hibbett and Thorn, 2000) and many other homobasidiomycetes taxa, this work should also significantly contribute to the development of a molecular database for the identification of new taxa and fungi from environmental samples (Bruns et al., 1998).

3.1. Large-scale phylogenies and higher clades of homobasidiomycetes

A common question in molecular systematics concerns optimization of the sampling ratio between the number of taxa vs characters and the number of char-

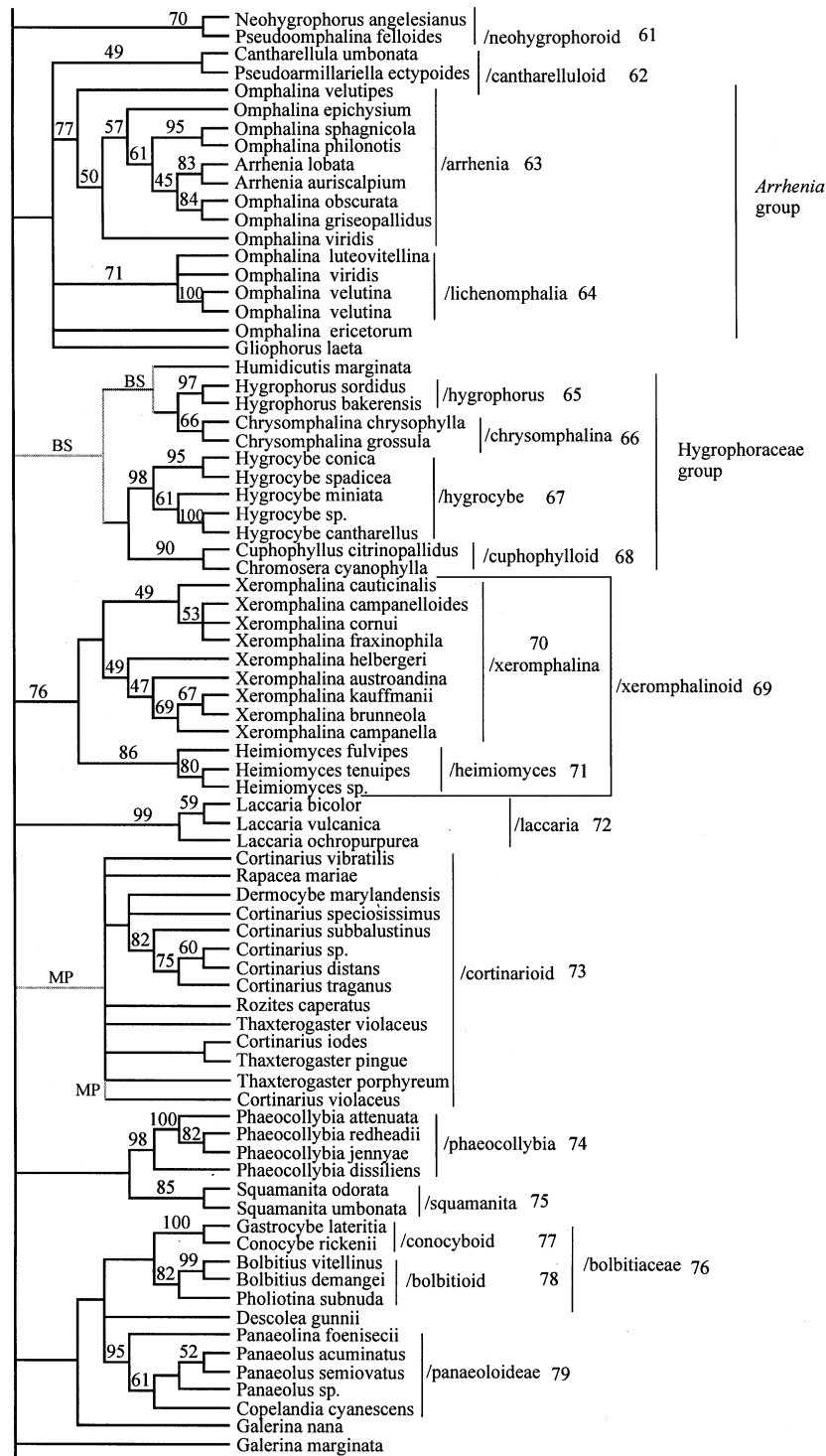


Fig. 2. (continued).

acters that are necessary to recover a correct phylogeny (Lecointre et al., 1994; Berbee et al., 2000). Both theoretical and empirical studies have demonstrated that increasing the taxa/characters ratio generally results in a decrease of statistical support in phylogenetic trees, especially at deeper nodes. However, it has also been shown that increasing taxon sampling increases accu-

racy of phylogenetic reconstruction (Hillis, 1996, 1998). In this study, the number of taxa sampled (877) was about twice higher than the number of parsimony-informative characters sampled (445). Therefore, high statistical support for deeper nodes was unlikely to be attainable. In contrast, the recent homobasidiomycetes phylogeny of Binder and Hibbett (2002) used a much

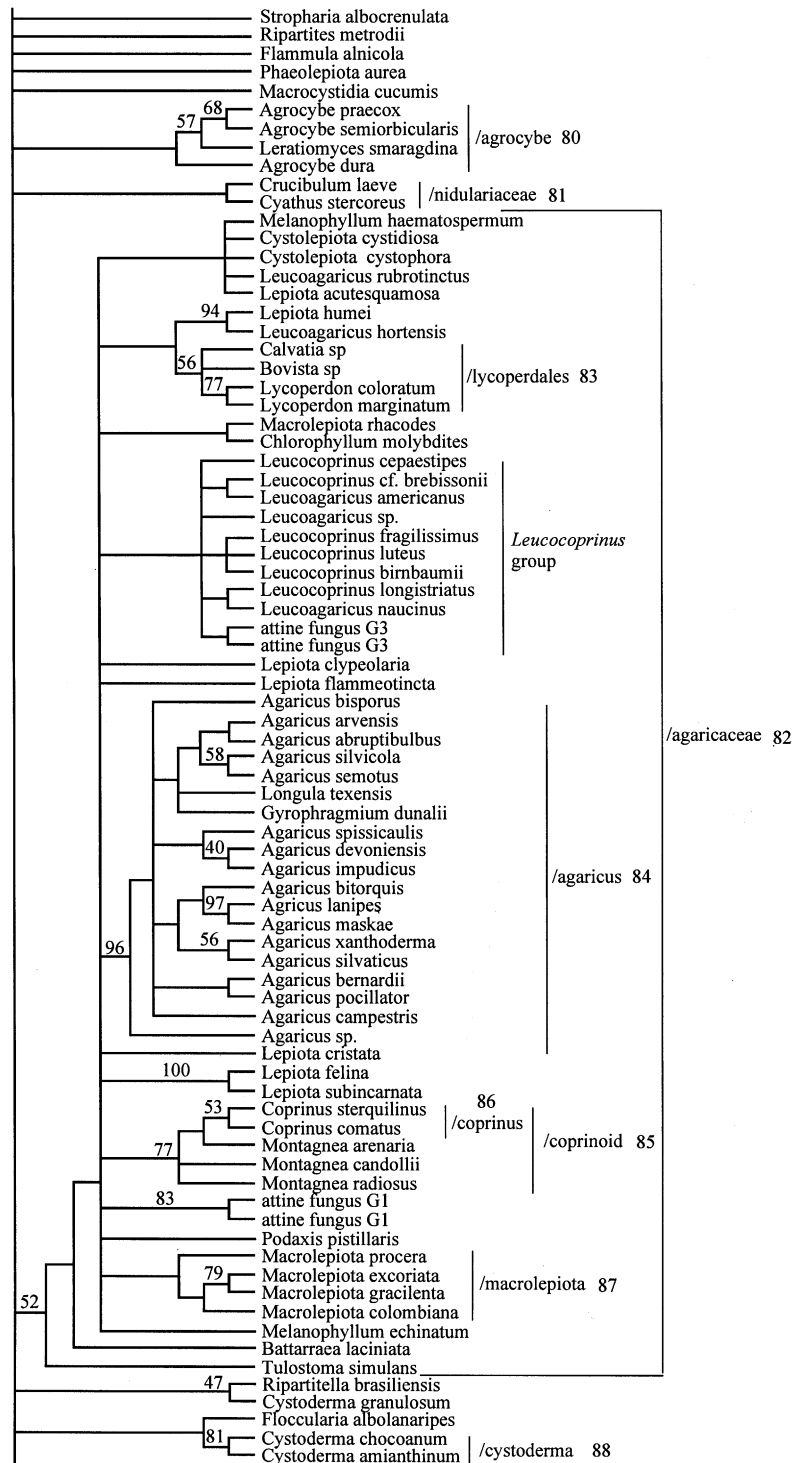


Fig. 2. (continued).

lower taxa/characters ratio, consisting of 83 taxa and 1114 parsimony-informative characters (produced from sequence data from four ribosomal genes). It is therefore helpful to compare results from these two studies.

Our analyses recover six of the eight homobasidiomycetes clades revealed in Binder and Hibbett (2002), but with lower bootstrap support. Both studies poorly

resolve basal relationships between the homobasidiomycetes lineages, but both suggest a more basal position of the cantharelloid, gomphales–phallales, and telephoroid clades. A major result in Binder and Hibbett (2002) was the strong bootstrap statistical support for a sister group relationship between the euagarics and the boletes (90% BS). This relationship

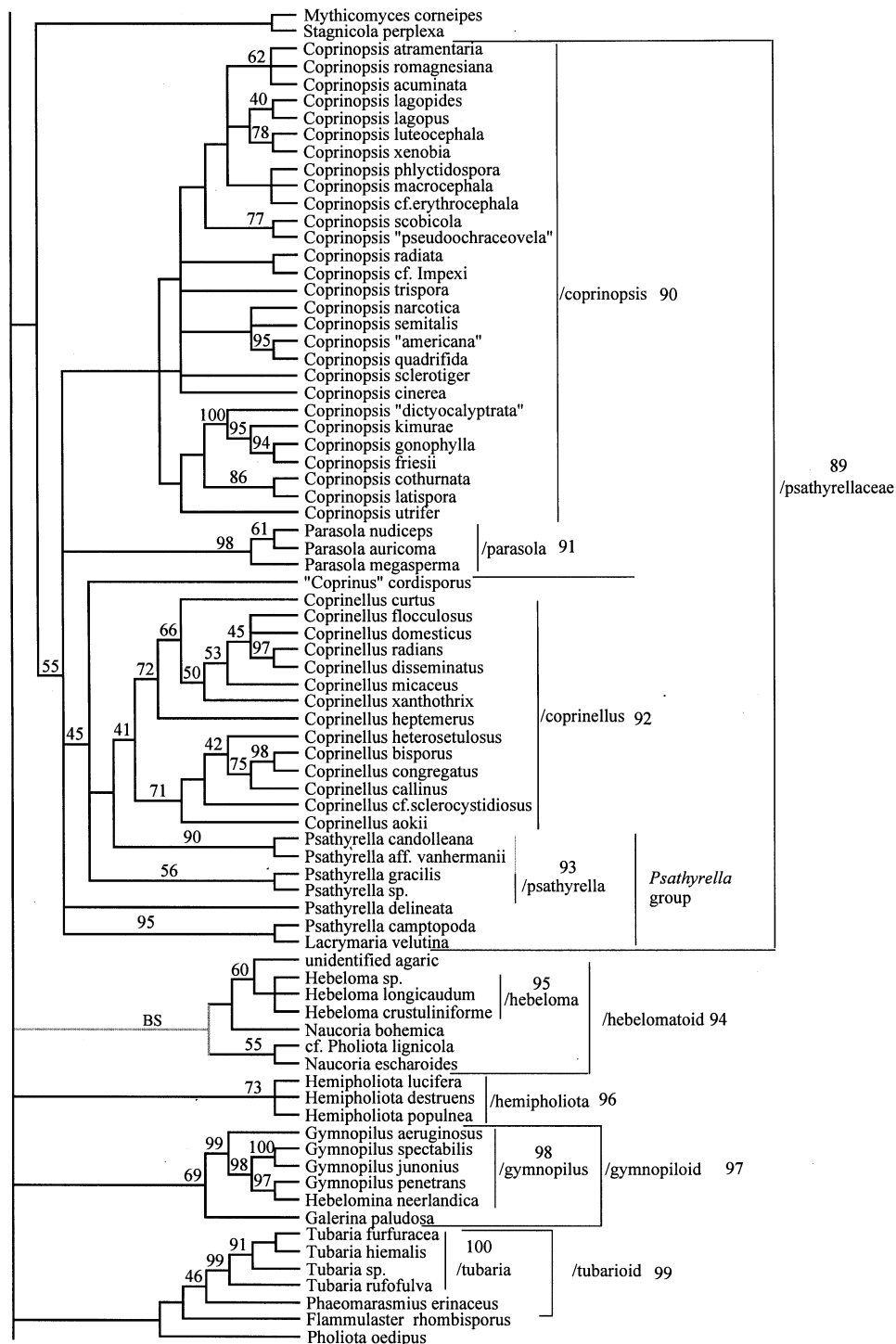


Fig. 2. (continued).

was only weakly suggested in earlier studies that sampled fewer characters (Hibbett et al., 1997; Fig. 5 in Moncalvo et al., 2000) and in the large-scale analysis presented here (< 40% BS; Fig. 2). Another significant result in Binder and Hibbett (2002) was the well-supported placement of *Hygrocybe* and *Humidicutis* (Hygrophoraceae) at the base of the euagarics (85% BS),

which in other studies were found either inside (Moncalvo et al., 2000) or outside (Bruns et al., 1998) the euagarics in phylogenetic reconstructions. Based on nLSU evidence, support for a monophyletic Hygrophoraceae is still lacking, and there is no indication of a possible placement of *Hygrophorus*/*Humidicutis* at the base of the euagarics clade.

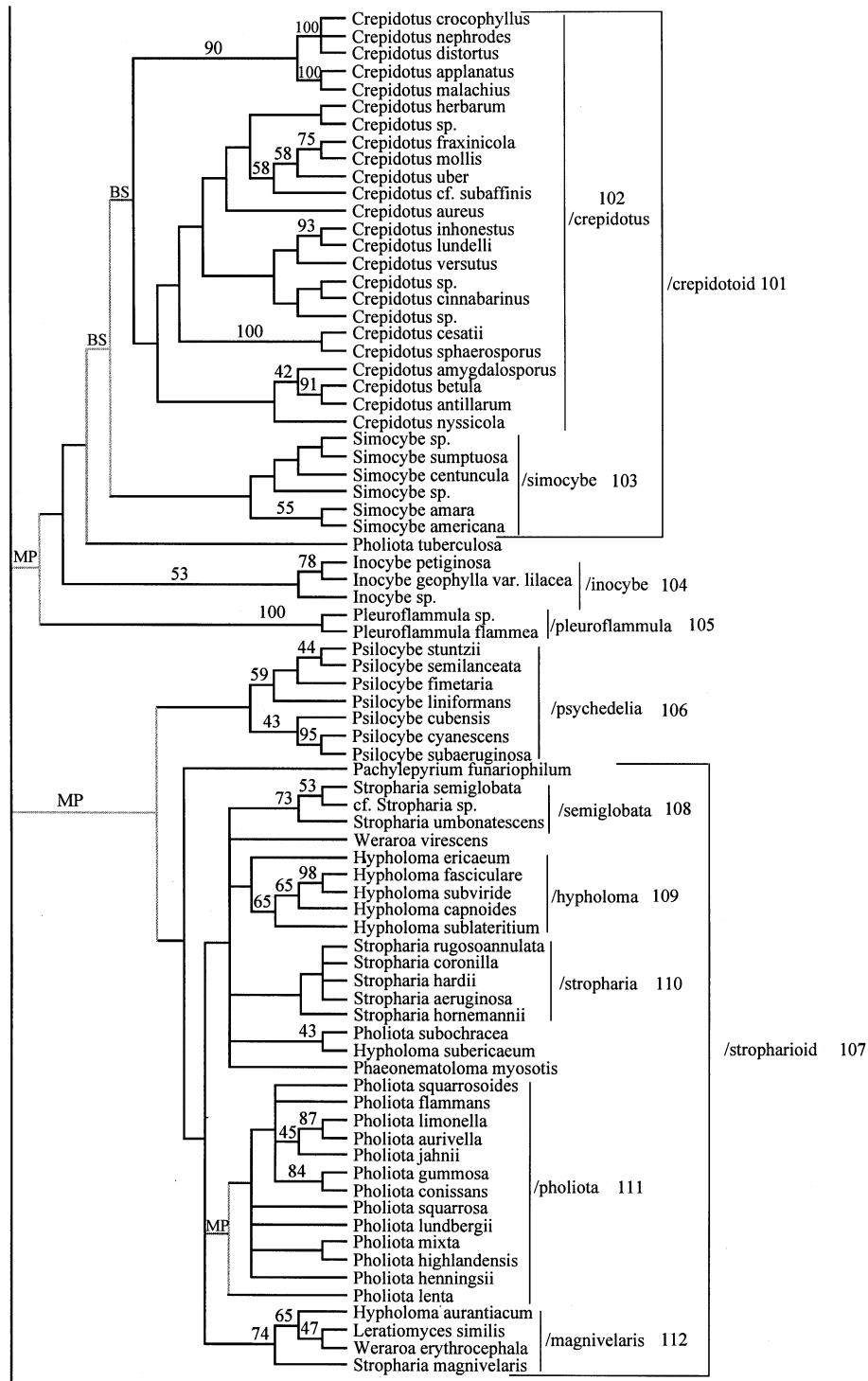


Fig. 2. (continued).

At least three conclusions with regard to homobasidiomycetes phylogeny can be drawn from these and earlier studies: (1) a dense taxon sampling using a limited number of phylogenetic characters—as conducted here—can still recover deeper nodes in the phylogeny and reveal many terminal clades with high bootstrap

statistical support; (2) a higher character/taxa ratio—as conducted in Binder and Hibbett (2002)—can boost bootstrap statistical support at deeper nodes, but not always; and (3) ribosomal genes alone are not sufficient to fully resolve natural relationships among higher clades of homobasidiomycetes.

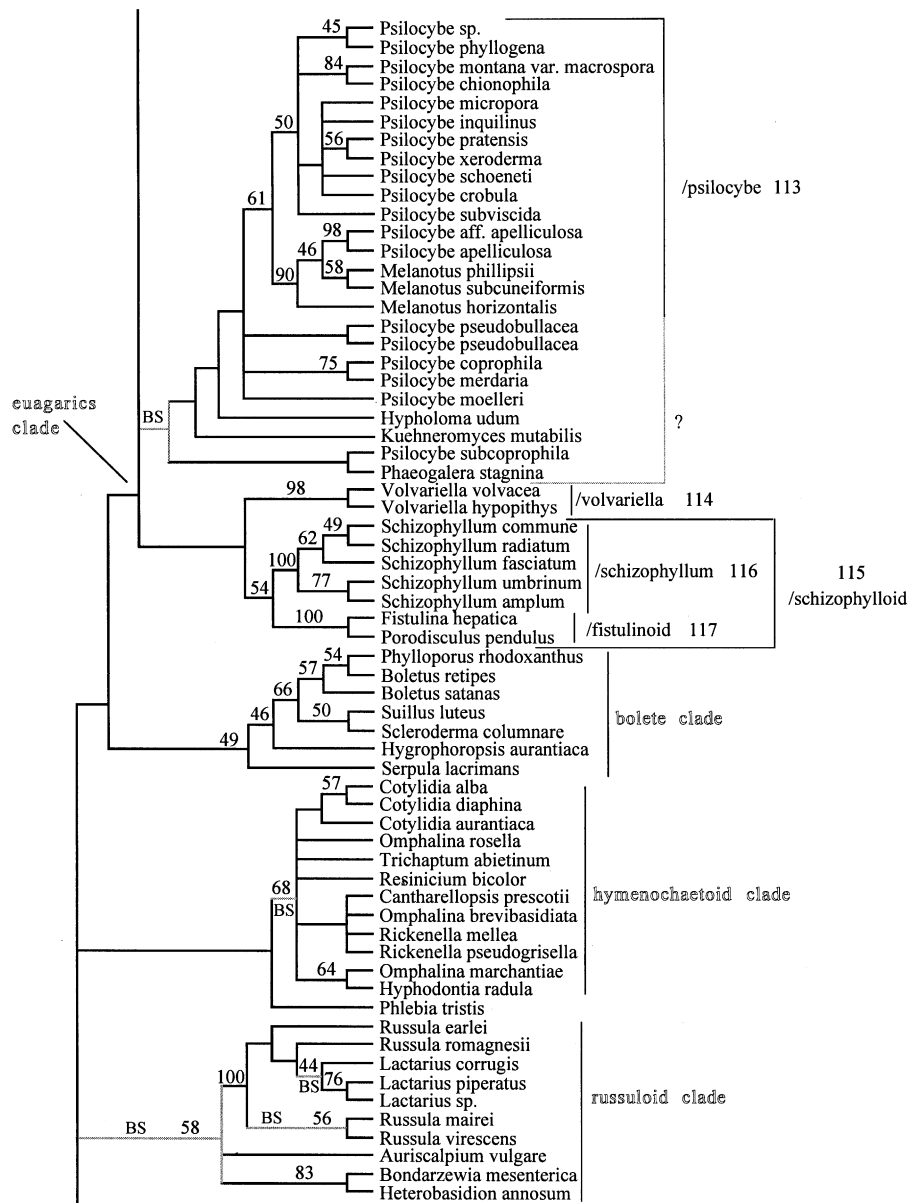


Fig. 2. (continued).

3.2. Morphological and ecological insights derived from the euagarics phylogeny

Gasteromycetization. The nesting of gasteromycetes taxa (e.g., puffballs and allies) among various groups of homobasidiomycetes was already indicated in earlier works (e.g., Baura et al., 1992; Bruns et al., 1989; Kretzer and Bruns, 1997; Hibbett et al., 1997; Peintner et al., 2001). However, as summarized in Table 1, this study is the first to unambiguously place several orders, families, and genera of gasteromycetes within the euagarics. Some of these relationships were already suggested by morphotaxonomists, including affinities between *Torrentia* and *Amanita*, between *Thaxterogaster* and *Cortinarius*, and between *Longula* and *Agaricus*

(Malencon, 1931, 1955; Savile, 1955, 1968; Heim, 1971; Smith, 1973; Bas, 1975; Thiers, 1984; Miller and Walting, 1987; Reijnders, 2000), but others were not. For instance, the placement of the true puffballs (*Lycoperdales*; clade 83 in Fig. 2) and *Tulostoma* and *Battarraea* in *agaricaceae* (clade 82) was not previously suspected by morphotaxonomists. However, it has already been shown that *Agaricus* mushrooms have many biochemical features in common with members of the *Lycoperdales* (see below). Gasteromycetization appears to have occurred more frequently in certain clades, in particular in *agaricaceae* and brown-spored groups.

Cyphelloid and reduced forms. Another syndrome of agaricoid fungi is the reduction of form or cyphellization, which has also occurred multiple times (Fig. 2 and

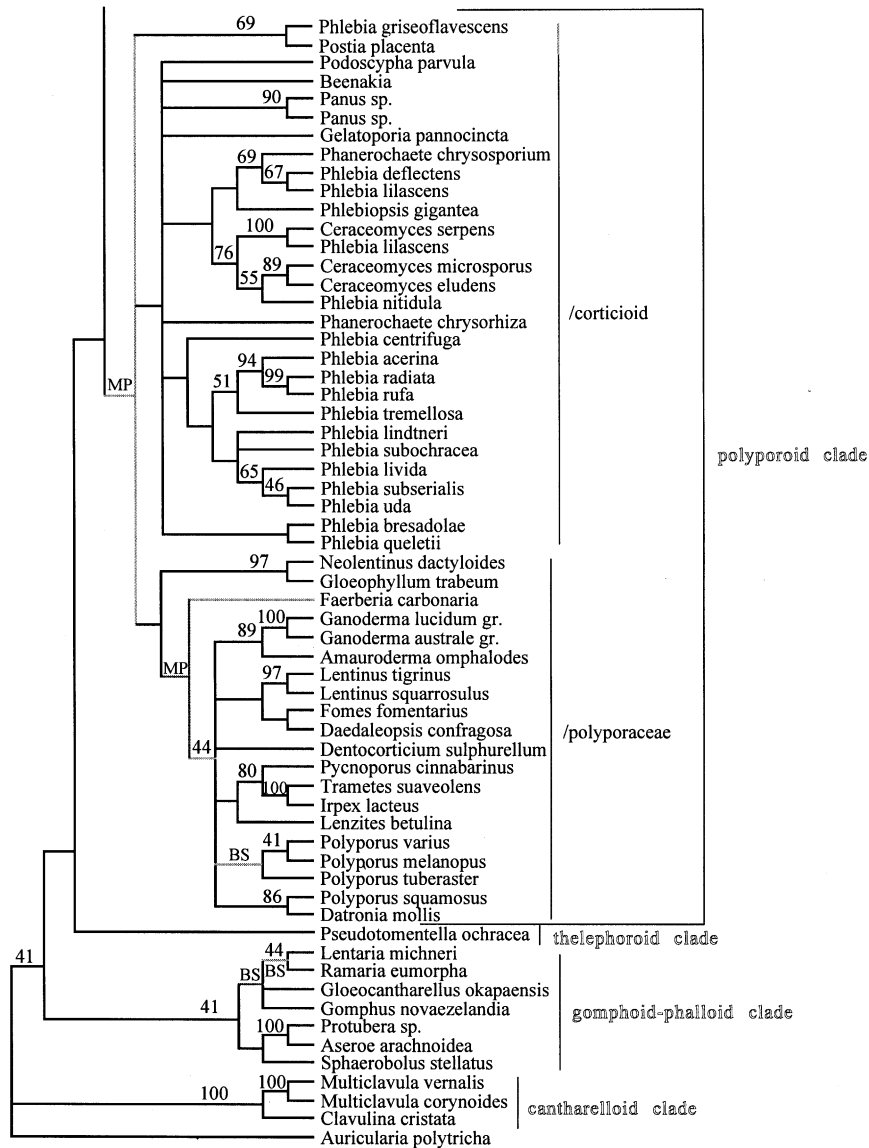


Fig. 2. (continued).

Table 2). For instance, we have identified *Caripia* as a reduced *Gymnopus* (in clade 5), *Stigmatolemma* as a cyphelloid *Resupinatus* (in clade 25), and *Porotheleum* as a cyphelloid member of /hydropoid (clade 27). Reduction and cyphellization are not unique to the euagarics, however, as shown by the placement of *Podoscypha* within the polyporoid clade and of *Cotylidia* within the hymenochaetoid clade.

Polyphyletic origin and instability of the lamellate hymenium. Results from this study support earlier findings that demonstrate the multiple origins of the lamellate hymenium within the basidiomycetes (Hibbett et al., 1997; Thorn et al., 2000; Moncalvo et al., 2000) and reveal for the first time that the hymenochaetoid clade might also include gilled fungi (*Rickenella*, *Cantharellopsis*, and *Omphalina* pro parte; Fig. 2). A lamellate hymenium is also known in the bolete

clade (*Phylloporus*; Bruns et al., 1998, Fig. 2), the polyporoid clade (*Lentinus*, *Neolentinus*, *Heliocybe*, and *Faerberia*; Hibbett and Vilgalys, 1993; Hibbett et al., 1997; Thorn et al., 2000, Fig. 2), the russuloid clade (Russulaceae; Hibbett et al., 1997; Moncalvo et al., 2000, Fig. 1), and the cantharelloid clade (Hibbett et al., 1997). Fig. 2 also indicates that transition from a gilled ancestor to a poroid hymenophore architecture has occurred at least three times within the euagarics: /fistulinoid (clade 117) in clade 115 and two times within /mycenaceae (clade 47). In the latter clade, *Dictyopanus* is in a derived position in /panelloid (clade 48), and /favolaschia and /porolaschia (clades 49 and 50) have probably both been derived from a common gilled ancestor.

Ectomycorrhizal vs saprophyte habit. Most clades revealed in this study are only composed of either

Table 1
Classification of gasteromycetoid taxa among the euagarics clade as indicated by molecular data

Gasteromycete taxa	Euagarics clade	References
Lycoperdales	/agaricaceae	This work
<i>Tulostoma</i>	/agaricaceae	This work
<i>Battarraea</i>	/agaricaceae	This work
<i>Podaxis</i>	/agaricaceae	Hopple and Vilgalys, 1999 This work
<i>Montagnea</i>	/agaricaceae/coprinus	This work
<i>Longula</i>	/agaricaceae/agaricus	This work
<i>Gyrophragmium</i>	/agaricaceae/agaricus	This work
<i>Trendia</i>	/amanita/caesareae	This work
<i>Thaxterogaster</i>	/cortinarioid	This work; Peintner et al., 2001
<i>Protoglossum</i>	/cortinarioid	Peintner et al., 2001
<i>Hymenogaster</i> pro parte	/cortinarioid	Peintner et al., 2001
<i>Quadrispora</i>	/cortinarioid	Peintner et al., 2001
<i>Setchelliogaster</i>	<i>Descolea</i> spp.	Martin and Raccabruna, 1999 Peintner et al., 2001
<i>Descomyces</i>	<i>Descolea</i> spp.	Peintner et al., 2001
<i>Hymenogaster</i> pro parte	/hebelomatoid	Peintner et al., 2001
<i>Gastrocybe</i>	/conocyboid	Hallen and Adams, 2000; this work
<i>Leratiomyces smaragdina</i>	/agrocyebe	This work
<i>Leratiomyces similis</i>	/stropharioid/ magnivelaris	Binder et al., 1997; This work
<i>Weraroa</i>	/stropharioid	Binder et al., 1997; this work
<i>Nia</i>	/schizophylloid	Binder et al., 2001
Nidulariales	unresolved position	Hibbett et al., 1997; this work

Table 2
Classification of reduced forms among the euagarics clade as indicated by molecular data

Reduced taxa	Euagarics clade	References
<i>Caripia</i>	/omphalotaceae/micromphale	This work
<i>Physalacria</i>	/physalacriaceae/physalacria	This work
<i>Lachnella</i>	euagarics	This work
<i>Gloeostereum</i>	/gloeostereae	This work
<i>Calyptella</i>	/hemimycena	This work
<i>Clavaria fusiformis</i>	? /tricholomopsis	This work
<i>Stigmatolemma</i>	/resupinatus	This work
<i>Porotheleum</i>	/hydropoid	This work
<i>Typhula phacorrhiza</i>	/phyllotopsis	This work
<i>Stereopsis humphreyi</i>	euagarics	This work
<i>Porodisculus</i>	/fistulinoid	This work
<i>Plicaturopsis</i>	euagarics; <i>Clitocybe</i> group?	This work

obligatory saprophytic or ectomycorrhizal taxa. For instance, all members of the larger /agaricaceae (clade 82), /mycenaceae (clade 47), /psathyrellaceae (clade 89), /stropharioid (clade 107), and the possibly monophyletic larger group that includes clades 1–26 are saprophytic. Clades composed only of putatively obligatorily ecto-

mycorrhizal taxa (Singer, 1986; Cléménçon, 1997; Norvell, 1998) include /tricholoma (clade 37), /amanita (clade 55), /hygrophorus (clade 65), /cortinarioid (clade 73), /phaeocollybia (clade 74), /hebeloma (clade 95), and /inocybe (clade 104). The existence of numerous, relatively large clades composed of either saprophytic or ectomycorrhizal fungi indicates that these two ecological habits have been relatively stable at least during the more recent radiation of the euagarics. Because of a lack of resolution of basal relationships, our phylogeny can neither fully support nor contradict results from a recent study by Hibbett et al. (2000) suggesting that the ancestor of the euagarics was ectomycorrhizal and that there have been multiple reversals to the saprophytic habit within this clade. However, there are several cases in our phylogeny that suggest that a transition from a saprophyte to a mycorrhizal habit is also possible. For instance, the putatively obligatorily ectomycorrhizal genus *Descolea* (Horak, 1971) is nested among saprophyte genera of clades 76–79, and both /amanita (clade 55) and /tricholoma (clade 37) also appear to be in derived, rather than basal, positions. All taxa in the *Lycophyllae* group are known to be saprophytes (Singer, 1986); therefore, the facultative mycorrhizal habit in *Lyophyllum shimeji* (Ohta, 1994; Agerer and Beenken, 1998), an ally to *L. decastes* (Moncalvo et al., 1993) in clade 34, is likely to be derived.

Relationships with other cryptogams. Transition from a free-living to an obligatory lichenized habit has occurred at least three times independently within the homobasidiomycetes, as indicated from both anatomical (Oberwinkler, 1984; Redhead and Kuyper, 1987) and molecular (Gargas et al., 1995) evidence. It occurred at least once in the euagarics, with the radiation of /lichenomphalia (clade 64) from within the *Arrhenia* group. A second group of lichenized basidiomycetes, *Dictyonema*, may also possibly belong to the euagarics (Gargas et al., 1995); however, this taxon has not been sampled here and its phylogenetic affinities still remain unclear. The third known lichenization event in the homobasidiomycetes has occurred in the cantharelloid clade (*Multi-clavula*), as indicated in both Fig. 2 and Hibbett et al. (1997). A suspected lichen parasite, *Gamundia leucophylla* (Bigelow, 1979), belongs to the euagarics and nests in a derived position in /fayodioid (clade 28).

The biology of the association between agaric fungi and bryophytes is still not well known, but has been documented in several studies (e.g., Redhead, 1981, 1984). The phylogeny depicted in Fig. 2 reveals that transition to a facultative or an obligatory bryophilous habit has occurred several times independently, apparently always from a saprophyte ancestor. For instance, *Lyophyllum palustris* (parasite on *Sphagnum*; Redhead, 1981) is derived from within the *Lyophylleae* group (which encompasses clades 30–35). *Galerina paludosa* (also a parasite on *Sphagnum*; Redhead, 1981, 1984) is

possibly sister group to /gymnopilus (clade 98). The bryophilous or peat-inhabiting species *Hypholoma ericaeum*, *Pholiota myosotis*, and *Pholiota henningsii* (Noordeloos, 1999) are all independently derived from within /stropharioid (clade 107). *Hypholoma uda* and *Phaeogalera stagnina* (Redhead, 1979) are independently derived from psilocybeoid taxa (at the base of clade 113 in Fig. 2). The fungus–bryophyte association does not appear to be evolutionarily very successful, judging from the limited radiation of bryophyte-associated clades. We observe only four instances of such radiations. (1) *Psilocybe montana* and *P. chionophila* are both often associated with mosses (Lamoure, 1977) and are uniquely derived from within /psilocybe (clade 113). (2) The /omphalina (clade 60) is composed of bryophilous species (*Omphalina pyxidata* and *O. rivulicola*; Lamoure, 1974) that are possibly a sister group of saprophytic species of *Clitocybe* and monophyletic with another bryophilous taxon, *Rimbachia* (Redhead, 1984) (*Omphalina* group in Fig. 2), hence representing one to two independent origins. (3) Nearly all members of /arrhenia (clade 63) are associated with bryophytes (Redhead, 1984). (4) All gilled taxa of /hymenochaete (*Omphalina rosella*, *O. brevbasisidita*, *O. marchantiae*, *Cantharellopsis prescottii*, *Rickenella mellea*, and *R. pseudogrisella*) are bryophilous as are some *Cotylidia* species (S.A. Redhead et al., unpublished), and all may have a single origin (Fig. 2).

Relationships with insects. Chapela et al. (1994) identified three groups of ant-associated fungi (labeled G1–G3). The phylogeny depicted in Fig. 2 indicates that two groups, G1 and G3, are independently derived from within /agaricaceae (clade 82), G3 being possibly monophyletic with members of the *Leucocoprinus* group (Johnson and Vilgalys, 1998). Group G2 is weakly supported (45% BS) as a sister group of /hydropoid (clade 27). The relatively large, obligatory termite-associate genus *Termitomyces* (Heim, 1977) forms clade 35 within the *Lyophylleae* group. The association between euagarics and insects has therefore developed independently several times. These associations appear to be evolutionarily stable, as indicated in our phylogeny by taxonomic radiation of the fungal partner and lack of observed reversal to a free-living habit.

Overall, it appears that ecology supports many natural groups of euagarics better than morphology. It is therefore striking to observe that all earlier major treatments of the Agaricales focused primarily on morphology and microanatomy (e.g., Kühner, 1980; Singer, 1986; Pegler, 1983; Bas et al., 1988; Jülich, 1981; Cléménçon, 1997), with limited attention being given to the taxonomic significance of physiological and ecological traits. This might explain why several taxonomic groups erected in the past are not natural. Redhead and Ginns (1985) were the first to introduce the idea of defining agaric genera based in part on their nutritional mode, but also supported by anatomical data, mating

strategies, and nuclear status. Based upon wood rot capability, mycorrhizal formation, and nematophagy these authors refined several generic concepts (e.g., in *Lentinula*, *Lentinus*, *Pleurotus*, and *Hypsizygus*) and created new genera (e.g. *Neolentinus* and *Ossicaulis*) that are also supported by the molecular data presented here. For instance, our results support the distinction between *Lentinula* (in clade 8), *Lentinus*, and *Neolentinus* (the latter two being in /polyporaceae in the polyporoid clade; Fig. 2), in agreement with Thorn et al. (2000), and the segregation of *Ossicaulis* and *Hypsizygus* (both in the *Lyophylleae* group) from *Pleurotus* (in clade 59).

3.3. Clades of euagarics

The reconstruction of a monophyletic euagarics results in the exclusion from that clade of several groups of gilled fungi traditionally classified in the Agaricales (e.g., the Russulaceae and *Rickenella*) and necessitates the inclusion in the clade of several clavarioid, poroid, secotioid, gasteroid, and reduced forms (Tables 1 and 2) that were traditionally classified in other orders of basidiomycetes or else controversially classified. Morphological, physiological, or ecological synapomorphies for the euagarics clade are unknown.

Below, we list and briefly discuss the 117 euagarics clades recognized in Fig. 2. Many clades are directly rooted to the euagarics node. When a clade is not directly rooted to the euagarics node, its containing clade(s) is (are) indicated. For instance, to indicate that clade 3 (/omphalotus) nests in clade 2 (/omphalotoid), which is contained in clade 1 (/omphalotaceae), the following notation is used: /omphalotaceae/omphalotoid/omphalotus. These notations are practical. In future studies, it might be possible to reconcile phylogenetic systematic and traditional taxonomy.

Clade 1 (87% BS): /omphalotaceae. Representative taxa: /lentinuloid and /omphalotoid. This clade includes several genera that were traditionally classified in various families or tribes of Agaricales (Singer, 1986) and one reduced form (*Caripia montagnei*) that was generally placed in the Stereales (Hawksworth et al., 1995). All /omphalotaceae are saprophytic or necrotrophic on wood or litter and have nonamyloid basidiospores that lack a germ pore.

Clade 2 (64% BS): /omphalotoid. Containing clade: /omphalotaceae. Representative taxa: *Anthracophyllum*, *Omphalotus*, *Lampteromyces*, and *Neonothopanus*. The MPF tree indicates that /omphalotoid is possibly paraphyletic, but monophyly is relatively well supported by bootstrapping (64% BS) and by equally weighted parsimony analysis (data not shown). All members of this clade are lignicolous and have basidiomata with decurrent lamellae or that lack a well-formed central stipe. In general, the context tissues of the basidiomata are poorly differentiated and cystidia are absent. *Anthraco-*

phyllum, *Lampteromyces*, and *Omphalotus* species have all been shown to contain atromentin, as do other unrelated taxa (e.g., several boletes; Gill and Steglich, 1987). *Lampteromyces* and *Omphalotus* species also contain illudins and are luminescent and toxic (Singer, 1986). *Neonothopanus nambi* (reported as *Pleurotus eugrammus*; see Petersen and Krisai-Greilhuber, 1999) has also been reported to be luminescent (Corner, 1981), but this report needs confirmation.

Clade 3 (75% BS): *lomphalotus*. Containing clades: /omphalotaceae/omphalotoid. Representative taxa: *Omphalotus* spp. and *Lampteromyces japonicus*. The tree topology in Fig. 2 suggests that these two generic names are possibly synonymous.

Clade 4 (88% BS): *lentinuloid*. Containing clade: /omphalotaceae. Representative taxa: *Caripia*, *Gymnopus*, *Lentinula*, *Marasmiellus* pro parte, *Marasmius* pro parte [excl. type], *Micromphale*, *Rhodocollybia*, and *Setulipes*. Close affinities between members of this clade have not been previously suggested. However, members of *lentinuloid* share several characteristics. They all have pale, nonamyloid spores with a thin or secondarily thickened wall and no germ pore. Hyphae in the basidiomata often thicken and subsequently impart revivability to the carpophores. Several lentinuloideae taxa produce glutamyl-peptides which are precursors of compounds with a polysulfide smell (Gmelin et al., 1976).

Clade 5 (76% BS): *lmicromphale*. Containing clades: /omphalotaceae/lentinuloid. Representative taxa: *Gymnopus* pro parte, *Caripia*, *Setulipes*, and *Micromphale*. The type species of both *Setulipes* (*S. androsaceus*) and *Micromphale* (*M. foetida*) nest in this clade. Our results support segregation of *Setulipes* from *Marasmius* (Antonin, 1987) since the type of the latter genus, *M. rotula*, is in Clade 21. *Micromphale* is polyphyletic since *M. perforans*, although also belonging to this clade, does not cluster with *M. foetida*. *Gymnopus* sensu Halling (1983) and Antonin et al. (1997) is also polyphyletic, with its members nesting in both this clade and clade 7. *Caripia*, which produces highly reduced basidiomata, is apparently derived from *Gymnopus* species, which has not been previously suspected.

Clade 6 (97% BS): *lscorodonius*. Containing clades: /omphalotaceae/lentinuloid. Representative taxa: *Marasmius scorodonius* and *Marasmiellus opacus*. A possible relationship between these two species has never been suspected before and is difficult to explain based on morphological or anatomical characters.

Clade 7 (58% BS): *lrhodocollybia*. Containing clades: /omphalotaceae/lentinuloid. Representative taxa: *Rhodocollybia maculata*, *Marasmiellus ramealis*, and *Gymnopus* pro parte. *Marasmiellus* is polyphyletic, with *M. ramealis* clustering in *lrhodocollybia* and *M. opacus* in *lscorodonius*. It still remains unknown where its type species, *M. juniperinus*, belongs.

Clade 8 (89% BS): *lentinula*. Containing clades: /omphalotaceae/lentinuloid. This clade corresponds to the genus *Lentinula* Earle.

Clade 9 (71% BS): *lphysalacriaceae*. Representative taxa: *lphysalacrioid* and *Armillaria*. Although *Physalacriaceae* was originally conceived for clavarioid fungi (Corner, 1970), inclusion of *Physalacria* in the Agaricales in the vicinity of *Gloiocephala* by Singer (1951, 1986) is congruent with nLSU phylogeny. *Physalacriaceae* is apparently the oldest available family name for clade 9; however, it still remains to be demonstrated if the type species of *Physalacria* *P. inflata* belongs to this clade.

Clade 10 (65% BS): *lphysalacrioid*. Containing clade: *lphysalacriaceae*. Representative taxa: *Cyptotrampa*, *Flammulina*, *Gloiocephala*, *Oudemansiella*, *Physalacria* aff. *orinocensis*, *Rhizomarasmius*, *Strobilurus*, *Xerula*, and *Oudemansiella*. Several morphological similarities exist among these taxa. Most members of *lphysalacrioid* have a hymeniform pileipellis composed of smooth and clavate cells that are often embedded in a gel, and several are characterized by the abundance of secretory, large, presumably multinucleate cystidia either in the hymenium, lamellar edges, pilear, and/or stipe surfaces. Strobilurins (antibiotics) are produced by *Oudemansiella*, *Strobilurus*, and *Xerula*, but also occur in other lineages (Anke, 1997). *lphysalacrioid* are primary colonizers of dead wood or leaves and do not demonstrate competitive ability of the mycelium to proliferate in soils and heavily colonized or rotten substrates. *Flammulina*, *Rhizomarasmius*, *Strobilurus*, and *Xerula* are also adapted for colonization of subterranean material. Our results also support the segregation of *Marasmius pyrrocephalus* into *Rhizomarasmius*, as proposed by Petersen (2000), and indicate polyphyly of *Gloiocephala* sensu Singer (1986).

Clade 11 (65% BS): *lphysalacria*. Containing clades: *lphysalacriaceae/physalacrioid*. Representative taxa: *Physalacria* aff. *orinocensis* and *Gloiocephala spathularia*. Both taxa are reduced agarics.

Clade 12 (95% BS): *loudemansiella*. Containing clades: *lphysalacriaceae/physalacrioid*. Representative taxa: *Oudemansiella* and *Xerula*. The two names are sometimes considered synonyms (Singer, 1986). A close relationship of these two taxa is confirmed here.

Clade 13 (97% BS): *larmillaria*. Containing clade: *lphysalacriaceae*. This clade corresponds to the genus *Armillaria* (Fr.) Staude.

Clade 14 (52% BS): *lgloeostereae*. Representative taxa: *Gloeostereum* and *Cheimonophyllum*. Both taxa are lignicolous, have fleshy and conchate pilei and inamyloid and white spores, and produce sequiterpene-based antibiotics (Takazawa and Kashino, 1991; Stadler et al., 1994). They have been classified together in the tribus *Gloeostereae* Ito & Imai (Parmasto, 1968) in the Stereales. *Cheimonophyllum*, but not *Gloeostereum*, was

placed in the Agaricales by Singer (1986). It was recently debated whether *Gloeostereum* is closer to *Phlebia* (/corticoid, in the polyporoid clade) or to the agarics (Petersen and Parmasto, 1993): this study indicates that it is phylogenetically related to the latter group.

Clade 15 (56% BS): /baeosporoid. Representative taxa *Baeospora* and *Hydropus scabripes*. Both taxa have amyloid spores, cheilocystidia, dermatocystidia, and sarcodimitic tissues (Redhead, 1987) and form masses of simple conidia in culture (S.A. Redhead, pers. observ.). *Hydropus scabripes* was originally described in *Mycena* but based on nLSU data it is phylogenetically unrelated to either the type of *Hydropus* (*H. fuliginarius*, in clade 27) or *Mycena* (*M. galericulata*, in clade 47). /Baeosporoid is difficult to separate morphologically from /hydropoid (clade 27).

Clade 16 (100% BS): /baeospora. Containing clade: /baeosporoid. This clade corresponds to the genus *Baeospora* Singer.

Clade 17 (48% BS): /marasmiaceae. Representative taxa: /tetrapyrgoid and /marasmioid. All members of this clade have pale spores and are saprophytes.

Clade 18 (100% BS): /tetrapyrgoid. Containing clade: /marasmiaceae. Representative taxa: *Campanella* and *Tetrapyrgos*. /Tetrapyrgoid is mostly composed of tropical species growing on woody debris. Basidiospores are hyaline, thin walled, smooth, inamyloid, and acyanophilous; the pilear trama is gelatinized (at least partly), inamyloid, with clamp connections; the epicutis has a well-developed or imperfect Rameales structure.

Clade 19 (87% BS): /tetrapyrgos. Containing clades: /marasmiaceae/tetrapyrgoid. This clade corresponds to the genus *Tetrapyrgos* Horak. It differs from its sister group, /campanella, by having tetradial basidiospores and a centrally or laterally attached pileus.

Clade 20 (61% BS): /campanella. Containing clades: /marasmiaceae/tetrapyrgoid. Representative taxa: *Campanella* spp. and an unidentified agaric. The two unidentified collections sampled from the mostly tropical genus *Campanella* exhibit the typical characters of the genus, as described in Singer (1986). The sister taxon (100% BS) of these two collections is another tropical, unidentified, centrally stipitate fungus with distant but well-developed gills connected with lower ridges or anastomoses (collection JMCR.34). Following Singer (1986), this collection would be classified as a *Marasmiellus* sensu lato, but its trama is similar to that of *Campanella* species.

Clade 21 (85% BS): /marasmioid. Containing clades: /marasmiaceae. Representative taxa: *Chaetocalathus*, *Crinipellis*, *Marasmius* (incl. *Hymenogloea*).

Clade 22 (71% BS): /crinipellis. Containing clades: /marasmiaceae/marasmioid. This clade corresponds to the genus *Crinipellis* Pat., which can be distinguished from other members of marasmioid by the presence of pseudoamyloid hairs on the pileus.

Clade 23 (100% BS): /hemimycena. Representative taxa: *Hemimycena* spp. and *Calyptella copula*. Our results support the segregation of *Hemimycena* Singer from the bulk species of *Mycena* (clade 47) and indicate that the cyphelloid fungus *Calyptella copula* is derived from *Hemimycena*.

Clade 24 (100% BS): /tricholomopsis. Representative species: *Tricholomopsis rutilans*, *Collybia aurea*, and *Marasmius rhyssophyllus*. A close relationship between the taxa of this clade has never been suspected before. All are saprophytic.

Clade 25 (82% BS): /resupinatus. Representative taxa: *Resupinatus* and *Stigmatolemma*. Molecular data are in agreement with Singer (1986), who indicated a close relationship between *Resupinatus* and the reduced fungus *Stigmatolemma*. Our results additionally show that *Stigmatolemma* is derived from within *Resupinatus*, making the latter paraphyletic.

Clade 26 (42% BS): /adonis. Representative species: *Mycena aurantiidisca*, *M. adonis*, and an unidentified marasmioid, bioluminescent fungus from the neotropics. These species differ from *Mycena* sensu stricto (clade 47) by having inamyloid spores.

Clade 27 (75% BS): /hydropoid. Representative taxa: *Hydropus* sensu stricto, *Gerronema* pro parte, *Megacollobia*, *Clitocybula*, and *Porotheleum fimbriatum*. The type of the genus *Hydropus*, *H. fuliginarius*, clusters here, whereas *H. scabripes* is in clade 16. Therefore, *Hydropus* sensu Singer (1986) is polyphyletic and should probably be restricted to species with amyloid spores, lacking pleurocystidia, and producing latex, as originally conceived by Kühner (1938). Our results also support Kühner's (1980) placement of *Megacollobia* and *Clitocybula* close to *Hydropus* and indicate that the reduced fungus *Porotheleum fimbriatum* is derived from *Hydropus* species. *Gerronema* sensu Singer (1986) is polyphyletic (Lutzoni, 1997; Moncalvo et al., 2000), but is monophyletic as restricted by Norvell et al. (1994).

Clade 28 (47% BS): /fayodiod. Representative taxa: *Gamundia leucophylla*, *Caulorhiza hygrophoroides*, *Conchomyces bursaeformis*, *Myxomphalia maura*, and *Fayodia gracilipes*. Although the presence of the latter taxon in this clade is moderately supported, there is good statistical support for the monophyly of the other taxa (75% BS). Singer (1986) already recognized affinities between some members of this clade as he considered *Gamundia* and *Myxomphalia* synonyms of *Fayodia*. However, a possible relationship between these taxa and *Caulorhiza* and *Conchomyces* has never been suspected before.

Possible monophyly of clades 29–46. The MPF and slightly longer trees and trees produced with reduced data sets (data not shown) all consistently indicate the possible monophyly of a larger clade that includes the *Collybia*–*Clitocybe* (pro parte) group, the *Lyophylleae* group, /tricholomatoid, and Entolomataceae. However,

there is presently no statistical support to formally recognize this putative clade. Natural relationships between *Tricholoma*, *Lyophylleae*, and Entolomataceae have been speculated by Cléménçon (1978, 1997) from similarities in the cell walls of basidiospores and the presence of siderophilous granules in the basidia in *Lyophylleae* and some Entolomataceae taxa.

The Collybia–Clitocybe group. In all our analyses /collybia, *Clitocybe* spp., *Lepista* spp., *Dendrocollybia*, *Omphaliaster*, and the reduced form *Plicaturopsis crispata* are recovered as a mono- or paraphyletic group attached to either the *Lyophylleae* group or /tricholomatoid.

Clade 29 (70% BS): /collybia. This clade includes the type species of *Collybia* Kummer, *C. tuberosa*. *Collybia* should be restricted to its type and closely related taxa (including *C. cirrhata* and *C. cookei*; Fig. 2; Hughes et al., 2001).

The Lyophylleae group. Both the MPF tree and the bootstrap tree produced in this study (Fig. 2) are in agreement with earlier studies that place *Termitomyces* in the *Lyophylleae* (Moncalvo et al., 2000; Hofstetter, 2000). Here we show that *Ossicaulis* may possibly also belong to this group (a sequence labeled *Ossicaulis* (GenBank Accession No. AF042625) that clustered with *Macrocybe* in Moncalvo et al. (2000) has been reidentified as a sequence of *Callistosporium*).

However, statistical support for recognizing a larger, monophyletic *Lyophylleae* is weak. In particular, the exact positions of *Ossicaulis* (the only taxon of this clade lacking siderophilous granules) and *Hypsizygus* (which clusters outside the group in several suboptimal trees examined) remain unclear. The clades recognized below in the *Lyophylleae* group are in agreement with results of a broader, multigene systematic study of the *Lyophylleae* (Hofstetter, 2000).

Clade 30 (98% BS): /asterophora. This clade belongs to the *Lyophylleae* group and corresponds to *Asterophora* Ditmar ex. Link (Redhead and Seifert, 2001). In Fig. 2, the sister group of *asterophora* is *Tricholomella constricta*.

Clade 31 (100% BS): /myochromella. This clade belongs to the *Lyophylleae* group. Representative species: *Lyophyllum boudieri* and *L. inolens*. /Myochromella is composed of small, collybioid species formerly classified in either *Lyophyllum* or *Tephrocybe*, which can be separated from these genera by having a striate and hygrophanous cap (Hofstetter, 2000).

Clade 32 (74% BS): /lyophylloid. This clade belongs to the *Lyophylleae* group. Representative taxa: *Lyophyllum leucophaeatum* (type of *Lyophyllum* Karst.), *L. favrei*, *L. ochraceum*, and *Calocybe* spp.

Clade 33 (63% BS): /calocybe. Containing clade: /lyophylloid, in the *Lyophylleae* group. This clade corresponds to the genus *Calocybe* sensu Singer (1986) with the exclusion of *C. constricta* and the inclusion of *Lyophyllum favrei* and *L. ochraceum*. Therefore, our results

support both the segregation of *C. constricta* in *Tricholomella* (Kalamees, 1992) and a close relationship between *L. favrei* and *L. ochraceum* with *Calocybe* species as indicated in Kühner and Romagnesi (1953).

Clade 34 (62% BS): /paralyophyllum. This clade belongs to the *Lyophylleae* group. Representative taxa: *Lyophyllum ambustum*, *L. decastes*, *L. semitale*, *L. caeruleuscens*, *L. anthracophilum*, and *L. atratum*.

Clade 35 (100% BS): /termitomyces. This clade belongs to the *Lyophylleae* group. It corresponds to the termite-associated genus *Termitomyces* Heim (including *Podabrella* Singer), which is sister group to the type species of *Tephrocybe* (*T. rancida*) in Fig. 2.

Clade 36 (40% BS): /tricholomatoid. Representative taxa: *Tricholoma*, *Leucopaxillus*, and *Porpoloma*. This clade is composed of fungi with a tricholomatoid habit and a white spore deposit. Our sampling of *Porpoloma* was restricted to a single, unidentified species; therefore a closer examination of this genus is still necessary to fully address its phylogenetic affinities. *Tricholoma* is held to be obligatorily ectomycorrhizal, whereas it is still controversial whether *Porpoloma* and *Leucopaxillus* are ectomycorrhizal or saprophytic (Singer, 1986; Cléménçon (1997; G. Thorn, pers. obs.)).

Clade 37 (68% BS): /tricholoma. Containing clade: /tricholomatoid. This clade corresponds to *Tricholoma* (Fr.) Staude, which is monophyletic only when restricted to ectomycorrhizal taxa (Pegler et al., 1998; Moncalvo et al., 2000).

Clade 38 (82% BS): /leucopaxillus. Containing clade: /tricholomatoid. This clade corresponds to the genus *Leucopaxillus* Boursier as described in Singer (1986). In Fig. 2, *Leucopaxillus* is phylogenetically distinct from *Tricholoma* in contrast to a previous report (Moncalvo et al., 2000) that used a mislabeled sequence (*L. albissimus* SAR1-2-90, GenBank Accession No. AF042592, excluded from this study). *Porpoloma* is weakly supported as sister group of /leucopaxillus (Fig. 2).

Clade 39 (100% BS): /catathelasma. This clade corresponds to *Catathelasma* Lovejoy, a taxon with problematic classification (Kühner, 1980; Singer, 1986). Analyses of nLSU sequence data consistently place it with two *Rhodocybe* species (Fig. 2), although without significant statistical support. We are not aware of any obvious anatomical, physiological, or ecological similarity between these taxa. Therefore, we consider /catathelasma to have unknown phylogenetic affinity in the euagarics.

Entolomataceae (rhodocybeoid and entolomatoid groups in Fig. 2). Modern agaricologists have agreed that the angular-pink-spored agarics (*Entoloma* sensu lato, *Clitopilus*, and *Rhodocybe*) represent a natural group, Entolomataceae (Singer, 1986; Kühner, 1980; Horak, 1980; Baroni, 1981; Baroni and Lodge, 1998). However, there is virtually no molecular support for a monophyletic Entolomataceae in our analyses, but this

hypothesis cannot be rejected from our data. In Fig. 2, the Entolomataceae segregates into two statistically weakly supported groups: a rhodocyboid group (*Rhodocybe* and *Clitopilus*) and an entolomatoid group (*Entoloma* sensu lato). Consistently nested in the former group is *Icatathelasma* (clade 39), and frequently nested within the latter group is *Icallistosporoid* (clade 41).

Clade 40 (69% BS): *Iclitopilus*. This clade belongs to the rhodocyboid group in the Entolomataceae. Representative taxa: *Clitopilus* spp. (including the type, *C. prunulus*) and *Clitopilopsis hirneola*.

Clade 41 (97% BS): *Icallistosporoid*. Representative taxa: *Callistosporium*, *Macrocybe*, and *Pleurocollybia*. This clade has not previously been recognized. All *Icallistosporoid* are saprophytic and have a white spore print and hyaline, smooth, and inamyloid spores. Pigments are intracellular when present, and the epicutis is composed of filamentous hyphae that are either repent (*Callistosporium* and *Pleurocollybia*) or strongly interwoven (*Macrocybe*).

Clade 42 (99% BS): *Imacrocybe*. Containing clade: *Icallistosporoid*. This clade corresponds to *Macrocybe* Pegler.

Clade 43 (99% BS): *Icallistosporium*. Containing clade: *Icallistosporoid*. This clade corresponds to *Callistosporium* Singer. Its sister group is *Pleurocollybia brunnescens* (79% BS).

Clade 44 (59% BS): *Iabortivum*. This clade belongs to the entolomatoid group in the Entolomataceae. Representative species: *Entoloma undatum*, *E. abortivum*, *E. sericeonitida*, and *Leptonia gracilipes*.

Clade 45 (< 40% BS): *Inolanea*. This clade belongs to the entolomatoid group in the Entolomataceae. It corresponds to the genus *Nolanea* (Fr.) Quélet, which may therefore warrant distinction from *Entoloma*.

Clade 46 (59% BS): *Iinocephalus*. This clade belongs to the entolomatoid group in the Entolomataceae. It corresponds to the genus *Inocephalus* (Noordeloos) P.D. Orton (Baroni and Hailing, 2000), with the inclusion of *Entoloma canescens*.

Clade 47 (76% BS): *Imycenaceae*. Representative taxa: *Mycena* pro parte (including its type, *M. galericulata*), *Resinomyцена*, *Panellus stypticus* (type of *Panellus*), *Dictyopanus*, *Favolaschia*, *Poromyцена* and *Filoboletus* spp., *Prunulus*, and *Mycenoporella griseipora*. Members of this clade of pale-spored agarics are morphologically very diverse, but amyloid spores are nearly always formed and dextrinoid tissues are frequent. Nearly all are primary colonizers of wood or leaves (they are rarely found on humus). *Mycena* sensu Singer (1986) is a polyphyletic genus with members clustering both in this clade and *Iadonis* (clade 26). It should therefore be restricted to taxa around its type species, *M. galericulata*. This study reveals a previously unsuspected relationship between *Mycena* and *Panellus* (including *Dictyopanus*). It also unambiguously places

the tropical, poroid genus *Favolaschia* among the euagarics.

Clade 48 (49% BS): *Ipanelloid*. Containing clade: *Imycenaceae*. Representative taxa: *Resinomyцена*, *Panellus*, *Dictyopanus*, and *Mycena viscidocruenta*. A natural relationship between these taxa has never been suspected before.

Clade 49 (<50% BS): *Ifavolaschia*. Containing clade: *Imycenaceae*. This clade corresponds to the genus *Favolaschia* (Pat.) Pat.

Clade 50 (76% BS): *Iporolaschia*. Containing clade: *Imycenaceae*. Representative taxa: *Poromyцена* and *Filoboletus* spp. and *Mycenoporella griseipora*. All members of this clade have a poroid hymenium. However, it also appears that additional sampling of *Imycenaceae* from the tropics breaks down generic distinction between poroid and gilled *Imycenoid* taxa (J. M. Moncalvo, pers. obs.).

Clade 51 (90% BS): *Iprunulus*. Containing clade: *Imycenaceae*. This clade corresponds to *Mycena* sect. *Purae* in Singer (1986), for which the generic name *Prunulus* S.F. Gray is available (Redhead et al., 2001).

Clade 52 (64% BS): *Iphylloopsis*. Representative taxa: *Phylloopsis nidulans*, *Pleurocybella porrigens*, and *Typhula phacorrhiza*. *Typhula* was previously classified in the Cantharellales (Hawksworth et al., 1995), but shown to be among the euagarics by Hibbett et al. (1997). Relationships between taxa of this clade have not been previously suspected, and we are still unaware of any morphological or anatomical character that could unify them.

Clade 53 (90% BS): *Ipluteus*. This clade corresponds to *Pluteus* Fries. At least two well-supported clades can be distinguished within this genus: one clade (63% BS) includes only species of section *Pluteus*, and one clade (92% BS) is composed of members of both sections *Hispidoderma* Fayod and *Celluloderma* Fayod.

Clade 54 (98% BS): *Imelanoleuca*. This clade corresponds to *Melanoleuca* Pat. This genus can be distinguished by several unique characters, but its relationships with other pale-spored agarics have never been clear (see for instance Singer, 1986). In our analyses, *Melanoleuca* clusters with *Pluteus* but with weak bootstrap support (<40%). The two taxa share similar stature and pigments, but differ significantly in their microanatomy.

Clade 55 (97% BS): *Iamanita*. This clade corresponds to the genus *Amanita* Persoon. Monophyly of the ectomycorrhizal *Amanita* taxa is strongly supported (97% BS); a potentially nonectomycorrhizal species, *A. armillariformes* (Miller et al., 1990), clusters weakly with *Iamanita* in the bootstrap tree and is not monophyletic with other *Amanita* species in the MPF tree. There is a good agreement between molecular and morphological data for infrageneric segregation of the genus, as shown in Fig. 2 and in earlier studies (Drehmel et al., 1999; Weiss et al., 1998; Moncalvo et al., 2000b). This work

shows for the first time that the secotioid fungus *Torrendia* belongs to *Amanita* subsection *Caesareae* (99% BS).

Clade 56 (<40% BS): *Limacella*. This clade corresponds to the genus *Limacella* Earle, with inclusion of the monotypic genus *Catatrampa* (Franco-Molano, 1991). The two taxa share a bilateral lamellar trama, viscid pilei, and amyloid spores. A sister group relationship between *Limacella* and *Amanita* (Amanitaceae) is weakly supported in our analyses.

Clade 57 (91% BS): *lpleurotaceae*. Representative taxa: *Hohenbuehlia* (including its *Nematoctonus* anamorphs) and *Pleurotus*. The production of nematode-trapping organs and nematophagy are synapomorphies for this clade (Moncalvo et al., 2000; Thorn et al., 2000).

Clade 58 (94% BS): *lhohenbuehlia*. Containing clade: *lpleurotaceae*. This clade corresponds to the genus *Hohenbuehlia* Schulzer, including its *Nematoctonus* anamorphs.

Clade 59 (93% BS): *lpleurotus*. Containing clade: *lpleurotaceae*. This clade corresponds to the genus *Pleurotus* (Fr.) Quélet.

Omphalinoid and hygrophoroid taxa. Most members of *Omphalina* sensu lato and *Hygrophoraceae* sensu singer (1986) are intermixed in clades 60–71 and related groups. These taxa have white, generally smooth, thin-walled spores; pilei are generally brightly pigmented and often have attached or decurrent gills. Many omphalinoid and hygrophoroid taxa form obligatory or facultative association with bryophytes or algae (see above). Three groups can be recognized in Fig. 2, although statistical support for each group remains weak: they are the *Omphalina* group, the *Arrhenia* group, and the *Hygrophoraceae* group.

Clade 60 (81% BS): *lomphalina*. Representative taxa: *Omphalina pyxidata* and *O. rivulicola*. Both species are bryophilous (Lamoure, 1974). The former species is the conserved type for *Omphalina* (Greuter et al., 2000). *Omphalina* s.s. Singer (1986) has already been shown to be polyphyletic (Lutzoni, 1997; Moncalvo et al., 2000). In Fig. 2, *Omphalina* species sensu lato are in this clade and in the *Arrhenia* group and the hymenochaetoid clade. Both the MPF tree and the bootstrap (<50% BS) tree indicate possible monophyly of *lomphalina* with another bryophyte-associate taxon, *Rimbachia* (see above), and saprophyte *Clitocybe* species (*Omphalina* group; Fig. 2).

Clade 61 (70% BS): *lneohygrophoroid*. Representative taxa: *Neohygrophorus angelesianus* and *Pseudoomphalina felloides*. A close phylogenetic relationship between these two species has never been suspected before.

The *Arrhenia* group (clades 61–64). Both the MPF tree and the bootstrap (<50% BS) tree indicate possible monophyly of the core *Omphalina* (excluding the type species) with members of *Arrhenia*, *Cantharellula*,

Pseudoarmillariella, and *Gliophorus*. Several taxa in this group are associated with cryptogams (see above).

Clade 62 (49% BS): *lcantharelluloid*. This clade belongs to the *Arrhenia* group. Representative taxa: *Cantharellula umbonata* and *Pseudoarmillariella ectypoides*. Affinities between these two taxa were already suspected by Singer, who first recognized *Pseudoarmillariella* as a subgenus of *Cantharellula* before recognizing it at the genus level (Singer, 1986).

Clade 63 (77% BS): *larrhenia*. This clade belongs to the *Arrhenia* group. Representative taxa: *Arrhenia auriscalpium*, *A. lobata*, *Omphalina velutipes*, *O. epichysium*, *O. sphagnicola*, *O. philonotis*, *O. obscurata*, *O. griseopallidus*, and *O. viridis*. Clade 63 includes the type species of *Arrhenia* (*A. auriscalpium*) and the core of the nonlichenized *Omphalina* species.

Clade 64 (71% BS): *llichenomphalia*. This clade belongs to the *Arrhenia* group. Representative taxa: *Omphalina luteovitellina*, *O. hudsoniana*, *O. velutina*, and *O. grisella*. Lichenization is a synapomorphy for this clade. Monophyly of *llichenomphalia* with another lichenized fungus, *O. ericetorum*, is not evident in Fig. 2 but has been shown in Lutzoni (1997). These species correspond to “*Phytoconis*” sensu Redhead and Kuyper (1987).

The *Hygrophoraceae* group (clades 65–68). There is virtually no support for a monophyletic *Hygrophoraceae* sensu auth. in our analyses, as indicated by the placement of *Gliophorus laeta* in the *Arrhenia* group and the possible relationship between *Hygrophorus* and *Chrysomphalina* species (the latter being traditionally classified in the *Tricholomataceae*). However, the core genera of *Hygrophoraceae* (*Hygrophorus*, *Hygrocybe*, *Humidicutis*, and *Cuphophyllus*) cluster together in the bootstrap tree (<40% BS).

Clade 65 (97% BS): *lhygrophorus*. This clade belongs to the *Hygrophoraceae* group and corresponds to *Hygrophorus* Fr., a genus that can be distinguished by its ectomycorrhizal habit and the presence of a bilateral lamellar trama.

Clade 66 (66% BS): *lchrysomphalina*. This clade belongs to the *Hygrophoraceae* group. It corresponds to the genus *Chrysomphalina* Cléménçon. Our results support the segregation of this genus from both *Gerronema* and *Omphalina*, as discussed in Cléménçon (1982).

Clade 67 (98% BS): *lhygrocybe*. This clade belongs to the *Hygrophoraceae* group. It corresponds to the genus *Hygrocybe* Kummer, including *Pseudohygrocybe* Kovalenko. In Fig. 2, species of *Pseudohygrocybe* (61% BS) are separated from *Hygrocybe* sensu stricto (95% BS).

Clade 68 (90% BS): *lcuphophylloid*. This clade belongs to the *Hygrophoraceae* group. Representative taxa: *Chromosera cyanophylla* and *Cuphophyllus citrinopallidus*. These two genera were segregated from *Hygrocybe* (see Redhead et al., 1995). Results of our analysis indicate that *lcuphophylloid* could be sister group of *hygrocybe*, but statistical support is weak (<40% BS).

Clade 69 (76% BS): *Xeromphalinoi*. Representative taxa: *Xeromphalina* and *Heimiomyces*. A close relationship between these two genera was already recognized by Singer (1986), who considered *Heimiomyces* a subgenus of *Xeromphalina*.

Clade 70 (<40% BS): *Xeromphalina*. Containing clade: *Xeromphalinoi*. This clade corresponds to *Xeromphalina* Kühner & Maire.

Clade 71 (86% BS): *Heimiomyces*. Containing clade: *Xeromphalinoi*. This clade corresponds to *Heimiomyces* Singer.

Clade 72 (99% BS): *Laccaria*. This clade corresponds to *Laccaria* Berk. & Br. Monophyly of this ectomycorrhizal, white-spored genus is strongly supported by nLSU sequence data. However, its phylogenetic relationships are still unresolved. In earlier studies (Bruns et al., 1998; Moncalvo et al., 2000) *Laccaria* clustered with brown-spored taxa, but statistical support was weak.

Clade 73 (0% BS): *Cortinarioid*. Representative taxa: *Cortinarius*, *Rozites*, *Dermocybe*, *Rapacea*, and the gasteromycete *Thaxterogaster*. All members of this clade are obligatorily ectomycorrhizal. Monophyly of these taxa is weakly supported in our analyses. However, the MPF tree is consistent with the multigene phylogeny of U. Peintner et al. (unpublished).

Clade 74 (98% BS): *Phaeocollybia*. This clade corresponds to *Phaeocollybia* Heim.

Clade 75 (85% BS): *Isquamanita*. This clade corresponds to *Squamanita* Imbach.

Clade 76 (<40% BS): *Bolbitiaceae*. Representative taxa: *Bolbitioid* and *Conocyboid*. This clade corresponds in part to the family Bolbitiaceae in Singer (1986). It is possibly a sister group of *Panaeoloideae*. *Descolea*, included in Bolbitiaceae by Singer (1986), nests in an unresolved position between *Bolbitiaceae* and *Panaeoloideae* (Fig. 2).

Clade 77 (100% BS): *Conocyboid*. Containing clade: *Bolbitiaceae*. Representative taxa: *Gastrocybe* and *Conocybe*. *Gastrocybe* appears to be a secotioid *Conocybe* (Hallen and Adams, 2000; Fig. 2).

Clade 78 (82% BS): *Bolbitioideae*. Containing clade: *Bolbitiaceae*. Representative taxa: *Bolbitius* and *Pholiotina subnuda*. *Pholiotina* has an overall morphology closer to *Conocybe* (Singer, 1986) but *P. subnuda* appears to be phylogenetically closer to *Bolbitius*.

Clade 79 (95% BS): *Panaeoloideae*. Representative taxa: *Panaeolina*, *Panaeolus*, and *Copelandia*. This clade corresponds to *Panaeoloideae* Singer (1986) in *Coprinaceae* (= *Psathyrellaceae*; Redhead et al., 2001), but our results indicate that it is possibly closer to *Bolbitiaceae*.

Clade 80 (<40% BS): *Agrocybe*. This clade corresponds to the genus *Agrocybe* Fayod with the inclusion of the gasteromycete *Leratiomyces smaragdina*. *Leratiomyces* appears to be polyphyletic, with *L. similis* nesting in clade 113.

Clade 81 (<40% BS): *Nidulariaceae*. Representative taxa: *Crucibulum laeve* and *Cyathus stercoreus*. The placement of the bird nest fungi (Nidulariales) in the euagarics was first demonstrated by Hibbett et al. (1997) and is supported in this study. However, its exact position among the euagarics remains unknown.

Clade 82 (52% BS): *Lagaricaceae*. Representative taxa: *Lycoperdales*, *Lagaricus*, *Leucocoprinus*, *Coprinoid*, *Macrolepiota*, *Podaxis*, *Lepiota*, *Leucoagaricus*, *Melanophyllum*, *Chlorophyllum*, *Cystolepiota*, *Battarraea*, *Tulostoma*, and two groups of attine fungi. This clade represents a morphologically highly diverse assemblage of taxa, including traditional orders and genera of gasteromycetes and hymenomycetes. However, virtually all the taxa in the clade occur on the soil (none are primary wood decay organisms and none are known to be ectomycorrhizal) and fairy ring formation is a common feature in the Agaricaceae. The true puffballs (*Lycoperdales*) have many biochemical features in common with *Agaricus*, such as formation of urea, concentration of silver, mercury, selenium, and arsenic, and biosynthesis of methylmercury and arsenobetaine (Byrne et al., 1979; Slejkovec et al., 1997; Tjakko Stijve, pers. comm. to H.C.).

Clade 83 (56% BS): *Lycoperdales*. Containing clade: *Agaricaceae*. This clade corresponds to the traditional gasteromycete order *Lycoperdales*.

Clade 84 (96% BS): *Lagaricus*. Containing clade: *Agaricaceae*. This clade corresponds to *Agaricus* Fries, with the inclusion of the secotioid genera *Gyrophragmium* and *Longula*.

Clade 85 (77% BS): *Coprinoid*. Containing clade: *Agaricaceae*. Representative taxa: *Coprinus* and *Montagnea*. A close affinity between *Coprinus sensu stricto* (Redhead et al., 2001) and the secotioid genus *Montagnea* is established here.

Clade 86 (53% BS): *Coprinus*. Containing clade: *Agaricaceae*. This clade corresponds to *Coprinus* Persoon as emended by Redhead et al. (2001).

Clade 87 (<40% BS): *Macrolepiota*. Containing clade: *Agaricaceae*. This clade corresponds to *Macrolepiota* Singer.

Clade 88 (81% BS): *Cystoderma*. Containing clade: *Agaricaceae*. Representative taxa: *Cystoderma amianthinum* (type of *Cystoderma* Fayod) and *C. chocoanum*. The separate placement of *Cystoderma granulorum*, which clusters with *Ripartitella* (Johnson and Vilgalys, 1998; Fig. 2) remains unexplained and needs further scrutiny. The placement of *Floccularia* as sister group to *Cystoderma* is weakly supported by bootstrapping (<50% BS), and there is no obvious morphological character to explain this relationship.

Clade 89 (55% BS): *Psathyrellaceae*. Representative taxa: *Psathyrella*, *Lacrymaria*, *Coprinopsis*, *Coprinellus*, and *Parasola*. This clade corresponds to the family *Psathyrellaceae* as defined in Redhead et al. (2001).

Clade 90 (<40% BS): *Icoprinopsis*. Containing clade: *psathyrellaceae*. This clade corresponds to the genus *Coprinopsis* as described in Redhead et al. (2001).

Clade 91 (98% BS): *Iparasola*. Containing clade: *psathyrellaceae*. This clade corresponds to the genus *Parasola* as described in Redhead et al. (2001).

Clade 92 (41% BS): *Icoprinellus*. Containing clade: *psathyrellaceae*. This clade corresponds to the genus *Coprinellus* as described in Redhead et al. (2001).

Clade 93 (56% BS): *Ipsathyrella*. Containing clade: *psathyrellaceae*. Representative species: *Psathyrella gracilis* (type species of *Psathyrella*). The results in Fig. 2 question monophyly of the large genus *Psathyrella*.

Clade 94 (<40% BS): *Ihebelomatoid*. Representative taxa: *Naucoria*, and *Ihebeloma*. This large-scale analysis supports a close relationship between the ectomycorrhizal genera *Hebeloma* and *Naucoria* and indicates that the latter genus is probably not monophyletic. These results are in agreement with other molecular studies (Aanen et al., 2000; E. Horak et al., unpublished; U. Peintner et al., unpublished). The placement in this clade of *Pholiota lignicola* is suspect and needs confirmation.

Clade 95 (60% BS): *Ihebeloma*. Containing clade: *Ihebelomatoid*. This clade corresponds to *Hebeloma* Kummer.

Clade 96 (73% BS): *Ihemipholiota*. This clade corresponds to *Hemipholiota* (Singer) Romagn. ex Bon.

Clade 97 (69% BS): *Igymnopiloid*. Representative taxa: *Igymnopilus* and *Galerina paludosa*. *Galerina* appears to be a polyphyletic genus, with its members clustering here and close to *Ipanaeolideae* (clade 79).

Clade 98 (99% BS): *Igymnopilus*. Containing clade: *Igymnopiloid*. This clade corresponds to the saprophytic genus *Gymnopilus* Karsten with the inclusion of *Hebelomina* Maire. *Hebelomina* was erected for taxa that resemble *Hebeloma* but are distinguished by having smooth and hyaline spores (Singer, 1986). This study confirms a close affinity of *Hebelomina* with dark-spored taxa, but indicates that the taxon is derived from within *Gymnopilus* rather than being close to *Hebeloma* (in clade 95). The ecology of *Hebelomina* is unclear. Singer (1986) wrote that the taxon is “probably ectomycorrhizal.” Because natural groups revealed by rDNA phylogenies are generally largely congruent with ecology and *Gymnopilus* is known not to be ectomycorrhizal, our results would suggest that *Hebelomina* is probably not ectomycorrhizal.

Clade 99 (46% BS): *Itubarioid*. Representative taxa: *Tubaria* and *Phaeomarasmius*. Singer (1986) classified the former genus in Crepidotaceae and the latter in Strophariaceae; however, a close relationship between these two taxa was already indicated by Kühner (1980).

Clade 100 (99% BS): *Itubaria*. Containing clade: *Itubarioid*. This clade corresponds to *Tubaria* (W.G. Smith) Gillet, as described in Singer (1986).

Clade 101 (<40% BS): *Icrepidotoid*. Representative taxa: *Crepidotus* and *Simocybe*. These two genera are reciprocally monophyletic in the bootstrap analysis, but not in the MPF tree. Reciprocal monophyly is also supported from an independent phylogenetic analysis in Aime (2001). A close relationship between *Crepidotus* and *Simocybe* is also apparent from morphology (Singer, 1986; Kühner, 1980).

Clade 102 (<40% BS): *Icrepidotus*. Containing clade: *Icrepidotoid*. This clade corresponds to *Crepidotus* Kummer.

Clade 103 (<40% BS): *Isimocybe*. Containing clade: *Icrepidotoid*. This clade corresponds to *Simocybe* Karsten.

Clade 104 (53% BS): *Iinocybe*. This clade corresponds to the genus *Inocybe* Fries. In both the MPF tree and the bootstrap tree *Iinocybe* comes close to *Icrepidotoid*, but with weak statistical support (<40% BS).

Clade 105 (100% BS): *Ipleuroflammula*. This clade corresponds to *Pleuroflammula* Singer.

Clade 106 (<40% BS): *Ipsychedelia*. Representative taxa: *Psilocybe cubensis*, *P. semilanceata*, *P. stuntzii*, *P. fmetaria*, *P. liniformans*, *P. cyanescens*, and *P. subaeruginosa*. This clade is composed only of psilocybin-containing (hallucinogenic) species of *Psilocybe*, whereas nonhallucinogenic *Psilocybe* species are in clade 112. Psilocybin is also produced in other mushrooms, for instance in *Copelandia* and *Panaeolus* (in clade 79) and several *Pluteus* species (in clade 53) (Stijve and Bonnard, 1986; Stamets, 1996). *Ipsychedelia* is monophyletic with *Istropharioid* in the MPF tree, but this relationship is not supported by bootstrapping.

Clade 107 (<40% BS): *Istropharioid*. Representative taxa: *Istropharia*, *Ipholiota*, *Isemiglobata* *I magnivelaris*, *Phaeonematoloma*, *Hypholoma* spp, and the secotioids *Weraroa* spp. and *Leratiomyces similis*. Chrysocystidia are present in all members of this clade, except in some species in *I magnivelaris* (e.g., in *Stropharia magnivelaris*). They are also absent in *Pachylepyrium*, the putative sister group of *Istropharioid* (Fig. 2).

Clade 108 (73% BS): *Isemiglobata*. Containing clade: *Istropharioid*. Representative taxa: *Stropharia semiglobata* and *S. unbonatenscens*. These two *Stropharia* species may not be monophyletic with the type of the genus, *S. aeruginosa*.

Clade 109 (<40% BS): *Ihypholoma*. Containing clade: *Istropharioid*. Representative taxa: *Hypholoma sublateritium*, *H. capnoides*, *H. subviride*, *H. fasciculare*, and *H. ericaeum*. This clade is composed of the core species of *Hypholoma* Kummer. However, this genus is probably polyphyletic: in our analyses *H. subericaeum* clusters with *Pholiota subochracea*, *H. aurantiacum* is in clade 111, and *H. udum* is basal to *Psilocybe* spp. in clade 113. *H. udum* is the only species with chrysocystidia that classifies outside *Istropharioid*; the placement of this species therefore needs further scrutiny.

Clade 110 (<40% BS): *Istropharia*. Containing clade: /stropharioid. Representative taxa: *Stropharia aeruginosa*, *S. rugosoannulata*, *S. coronilla*, *S. hardii*, and *S. hornemannii*. This clade includes the type of the genus *Stropharia*, *S. aeruginosa*, and closely related species. Our results suggest that *Stropharia magnivelaris* (in clade 112), *S. albocrenulata* (in an isolated position outside /stropharioid), and possibly also *S. semiglobata* and *S. umbonatescens* (both in clade 108) should be excluded from this genus.

Clade 111 (<40% BS): *lpholiota*. Containing clade: /stropharioid. This clade corresponds to the core of the genus *Pholiota* Kummer, including its type species (*P. squarrosa*). Our results support the separation of *Hemipholiota* (clade 96) from *Pholiota* and suggest the exclusion from *Pholiota* of *P. oedipus* (close to clade 99), *P. tuberculosa* (in an isolate position between clades 103 and 104 in Fig. 2), and possibly *P. subochracea* (which clusters with *Hypholoma subericaceum* in /stropharioid) and *P. lignicola* (in a doubtful position in clade 94).

Clade 112 (74% BS): *lmagnivelaris*. Containing clade: /stropharioid. Representative taxa: *Stropharia magnivelaris*, *Hypholoma aurantiacum*, and the secotioids *Leratiomyces similis* and *Weraroa erythrocephala*.

Clade 113 (61% BS): *lpsilocybe*. Representative taxa: *Psilocybe montana* (type of *Psilocybe* in Singer, 1986) and related non-*psilocybe*-containing species (as listed in Fig. 2), including *Melanotus*. Monophyly of *Psilocybe* is questioned by nLSU data: hallucinogenic species are separated in clade 106, and *Psilocybe subcoprophila* clusters with *Phaeogalera stagnina* at the base of clade 113. Based on Fig. 2, *lpsilocybe* may possibly also include *Kuehneromyces*, *Phaeogalera*, and *Hypholoma udum*.

Clade 114 (98% BS): *lvolvariella*. This clade corresponds to *Volvariella* Spegazzini. In the results depicted in Fig. 2 and other analyses (data not shown) /volvariella consistently clusters with /schizophylloid but always with a weak statistical support.

Clade 115 (54% BS): *lschizophylloid*. Representative taxa: *Schizophyllum*, *Fistulina*, and *Porodiscus pendulus*. This study supports the findings by Hibbett et al. (1997) showing that *Schizophyllum* and *Fistulina* are closely related and belong to the euagarics.

Clade 116 (100% BS): *lschizophyllum*. Containing clade: /schizophylloid. Clade 116 corresponds to *Schizophyllum* Fr.

Clade 117 (100% BS): *lfistulinoid*. Containing clade: /schizophylloid. Representative taxa: *Fistulina* and the reduced fungus *Porodiscus pendulus*. A possible affinity of *Fistulina* with both agarics and reduced forms was already indicated by Singer (1986, p. 843) who stated that “the gelatinizing of the trama of *Fistulina* and the acanthophyoid hairs of *Pseudofistulina* suggest [...] strong similarities with cyphelloid reduced agarics [...]. I am not at present ready to introduce *Fistulinaceae* as a

family of the Agaricales, because I believe that additional studies will be required to substantiate this position.”

Euagarics Incertae Sedis. Natural relationships of several species included in this study remain unresolved. However, our results support the placement in the euagarics of the following taxa: *Clavaria fusiformis* (possibly related to *Tricholomopsis* in clade 24), *Pleurotopsis longinqua*, *Lachnella alboviolascens*, *Tectella patellaris*, *Stereopsis humphreyi*, *Cantharocybe gruberi*, *Camarophyllus pratensis*, *Pseudoclitocybe cyathiformis*, *Stropharia albocrenulata*, *Ripartites*, *Flammula alnicola*, *Phaeolepiota aurea*, *Macrocystidia cucumis*, *Floccularia albolaripes*, *Pholiota oedipus*, *Pholiota tuberculosa*, *Laccaria*, *Squamanita*, *Phaeocollybia*, *Descolea*, *Galerina* spp. (this genus does not appear to be monophyletic), *Agrocybe*, *Cystoderma*, *Ripartitella*, *Mythicomyces*, *Stagnicola*, *Hemipholiota*, *Flammulaster*, *Inocybe*, *Pleuroflammula*, and *Nidulariaceae*.

4. Conclusions

Ribosomal DNA systematics has become a standard method in fungal taxonomy. It is therefore expected that in the coming years rDNA sequence data for the large majority of homobasidiomycetes will be produced. In nearly all studies published to date, rDNA data have been useful but not entirely sufficient for reconstructing fully resolved, well-supported phylogenies, for at least two reasons: (1) rDNA genes cannot always resolve relationships at every taxonomic level (Bruns et al., 1991) and (2) rDNA cannot provide the number of molecular characters needed to provide statistical support at all taxonomic levels (Berbee et al., 2000). In consequence, several laboratories are beginning to develop primers for PCR amplification and sequencing of additional mitochondrial and nuclear protein-coding genes in fungi (e.g., Thon and Royse, 1999; Kretzer and Bruns, 1999). Eventually, combining phylogenetic data from this work and others into a “supertree” (Sanderson et al., 1998) may boost our understanding of evolutionary relationships in the euagarics and other fungi and contribute to Darwin’s dream (as cited in Burkhardt and Smith, 1990:, p. 456): “The time will come [...] though I shall not live to see it, when we shall have fairly true genealogical trees of each kingdom of nature.”

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Appendix A. List of strains used with their sources and GeneBank accession numbers

Taxon	GenBank Accession No.	Source: Strain No. ^a
<i>Anthracoephyllum lateritium</i>	AF261324	This work: (T) CULTENN4419
<i>Neonothopanus nambi</i>	AF042577	Moncalvo et al., 2000 (as <i>Nothopanus eugrammus</i>)
	AF135175*	This work: (D) RVPR27
<i>Omphalotus olivascens</i>	AF261325	This work: (V) VT645.7
<i>Omphalotus nidiformis</i>	AF042621	Moncalvo et al., 2000
<i>Omphalotus olearius</i>	AF042010	Binder et al., 1997
<i>Lampteromyces japonicus</i>	AF135172	Moncalvo et al., 2000
	AF042008*	Binder et al., 1997
<i>Gymnopus polyphyllus</i>	AF042596	Moncalvo et al., 2000 (as <i>Collybia</i>)
<i>Gymnopus dryophilus</i>	AF042595	Moncalvo et al., 2000 (as <i>Collybia</i>)
<i>Gymnopus acervatus</i>	AF223172	This work: CBS174.48
<i>Gymnopus</i> sp.	AF261326	This work: (J) JEJ.PR.213
<i>Caripia montagnei</i>	AF261327	This work: (D) JMCR.143
<i>Setulipes androsaceus</i>	AF261585	This work: (D) HN4730
<i>Micromphale foetidum</i>	AF261328	This work: (J) JEJ.VA.567
<i>Marasmiellus opacus</i>	AF261329	This work: (J) JEJ.574
	AF261330*	This work: (D) HN2270
<i>Marasmius scorodonius</i>	AF261331	This work: (J) JEJ.586
	AF261332*	This work: DAOM175382
<i>Gymnopus</i> sp	AF261333	This work: (D) RVPR98.46
	AF261334*	This work: (D) RV.PR.98.08
<i>Gymnopus</i> sp.	AF261335	This work: (D) RVPR98.13
<i>Gymnopus bififormis</i>	AF261336	This work: (D) RV98/32
<i>Rhodocollybia maculata</i>	AF042597	Moncalvo et al., 2000 (as <i>Collybia</i>)
<i>Marasmiellus ramealis</i>	AF042626	Moncalvo et al., 2000
	AF042650*	Moncalvo et al., 2000
<i>Gymnopus peronatus</i>	AF223173	This work: CBS426.79
<i>Lentinula edodes</i>	AF042579	Moncalvo et al., 2000
	AF261557*	This work: (G) TMI1941
<i>Lentinula boryana</i>	AF261558	This work: (G) RGT960624
	AF261559*	This work: (D) HN2002
	AF261560*	This work: (D) R38
<i>Lentinula novaeseelandiae</i>	AF261561	This work: (G)TMI1172
<i>Lentinula lateritia</i>	AF261562	This work: (G) TMI1485
<i>Micromphale perforans</i>	AF042628	Moncalvo et al., 2000
	AF042651*	Moncalvo et al., 2000
<i>Tetrapyrgos nigripes</i>	AF261337	This work: DAOM186918
<i>Tetrapyrgos subdendrophora</i>	AF042629	Moncalvo et al., 2000 (as <i>Campanella</i>)
<i>Tetrapyrgos</i> sp.	AF261338	This work: (T) TENN7373
<i>Campanella</i> sp.	AF261339	This work: (D) RV-PR075
<i>Campanella</i> sp.	AF261340	This work: (D) RV98/79
Unidentified agaric	AF261341	This work: (D) JMCR.34

Appendix A. (continued)

Taxon	GenBank Accession No.	Source: Strain No. ^a
<i>Marasmius delectans</i>	U11922	Chapela et al., 1994
<i>Marasmius</i> sp.	AF261342	This work: (J) JEJ.PR.256
<i>Marasmius cladophyllus</i>	AF261343	This work: (D)JMCR. 121
<i>Hymenogloea papyracea</i>	AF261344*	This work: HALLING.5013
<i>Marasmius capillaris</i>	AF042631	Moncalvo et al., 2000
<i>Marasmius rotula</i>	AF261345	This work: (J) JEJ.VA.595
<i>Marasmius fulvoferrugineus</i>	AF261584	This work: (D) HN2346
<i>Chaetocalathus liliputianus</i>	AF261346	This work: DAOM175886
<i>Chaetocalathus</i> sp.	AF261347	This work: (T) TENN3572
<i>Crinipellis campanella</i>	U11916	Chapela et al., 1994
<i>Crinipellis maxima</i>	AF042630	Moncalvo et al., 2000
<i>Crinipellis</i> sp.	AF261348	This work: (D) RV.PR98/75
<i>Gloiocephala spathularia</i>	AF261349	This work: (D) JMCR.115
<i>Physalacria aff.orinocensis</i>	AF261350	This work: (T) TENN9134
<i>Rhodotus palmatus</i>	AF042565	Moncalvo et al., 2000
<i>Xerula megalospora</i>	AF042649	Moncalvo et al., 2000
<i>Xerula furfuracea</i>	AF042566	Moncalvo et al., 2000
<i>Oudemansiella canarii</i>	AF261351	This work: (D) RV.PR100
<i>Flammulina velutipes</i>	AF042641	Moncalvo et al., 2000
<i>Strobilurus trullisatus</i>	AF042633	Moncalvo et al., 2000
<i>Rhizomarasmius pyrrhocephalus</i>	AF261352	This work: (J) JEJ.596
	AF042605*	Moncalvo et al., 2000 (as <i>Marasmius</i>)
<i>Cyptotrama asprata</i>	AF261353	This work: (D) RV98/78
	AF042642*	Moncalvo et al., 2000
<i>Gloiocephala menieri</i>	AF042632	Moncalvo et al., 2000
<i>Gloiocephala</i> sp.	AF261354	This work: (T) TENN7573
<i>Armillaria tabescens</i>	AF042593	Moncalvo et al., 2000
<i>Armillaria "NABSI"</i>	AF261355	This work: (B) GC17
<i>Armillaria affinis</i>	AF261356	This work: (D) JMCR.126
<i>Cheimonophyllum candidissimum</i>	AF261357	This work: DAOM187959
<i>Gloeostereum incarnatum</i>	AF141637	Hallenberg and Parmasto (GenBank)
<i>Hemimycena delicatella</i>	AF261358	This work: DAOM187554
<i>Hemimycena ignobilis</i>	AF261359	This work: DAOM214662
<i>Calyptella capula</i>	AF261379	This work: (J) JAN.SW.21835
<i>Mycena aurantiidisca</i>	AF261360	This work: DAOM216791
<i>Mycena adonis</i>	AF261361	This work: DAOM174885
bioluminescent agaric	AF261362	This work: (D) JMCR.32
<i>Pleurotopsis longinqua</i>	AF042604	Moncalvo et al., 2000
<i>Baeospora myriadophylla</i>	AF042634	Moncalvo et al., 2000
<i>Baeospora myosura</i>	AF261363	This work: (T) TENN4256
<i>Hydropus scabripes</i>	AF042635	Moncalvo et al., 2000
<i>Gerronema strombodes</i>	U66433	Lutzoni, 1997
	AF261364*	This work: (J) JEJ580
<i>Gerronema subclavatum</i>	U66434	Lutzoni, 1997
<i>Gerronema</i> sp.	AF261365	This work: (V) OKM27143
<i>Megacollybia platyphylla</i>	AF261366	This work: DAOM195782
<i>Clitocybula oculus</i>	AF261367	This work: DAOM195995
<i>Hydropus fuliginarius</i>	AF261368	This work: DAOM196062
<i>Hydropus</i> sp.	AF261369	This work: (D) RV98/43
<i>Porothelium fimbriatum</i>	AF261370	This work: (S) HC.10/11/98.C
= <i>Stromatoscypha fimbriata</i>	AF261371*	This work: (J) FP102067
attine fungus G2	U11901	Chapela et al., 1994
	U11890*	Chapela et al., 1994

Appendix A. (continued)

Taxon	GenBank Accession No.	Source: Strain No. ^a
	U11905*	Chapela et al., 1994
<i>Resupinatus</i> sp.	AF042599	Moncalvo et al., 2000
<i>Resupinatus alboniger</i>	AF042600	Moncalvo et al., 2000
<i>Resupinatus dealbatus</i>	AF139944	Thorn et al., 2000 (as <i>Asterotus</i>)
<i>Stigmatolemma poriaeforme</i>	AF261372	This work: (J)RLG1156sp
cyphelloid sp.	AF261373	This work: HHB3534sp
<i>Phyllotopsis nidulans</i>	AF042578	Moncalvo et al., 2000
<i>Pleurocybella porrigens</i>	AF042594	Moncalvo et al., 2000
<i>Typhula phacorrhiza</i>	AF261374	This work: DAOM195241
<i>Gamundia leucophylla</i>	AF261375	This work: DAOM192749
<i>Caulorhiza hygrophoroides</i>	AF042640	Moncalvo et al., 2000
<i>Conchomyces bursaeformis</i>	AF042603	Moncalvo et al., 2000
	AF261376*	This work: (D) RV95/695
<i>Fayodia gracilipes</i>	AF261377	This work: DAOM187531
<i>Myxomphalia maura</i>	AF261378	This work: DAOM187839
<i>Floccularia albolaripes</i>	AF261380	This work: DAOM214667
<i>Mythicomyces corneipes</i>	AF261381	This work: DAOM178138
<i>Stereopsis humphreyi</i>	AF261382	This work: DAOM185795
<i>Pseudoclitocybe cyathiformis</i>	AF261383	This work: DAOM191063
<i>Collybia tuberosa</i>	AF261384	This work: (D) DUKE1424
	AF261385*	This work: DAOM191061
	AF261386*	This work: (T) TENN53630
<i>Collybia cirrhata</i>	AF261387	This work: (T) TENN53540
<i>Collybia cookei</i>	AF261388	This work: (T) TENN55143
<i>Dendrocollybia racemosa</i>	AF042598	Moncalvo et al., 2000 (as <i>Collybia</i>)
<i>Clitocybe dealbata</i>	AF042589	Moncalvo et al., 2000
	AF223175*	This work: (S) HC95/cp3
<i>Clitocybe connata</i>	AF042590	Moncalvo et al., 2000
<i>Lepista nuda</i>	AF042624	Moncalvo et al., 2000 (as <i>Clitocybe</i>)
<i>Lepista nuda</i>	AF139963	Thorn et al., 2000
<i>Clitocybe ramigena</i>	AF042648	Moncalvo et al., 2000
<i>Clitocybe glacialis</i>	AF261389	This work: DAOM208590
<i>Clitocybe odorata</i>	AF261390	This work: (D) RV98/145
<i>Lepista nebularis</i>	AF223217	This work: CBS362.65
<i>Plicaturopsis crispa</i>	AF261586	This work: (D) RV98/1
<i>Omphaliaster borealis</i>	AF261391	This work: DAOM189775
<i>Tricholoma atroviolaceum</i>	U76457	Shank and Vilgalys (GenBank)
<i>Tricholoma imbricatum</i>	U76458	Shank and Vilgalys (GenBank)
<i>Tricholoma focale</i>	U76460	Shank and Vilgalys (GenBank)
<i>Tricholoma myomyces</i>	U76459	Shank and Vilgalys (GenBank)
<i>Tricholoma vernaticum</i>	U76461	Shank and Vilgalys (GenBank)
<i>Tricholoma pardinum</i>	U76462	Shank and Vilgalys (GenBank)
<i>Tricholoma venenatum</i>	U76463	Shank and Vilgalys (GenBank)
<i>Tricholoma portentosum</i>	U76464	Shank and Vilgalys (GenBank)
<i>Tricholoma intermedium</i>	U76465	Shank and Vilgalys (GenBank)
<i>Tricholoma subaureum</i>	U76466	Shank and Vilgalys (GenBank)
<i>Tricholoma caligatum</i>	U76467	Shank and Vilgalys (GenBank)
	AF261392*	This work: (D) SAR1/2/88
<i>Tricholoma matsutake</i>	U62964	Hwang and Kim, 2000.
<i>Tricholoma</i> cf. <i>flavovirens</i>	U86672	Pegler et al., 1998
<i>Tricholoma vaccinum</i>	U86443-4	Nakasone and Rentmeester (GenBank)
<i>Leucopaxillus albissimus</i>	AF261393	This work: DAOM182713
<i>Leucopaxillus gentianeus</i>	AF261394	This work: (T) TENN5616

Appendix A. (continued)

Taxon	GenBank Accession No.	Source: Strain No. ^a
<i>Porpoloma</i> sp.	AF261395	This work: JLPR3395
<i>Hypsizygyus ulmarius</i>	AF042584	Moncalvo et al., 2000
<i>Ossicaulis lignatilis</i>	AF261396	This work: DAOM188196
	AF261397*	This work: (D, V) D604
	n.a.*	This work: DAOM211765
<i>Lyophyllum tylicolor</i>	AF139964	Thorn et al., 2000
	AF223193*	This work: (S) SAG5/271yo9
	AF223194*	This work: (S) SAG5/27.11
	AF223192*	This work: CBS362.80
	AF223195*	This work: BSI92/245
<i>Lyophyllum gibberosum</i>	AF223198	This work: CBS320.80
	AF223196*	This work: CBS321.80
	AF223197*	This work: CBS328.50
<i>Lyophyllum palustris</i>	AF223200	This work: CBS717.87
	AF223199*	This work: CBS714.87
<i>Tephrocycbe rancida</i>	AF223203	This work: CBS204.47
<i>Tricholomella constricta</i>	AF223187	This work: (S) HC80/148
	AF223186*	This work: CBS660.87
	AF223189*	This work: CBS320.85
	AF223188*	This work: (S) HC84/75
<i>Lyophyllum boudieri</i>	AF223206	This work: (S) HC78U
	AF223205*	This work: CBS379.88
	AF223204*	This work: BSI96/84
<i>Lyophyllum inolens</i>	AF223201	This work: CBS330.85
<i>Lyophyllum ambustum</i>	AF223215	This work: CBS451.87
	AF223216*	This work: CBS452.87
	AF223214*	This work: CBS450.87
<i>Lyophyllum anthracophilum</i>	AF223211	This work: BSI94/88
	AF223212*	This work: (S) HC79/132
	AF223213*	This work: CBS156.44
<i>Lyophyllum atratum</i>	AF042582	Moncalvo et al., 2000
	AF223210*	This work: CBS709.87
<i>Lyophyllum decastes</i>	AF042583	Moncalvo et al., 2000
<i>Lyophyllum caerulescens</i>	AF223209	This work: (S) HC80/140
<i>Lyophyllum sykosporum</i>	AF223208	This work: IFO30978
<i>Lyophyllum semitale</i>	AF042581	Moncalvo et al., 2000
<i>Termitomyces cylindricus</i>	AF042585	Moncalvo et al., 2000
<i>Termitomyces clypeatus</i>	AF261398	This work: (D) JMleg.MUID
<i>Termitomyces heimii</i>	AF042586	Moncalvo et al., 2000
<i>Termitomyces microcarpus</i>	AF042587	Moncalvo et al., 2000
<i>Termitomyces</i> sp.	AF261399	This work: (D) JJs.n.
<i>Termitomyces subhyalinus</i>	AF223174	This work: BSI93/3
<i>Lyophyllum leucophaeatum</i>	AF223202	This work: (S) HAe251/97
<i>Lyophyllum ochraceum</i>	AF223185	This work: BSI94/cp1
<i>Lyophyllum favrei</i>	AF223183	This work: (S) HAe.251.97
	AF223184*	This work: (S) HC96/cp4
	AF223182*	This work: BSI94/cp2
<i>Calocybe ionides</i>	AF223179	This work: (S) HC77/33
<i>Calocybe naucoria</i>	AF223180	This work: (S) HC80/103
<i>Calocybe obscurissima</i>	AF223181	This work: (S) HC79/181
<i>Calocybe cyanea</i>	AF261400	This work: (D) RVPR10 June 97
<i>Calocybe persicolor</i>	AF223176	This work: (S) HC80/99
<i>Calocybe gambosa</i>	AF223177	This work: (S) HC78/64

Appendix A. (continued)

Taxon	GenBank Accession No.	Source: Strain No. ^a
	U86441/2*	Nakasone and Rentmeester (GenBank)
<i>Calocybe carneum</i>	AF223178	This work: CBS552.50
<i>Asterophora lycoperdoides</i>	AF223190	This work: CBS170.86
<i>Asterophora parasitica</i>	AF223191	This work: CBS683.82
<i>Catathelasma ventricosa</i>	AF261401	This work: DAOM221514
<i>Catathelasma imperialis</i>	AF261402	This work: DAOM225247
<i>Rhodocybe fallax</i>	AF223166	This work: CBS129.63
	AF223165*	This work: CBS605.79
	AF261283	This work: (V) OKM25668
<i>Rhodocybe truncata</i>	AF223168	This work: CBS604.76
	AF223167*	This work: CBS482.50
<i>Rhodocybe caelata</i>	AF261282	This work: (C) TB5890
<i>Rhodocybe mundula</i>	AF261284	This work: (C) TB4698
<i>Rhodocybe popinalis</i>	AF261285	This work: (C) TB6378
<i>Clitopilus "flaviphyllus"</i>	AF261286	This work: (C) TB8067
<i>Clitopilus apalus</i>	AF261287	This work: (C) M536
<i>Clitopilus scyphoides</i>	AF261288	This work: (C) T777
<i>Clitopilus prunulus</i>	AF042645	Moncalvo et al., 2000
<i>Clitopilopsis hirneola</i>	AF223164	This work: CBS576.87
	AF223163*	This work: CBS577.87
<i>Entoloma bloxamii</i>	AF261289	This work: (C) TB6117
<i>Trichopilus porphyrophaeus</i>	AF261290	This work: (C) TB6957
<i>Leptonia subserrulata</i>	AF261291	This work: (C) TB6993
<i>Alboleptonia stylophora</i>	AF261292	This work: (C) TB8475
<i>Inopilus entolomoides</i>	AF261293	This work: (C) TB8507
<i>Entoloma lividum</i>	AF261294	This work: (C) TB5034
	AF261295	This work: (C) TB6807
<i>Entoloma nidorosum</i>	AF261296	This work: (C) TB6263
<i>Entoloma bicolor</i>	AF261297/8	This work: (C) TB4967
<i>Entoloma rhodopolium</i>	AF261299	This work: (C) TB6221
<i>Entoloma flavifolium</i>	AF261301	This work: (C) TB6215
<i>Entoloma alpicola</i>	AF261302	This work: (C) TB6415
<i>Inocephalus quadratus</i>	AF261303	This work: (C) TB7695
<i>Inocephalus lactifluus</i>	AF261304	This work: (C) TB7962
<i>Inocephalus murrarii</i>	AF261305/6	This work: (C) TB6038
<i>Entoloma canescens</i>	AF261307	This work: (C) TB5657
<i>Pouzarella nodospora</i>	AF261308	This work: (C) TB5716
<i>Entoloma haastii</i>	AF261309	This work: (C) BY21
<i>Entoloma odorifer</i>	AF261310	This work: (C) TB6366
<i>Entoloma unicolor</i>	AF261311/2	This work: (C) TB5520
<i>Leptonia carnea</i>	AF261313	This work: (C) TB5812
<i>Entoloma undatum</i>	AF261314	This work: (C) TB6398
<i>Entoloma abortivum</i>	AF223169	This work: CBS143.34
<i>Entoloma sericeonitida</i>	AF261315	This work: (C) TB7144
<i>Leptonia gracilipes</i>	AF261316	This work: (C) TB6033
<i>Nolanea conica</i>	AF261317	This work: (C) MB6
<i>Nolanea cetrata</i>	AF261319	This work: (C) TB7382
<i>Nolanea hirtipes</i>	AF261320	This work: (C) K1171992
<i>Nolanea conferenda</i>	AF261321	This work: (C) TB7660
<i>Nolanea strictia</i>	AF042620	Moncalvo et al., 2000 (as <i>Entoloma</i>)
<i>Nolanea sericea</i>	AF261318	This work: (C) TB6506
	AF223170*	This work: CBS237.50
	AF223171*	This work: CBS153.46

Appendix A. (continued)

Taxon	GenBank Accession No.	Source: Strain No. ^a
<i>Entoloma</i> sp.	AF261322	This work: (D) JM98/123
<i>Claudopus depluens</i>	AF261323	This work: (C) TB7522
<i>Collybia aurea</i>	AF261403	This work: (D) RV.PR98/27
<i>Tricholomopsis rutilans</i>	AF261404	This work: DAOM225484
<i>Marasmius rhyssophyllus</i>	n.a.	This work: JLPR5831
<i>Clavaria fusiformis</i>	n.a.	This work: (D) RV.98.143
<i>Macrocybe gigantea</i>	AF042591	Moncalvo et al., 2000
<i>Macrocybe titans</i>	U86437	Pegler et al., 1998
<i>Callistosporium luteoolivaceum</i>	AF261405	This work: (D) JM99/124
<i>Callistosporium xanthophyllum</i>	AF261406	This work: IB19770276
<i>Pleurocollybia brunnescens</i>	AF261407	This work: DAOM34832
<i>Mycena rorida</i>	AF261408	This work: DAOM215019
<i>Mycena leaiana</i>	AF261411	This work: DAOM167618
<i>Mycena inclinata</i>	AF042636	Moncalvo et al., 2000 (as <i>M. galericulata</i>)
<i>Mycena galericulata</i>	AF261412	This work: (T) TENN7495
<i>Mycena clavicularis</i>	AF042637	Moncalvo et al., 2000
<i>Mycena insignis</i>	AF261413	This work: DAOM208539
“ <i>Cotobrusia calostomoides</i> ”	AF261424	This work: (D)JMCR.100
cf. <i>Poromyceia</i>	AF261429	This work: (D) JM98/128
<i>Mycena viscidocruenta</i>	AF261414	This work: DUKE3411
<i>Resinomyceia acadensis</i>	AF042638	Moncalvo et al., 2000
<i>Resinomyceia rhododendri</i>	AF261415	This work: (J) JEJ.VA.599
<i>Dictyopanus pusillus</i>	AF261425	This work: (D) RV.PR98/36
<i>Dictyopanus</i> sp.	AF261426	This work: (T) CULTENN7699
<i>Panellus stypticus</i>	AF261427	This work: (J) CMC5
<i>Favolaschia cinnabarina</i>	AF261416	This work: (D) RVPR82
<i>Favolaschia calocera</i>	AF261417	This work: (J) SR.KEN.346
<i>Favolaschia</i> cf. <i>calocera</i>	AF261418	This work: (D) JM98/186
<i>Favolaschia</i> cf. <i>calocera</i>	AF261419	This work: (D) JM98/372
<i>Favolaschia</i> cf. <i>sprucei</i>	AF261420	This work: (D) TH6418
<i>Poromyceia</i> sp.	AF261421	This work: (D) RV.PR114
<i>Filoboletus gracilis</i>	AF261422	This work: (J) JEJ.PR.253
<i>Poromyceia manipularis</i>	AF261423	This work: (D) JM98/217
<i>Mycenoporella griseipora</i>	AF261428	This work: (D) JM98/156
<i>Prunulus rutilantiformis</i>	AF042606	Moncalvo et al., 2000 (as <i>Mycena</i>)
<i>Prunulus pura</i> cplx	AF261409	This work: (D) JMCR.101
<i>Prunulus pura</i> cplx	AF261410	This work: (D) JM98/136
<i>Tectella patellaris</i>	AF261430	This work: (D) TH6346
<i>Macrocystidia cucumis</i>	AF261431	This work: DAOM181084
<i>Hohenbuehelia</i> sp.	AF139960	Thorn et al., 2000
<i>Hohenbuehelia</i> cf. <i>atrolucida</i>	AF042603	Moncalvo et al., 2000
<i>Hohenbuehelia grisea</i>	AF139954/5	Thorn et al., 2000
<i>Hohenbuehelia petaloides</i>	AF139956*	Thorn et al., 2000
<i>Nematoctonus geogenius</i>	AF139957/8*	Thorn et al., 2000
<i>Hohenbuehelia</i> sp.	AF139950/1*	Thorn et al., 2000
<i>Hohenbuehelia portegna</i>	AF139959*	Thorn et al., 2000
<i>Nematoctonus robustus</i>	AF139952/3	Thorn et al., 2000
<i>Hohenbuehelia tristis</i>	AF042602	Moncalvo et al., 2000
	AF135171*	Thorn et al., 2000
<i>Pleurotus ostreatus</i>	U04140	Vilgalys and Sun, 1994
	U04160*	Vilgalys and Sun, 1994
	U04143*	Vilgalys and Sun, 1994
	U04144*	Vilgalys and Sun, 1994

Appendix A. (continued)

Taxon	GenBank Accession No.	Source: Strain No. ^a
	U04147*	Vilgalys and Sun, 1994
	U04142*	Vilgalys and Sun, 1994
<i>Pleurotus pulmonarius</i>	U04157*	Vilgalys and Sun, 1994
	U04152*	Vilgalys and Sun, 1994
	U04141*	Vilgalys and Sun, 1994
	U04151*	Vilgalys and Sun, 1994
	U04153*	Vilgalys and Sun, 1994
<i>Pleurotus populinus</i>	U04159	Vilgalys and Sun, 1994
<i>Pleurotus eryngii</i>	U04136	Vilgalys and Sun, 1994
	U04137*	Vilgalys and Sun, 1994
	U04155*	Vilgalys and Sun, 1994
	U04154*	Vilgalys and Sun, 1994
<i>Pleurotus abieticola</i>	AF135176	Thorn et al., 2000
<i>Pleurotus australis</i>	AF261432	This work: (D) RV95/568
<i>Pleurotus cornucopiae</i>	U04146	Vilgalys and Sun, 1994
	U04135*	Vilgalys and Sun, 1994
<i>Pleurotus djamor</i>	AF042575	Moncalvo et al., 2000
	U04139*	Vilgalys and Sun, 1994
	U04138*	Vilgalys and Sun, 1994
<i>Pleurotus calyptratus</i>	AF135177	Thorn et al., 2000
<i>Pleurotus cystidiosus</i>	U04148	Vilgalys and Sun, 1994
	U04149*	Vilgalys and Sun, 1994
<i>Pleurotus smithii</i>	U04150	Vilgalys and Sun, 1994
<i>Pleurotus laevis</i>	U04156	Vilgalys and Sun, 1994
	U04158*	Vilgalys and Sun, 1994
	AF139968*	Thorn et al., 2000
<i>Pleurotus dryinus</i>	AF135178	Thorn et al., 2000
<i>Pleurotus tuberregium</i>	AF135180	Thorn et al., 2000
<i>Pleurotus purpureoolivaceus</i>	AF042576	Moncalvo et al., 2000
	AF135179*	Thorn et al., 2000
<i>Pluteus petasatus</i>	AF042611	This work: (S) JB91/21
<i>Pluteus primus</i>	AF042610	This work: (S) JB94/24
<i>Pluteus brunneoradiatus</i>	AF261567	This work: (S) JB97/3
<i>Pluteus pouzarianus</i>	AF261568	This work: (S) JB94/26
<i>Pluteus pallidus</i>	AF261569	This work: (S) JB90/27
<i>Pluteus cervinus</i>	AF261570	This work: (S) JB97/19
<i>Pluteus pellitus</i>	AF261571	This work: (S) JB93/3
<i>Pluteus atromarginatus</i>	AF261572	This work: (S)JB97/14
<i>Pluteus salicinus</i>	AF261573	This work: (S) JB97/6
<i>Pluteus ephebeus</i>	AF261574	This work: (S) JB97/23
<i>Pluteus</i> “white”	AF042612	Moncalvo et al., 2000
<i>Pluteus</i> sp.	AF261576	This work: (S) JMCR.124
<i>Pluteus romellii</i>	AF261575	This work: (S) JB97/26
<i>Pluteus admirabilis</i>	AF261577	This work: DAOM193532
	AF261578*	This work: DAOM197226
<i>Pluteus aurantiorugosus</i>	AF261579	This work: DAOM197369
<i>Pluteus umbrosus</i>	AF261580	This work: DAOM197235
<i>Pluteus chrysophlebius</i>	AF261581	This work: DAOM 190194
<i>Melanoleuca cognata</i>	AF261433	This work: DAOM210221
<i>Melanoleuca alboflavida</i>	AF261434	This work: DAOM215874
	AF139965*	Thorn et al., 2000
<i>Amanita muscaria</i>	AF042643	Moncalvo et al., 2000
<i>Amanita roseitincta</i>	AF097369	Drehmel et al., 1999

Appendix A. (continued)

Taxon	GenBank Accession No.	Source: Strain No. ^a
<i>Amanita farinosa</i>	AF097370	Drehmel et al., 1999
<i>Amanita gemmata</i>	AF097371	Drehmel et al., 1999
<i>Amanita ceciliae</i>	AF097372	Drehmel et al., 1999
<i>Amanita fulva</i>	AF097373	Drehmel et al., 1999
<i>Amanita vaginata</i>	AF097375	Drehmel et al., 1999
<i>Amanita jacksonii</i>	AF097376	Drehmel et al., 1999
<i>Torrendia pulchella</i>	AF261566	This work: G.Platas
<i>Amanita citrina</i>	AF041547	Hopple and Vilgalys, 1999
<i>Amanita brunnescens</i>	AF097379	Drehmel et al., 1999
<i>Amanita flavoconia</i>	AF042609	Moncalvo et al., 2000
<i>Amanita rubescens</i>	AF042607	Moncalvo et al., 2000
<i>Amanita flavorubescens</i>	AF042609	Moncalvo et al., 2000
<i>Amanita franchetii</i>	AF097381	Drehmel et al., 1999
<i>Amanita bisporigera</i>	AF097384	Drehmel et al., 1999
<i>Amanita phalloides</i>	AF261435	This work: UPS2701
<i>Amanita virosa</i>	AF097386	Drehmel et al., 1999
<i>Amanita rhoadsii</i>	AF097391	Drehmel et al., 1999
<i>Amanita solitariiformis</i>	AF097390	Drehmel et al., 1999
<i>Amanita peckiana</i>	AF042608	Moncalvo et al., 2000
	AF097387*	Drehmel et al., 1999
<i>Amanita volvata</i>	AF097388	Drehmel et al., 1999
<i>Amanita rhopalopus</i>	AF097393	Drehmel et al., 1999
<i>Amanita armillariiformis</i>	AF261436	This work: DAOM216919
	AF261437*	This work: DAOM184734
<i>Limacella glischra</i>	U85301	Johnson and Vilgalys, 1998
<i>Limacella glioderma</i>	AF261438	This work: (V) VT(L18)
<i>Limacella illinata</i>	AF261439	This work: (V) VT8.9.96
<i>Catatrampa costaricensis</i>	AF261440	This work: DAOM211663
<i>Neohygrophorus angelesianus</i>	AF261441	This work: DAOM208569
<i>Pseudoomphalina felloides</i>	AF261442	This work: DAOM11115
<i>Cantharellula umbonata</i>	AF261443	This work: DAOM198740
<i>Pseudoarmillariella ectypoides</i>	AF261444	This work: DAOM191921
<i>Omphalina velutipes</i>	U66455	Lutzoni, 1997
<i>Omphalina epichysium</i>	U66442	Lutzoni, 1997
<i>Omphalina sphagnicola</i>	U66453	Lutzoni, 1997
<i>Omphalina philonotis</i>	U66449	Lutzoni, 1997
<i>Omphalina viridis</i>	U66456	Lutzoni, 1997
<i>Arrhenia lobata</i>	U66429	Lutzoni, 1997
<i>Arrhenia auriscalpium</i>	U66428	Lutzoni, 1997
<i>Omphalina obscurata</i>	U66448	Lutzoni, 1997
<i>Omphalina griseopallidus</i>	U66436	Lutzoni, 1997 (as <i>Phaeotellus</i>)
<i>Omphalina luteovitellina</i>	U66447	Lutzoni, 1997
<i>Omphalina velutina</i>	U66454	Lutzoni, 1997
<i>Omphalina velutina</i>	U66443	Lutzoni, 1997 (as <i>O. grisella</i>)
<i>Omphalina hudsoniana</i>	U66446	Lutzoni, 1997
<i>Omphalina ericetorum</i>	U66445	Lutzoni, 1997
	AF261445*	This work: DAOM180811
<i>Gliophorus laeta</i>	AF261446	This work: DAOM196394
<i>Omphalina pyxidata</i>	U66450	Lutzoni, 1997
<i>Omphalina rivulicola</i>	U66451	Lutzoni, 1997
<i>Clitocybe lateritia</i>	U66431	Lutzoni, 1997
<i>Clitocybe clavipes</i>	AF042564	Moncalvo et al., 2000
	AF261447*	This work: (J) JEJ.VA.587

Appendix A. (continued)

Taxon	GenBank Accession No.	Source: Strain No. ^a
	U86439/40*	Nakasone et al., (GenBank)
<i>Clitocybe</i> sp.	AF261448	This work: (J) JEJ.VA.581
<i>Rimbachia bryophila</i>	AF261449	This work: DAOM192811
<i>Humidicutis marginata</i>	AF042580	Moncalvo et al., 2000
<i>Hygrophorus sordidus</i>	AF042562	Moncalvo et al., 2000
<i>Hygrophorus bakerensis</i>	AF042623	Moncalvo et al., 2000
<i>Chrysomphalina chrysophylla</i>	U66430	Lutzoni, 1997
<i>Chrysomphalina grossula</i>	U66444	Lutzoni, 1997 (as <i>Omphalina</i>)
	U66457*	Lutzoni, 1997 (as <i>Omphalina wynniae</i>)
<i>Hygrocybe conica</i>	AF261450	This work: DAOM190581
<i>Hygrocybe spadicea</i>	AF261451	This work: DAOM171030
<i>Hygrocybe miniata</i>	AF261452	This work: DAOM169729
<i>Hygrocybe</i> sp.	AF261453	This work: (D) JM98/368
<i>Hygrocybe cantharellus</i>	AF261454	This work: (D) JM98/369
<i>Cuphophyllus citrinopallidus</i>	U66435	Lutzoni, 1997 (as <i>Hygrocybe</i>)
<i>Chromosera cyanophylla</i>	AF261455	This work: DAOM208603
= <i>Mycena lilacifolia</i>	AF261456	This work: (D) DUKE1645
<i>Camarophyllus pratensis</i>	AF261457	This work: DAOM215543
<i>Cotylidia alba</i>	AF261458	This work: (D) RV.PR98/28
<i>Cotylidia diaphina</i>	AF261459	This work: DAOM182136
<i>Cotylidia aurantiaca</i>	AF261460	This work: (D) JMCR.33
<i>Cantharellopsis prescottii</i>	AF261461	This work: DAOM225483
<i>Omphalina brevibasidiata</i>	U66441	Lutzoni, 1997
<i>Omphalina rosella</i>	U66452	Lutzoni, 1997
<i>Rickenella mellea</i>	U66438	Lutzoni, 1997
<i>Rickenella pseudogrisella</i>	U66437	Lutzoni, 1997
<i>Omphalina marchantiae</i>	U66432	Lutzoni, 1997 (as <i>Gerronema</i>)
<i>Xeromphalina caudicinalis</i>	AF042639	Moncalvo et al., 2000
<i>Xeromphalina campanelloides</i>	AF261462	This work: (T) TENN6368
<i>Xeromphalina cornui</i>	AF261463	This work: (T) TENN6397
<i>Xeromphalina fraxinophila</i>	AF261464	This work: (T) TENN6398
<i>Xeromphalina helbergeri</i>	AF261465	This work: (T) TENN6255
<i>Xeromphalina austroandina</i>	AF261466	This work: (T) TENN7392
<i>Xeromphalina kauffmanii</i>	AF261467	This work: (T) TENN6906
<i>Xeromphalina brunneola</i>	AF261468	This work: (T) TENN1179
<i>Xeromphalina campanella</i>	AF261469	This work: (T) TENN7250
<i>Heimiomyces fulvipes</i>	AF261470	This work: (T) TENN5864
<i>Heimiomyces tenuipes</i>	AF261471	This work: (T) TENN6908
<i>Heimiomyces</i> sp.	AF261472	This work: (D) RV95/396
<i>Ripartitella brasiliensis</i>	U85300	Johnson and Vilgalys, 1998
<i>Cystoderma granulosum</i>	U85299	Johnson and Vilgalys, 1998
<i>Cystoderma chocoanum</i>	U85302	Johnson and Vilgalys, 1998
<i>Cystoderma amianthinum</i>	AF261473	This work: DAOM188121
<i>Phaeolepiota aurea</i>	AF261474	This work: DAOM178195
<i>Lachnella alboviolascens</i>	AF261475	This work: DAOM223321
<i>Melanophyllum haematospermum</i>	AF261476	This work: DAOM197183
<i>Melanophyllum echinatum</i>	AF059231	Mitchell and Bresinsky, 1999
<i>Lepiota clypeolaria</i>	U85291	Johnson and Vilgalys, 1998
<i>Lepiota acutesquamosa</i>	U85293	Johnson and Vilgalys, 1998
<i>Lepiota cristata</i>	U85292	Johnson and Vilgalys, 1998
<i>Lepiota humei</i>	U85284	Johnson and Vilgalys, 1998
<i>Lepiota flammeotincta</i>	U85296	Johnson and Vilgalys, 1998
<i>Lepiota felina</i>	U85295	Johnson and Vilgalys, 1998

Appendix A. (continued)

Taxon	GenBank Accession No.	Source: Strain No. ^a
<i>Lepiota subincarnata</i>	U85294	Johnson and Vilgalys, 1998
<i>Cystolepiota cystidiosa</i>	U85298	Johnson and Vilgalys, 1998
<i>Cystolepiota cystophora</i>	U85297	Johnson and Vilgalys, 1998
<i>Macrolepiota caperatus</i>	U85277	Johnson and Vilgalys, 1998
	U11923*	Chapela et al., 1994
<i>Macrolepiota procera</i>	U85304	Johnson and Vilgalys, 1998
	U85275*	Johnson and Vilgalys, 1998
<i>Macrolepiota excoriata</i>	U85278	Johnson and Vilgalys, 1998
<i>Macrolepiota gracilentia</i>	U85279	Johnson and Vilgalys, 1998
<i>Macrolepiota colombiana</i>	U85276	Johnson and Vilgalys, 1998
<i>Leucocoprinus cepaestipes</i>	U85286	Johnson and Vilgalys, 1998
	U85305*	Johnson and Vilgalys, 1998
	U85306*	Johnson and Vilgalys, 1998
<i>Leucocoprinus fragilissimus</i>	AF041540	Hopple and Vilgalys, 1999
	U85289*	Johnson and Vilgalys, 1998
<i>Leucocoprinus luteus</i>	U11920	Chapela et al., 1994
<i>Leucocoprinus birnbaumii</i>	U85288	Johnson and Vilgalys, 1998
	AF041541*	Hopple and Vilgalys, 1999
<i>Leucocoprinus</i> cf. <i>brebissonii</i>	U85290	Johnson and Vilgalys, 1998
<i>Leucocoprinus longistriatus</i>	U85287	Johnson and Vilgalys, 1998
<i>Leucoagaricus rubrotinctus</i>	U85281	Johnson and Vilgalys, 1998
<i>Leucoagaricus naucinus</i>	U11921	Chapela et al., 1994
	U85280*	Johnson and Vilgalys, 1998
<i>Leucoagaricus</i> sp.	U85285	Johnson and Vilgalys, 1998
<i>Leucoagaricus hortensis</i>	U85283	Johnson and Vilgalys, 1998
<i>Leucoagaricus americanus</i>	U85282	Johnson and Vilgalys, 1998
<i>Chlorophyllum molybdites</i>	U11915	Chapela et al., 1994
	U85274*	Johnson and Vilgalys, 1998
	U85303*	Johnson and Vilgalys, 1998
attine fungus G1	U11902	Chapela et al., 1994
attine fungus G1	U11893	Chapela et al., 1994
attine fungus G3	U11895	Chapela et al., 1994
attine fungus G3	U11906	Chapela et al., 1994
<i>Agaricus bisporus</i>	U11911	Chapela et al., 1994
	AF059227*	Mitchell and Bresinsky, 1999
	AF059218*	Mitchell and Bresinsky, 1999
<i>Agaricus spissicaulis</i>	AF059220	Mitchell and Bresinsky, 1999
<i>Agaricus devoniensis</i>	AF059225	Mitchell and Bresinsky, 1999
<i>Agaricus impudicus</i>	AF059226	Mitchell and Bresinsky, 1999
<i>Agaricus bitorquis</i>	AF059217	Mitchell and Bresinsky, 1999
<i>Agaricus bernardii</i>	AF059215	Mitchell and Bresinsky, 1999
<i>Agaricus pocillator</i>	AF041542	Hopple and Vilgalys, 1999
<i>Agaricus campestris</i>	U85273	Johnson and Vilgalys, 1998
	AF059221*	Mitchell and Bresinsky, 1999
<i>Agaricus xanthoderma</i>	AF059222	Mitchell and Bresinsky, 1999
<i>Agaricus silvaticus</i>	AF059219	Mitchell and Bresinsky, 1999
<i>Agaricus arvensis</i>	U11910	Chapela et al., 1994
<i>Agaricus silvicola</i>	AF059223	Mitchell and Bresinsky, 1999
<i>Agaricus abruptibulbus</i>	AF059228	Mitchell and Bresinsky, 1999
<i>Agaricus lanipes</i>	AF059229	Mitchell and Bresinsky, 1999
<i>Agaricus maskae</i>	AF059230	Mitchell and Bresinsky, 1999
<i>Agaricus semotus</i>	AF059224	Mitchell and Bresinsky, 1999
<i>Agaricus</i> sp.	AF261477	This work: (D) JMCR.50

Appendix A. (continued)

Taxon	GenBank Accession No.	Source: Strain No. ^a
<i>Gyrophragmium dunalii</i>	AF261478	This work: leg.CALLAC
<i>Longula texensis</i>	AF261479	This work: (V) OKM19301
<i>Battarraea laciniata</i>	AF208534	This work: (V) OKM22810
<i>Coprinus sterquilinus</i>	AF041530	Hopple and Vilgalys, 1999
<i>Coprinus comatus</i>	AF041529	Hopple and Vilgalys, 1999
<i>Montagnea arenaria</i>	AF041538	Hopple and Vilgalys, 1999
<i>Montagnea radiosus</i>	AF261480	This work: (V) EK13
<i>Montagnea candollii</i>	AF261481	This work: (V) EK7
<i>Podaxis pistillaris</i>	AF041539	Hopple and Vilgalys, 1999
<i>Calvatia</i> sp.	AF261482	This work: (J) JRT008
<i>Bovista</i> sp.	AF261483	This work: (D) DUKE2395
<i>Lycoperdon coloratum</i>	AF261484	This work: (D) TYJ
<i>Lycoperdon marginatum</i>	AF261485	This work: (J) JEJ.NC.60
<i>Tulostoma simulans</i>	AF261486	This work: (D) DUKE3733
<i>Crucibulum laeve</i>	AF261582	This work: (G) T816
<i>Cyathus stercoreus</i>	AF261583	This work: (G) T815
<i>Coprinopsis atramentaria</i>	AF041484	Hopple and Vilgalys, 1999 (as <i>Coprinus</i>)
<i>Coprinopsis acuminata</i>	AF041485	Hopple and Vilgalys, 1999 (as <i>Coprinus</i>)
<i>Coprinopsis romagnesiana</i>	AF041486	Hopple and Vilgalys, 1999 (as <i>Coprinus</i>)
<i>Coprinopsis lagopides</i>	AF041488	Hopple and Vilgalys, 1999 (as <i>Coprinus</i>)
<i>Coprinopsis lagopus</i>	AF041490	Hopple and Vilgalys, 1999 (as <i>Coprinus</i>)
<i>Coprinopsis luteocephala</i>	AF041505	Hopple and Vilgalys, 1999 (as <i>Coprinus</i>)
<i>Coprinopsis xenobia</i>	AF041498	Hopple and Vilgalys, 1999 (as <i>Coprinus</i>)
<i>Coprinopsis phlyctidospora</i>	AF041499	Hopple and Vilgalys, 1999 (as <i>Coprinus</i>)
<i>Coprinopsis macrocephala</i>	AF041489	Hopple and Vilgalys, 1999 (as <i>Coprinus</i>)
<i>Coprinopsis</i> cf. <i>erythrocephala</i>	AF041496	Hopple and Vilgalys, 1999 (as <i>Coprinus</i>)
<i>Coprinopsis scobicola</i>	AF041491	Hopple and Vilgalys, 1999 (as <i>Coprinus</i>)
<i>Coprinopsis</i> cf. <i>Pseudoochraceovela</i>	AF041492	Hopple and Vilgalys, 1999 (as <i>Coprinus</i>)
<i>Coprinopsis radiata</i>	AF041493	Hopple and Vilgalys, 1999 (as <i>Coprinus</i>)
<i>Coprinopsis</i> cf. <i>Impexi</i>	AF041495	Hopple and Vilgalys, 1999 (as <i>Coprinus</i>)
<i>Coprinopsis trispora</i>	AF041504	Hopple and Vilgalys, 1999 (as <i>Coprinus</i>)
<i>Coprinopsis narcotica</i>	AF041506	Hopple and Vilgalys, 1999 (as <i>Coprinus</i>)
<i>Coprinopsis semitalis</i>	AF041508	Hopple and Vilgalys, 1999 (as <i>Coprinus</i>)
<i>Coprinopsis</i> cf. <i>americana</i>	AF041487	Hopple and Vilgalys, 1999 (as <i>Coprinus</i>)
<i>Coprinopsis quadrifida</i>	AF139945	Thorn et al., 2000 (as <i>Coprinus</i>)
<i>Coprinopsis cinerea</i>	AF041494	Hopple and Vilgalys, 1999 (as <i>Coprinus</i>)
<i>Coprinopsis sclerotiger</i>	AF041509	Hopple and Vilgalys, 1999 (as <i>Coprinus</i>)
<i>Coprinopsis</i> cf. <i>dictyocalyptrata</i>	AF041497	Hopple and Vilgalys, 1999 (as <i>Coprinus</i>)
<i>Coprinopsis kimurae</i>	AF041500	Hopple and Vilgalys, 1999 (as <i>Coprinus</i>)
<i>Coprinopsis gonophylla</i>	AF041502	Hopple and Vilgalys, 1999 (as <i>Coprinus</i>)
<i>Coprinopsis friesii</i>	AF041503	Hopple and Vilgalys, 1999 (as <i>Coprinus</i>)
<i>Coprinopsis utrifer</i>	AF041501	Hopple and Vilgalys, 1999 (as <i>Coprinus</i>)
<i>Coprinopsis cothurnata</i>	AF041507	Hopple and Vilgalys, 1999 (as <i>Coprinus</i>)
<i>Coprinopsis latispora</i>	AF041510	Hopple and Vilgalys, 1999 (as <i>Coprinus</i>)
<i>Parasola nudiceps</i>	AF041517	Hopple and Vilgalys, 1999 (as <i>Coprinus</i>)
<i>Parasola megasperma</i>	AF041518	Hopple and Vilgalys, 1999 (as <i>Coprinus</i>)
<i>Parasola auricoma</i>	AF041519	Hopple and Vilgalys, 1999 (as <i>Coprinus</i>)
“ <i>Coprinus</i> ” cf. <i>cordisporus</i>	AF041511	Hopple and Vilgalys, 1999 (as <i>Coprinus</i>)
<i>Coprinellus curtus</i>	AF041527	Hopple and Vilgalys, 1999 (as <i>Coprinus</i>)
<i>Coprinellus heterosetulosus</i>	AF041520	Hopple and Vilgalys, 1999 (as <i>Coprinus</i>)
<i>Coprinellus</i> cf. <i>sclerocystidiosus</i>	AF041521	Hopple and Vilgalys, 1999 (as <i>Coprinus</i>)
<i>Coprinellus bisporus</i>	AF041523	Hopple and Vilgalys, 1999 (as <i>Coprinus</i>)
<i>Coprinellus congregatus</i>	AF041528	Hopple and Vilgalys, 1999 (as <i>Coprinus</i>)

Appendix A. (continued)

Taxon	GenBank Accession No.	Source: Strain No. ^a
<i>Coprinellus callinus</i>	AF041524	Hopple and Vilgalys, 1999 (as <i>Coprinus</i>)
<i>Coprinellus aokii</i>	AF041526	Hopple and Vilgalys, 1999 (as <i>Coprinus</i>)
<i>Coprinellus flocculosus</i>	AF041515	Hopple and Vilgalys, 1999 (as <i>Coprinus</i>)
<i>Coprinellus xanthothrix</i>	AF041512	Hopple and Vilgalys, 1999 (as <i>Coprinus</i>)
<i>Coprinellus micaceus</i>	AF041513	Hopple and Vilgalys, 1999 (as <i>Coprinus</i>)
<i>Coprinellus domesticus</i>	AF041514	Hopple and Vilgalys, 1999 (as <i>Coprinus</i>)
<i>Coprinellus radians</i>	AF041516	Hopple and Vilgalys, 1999 (as <i>Coprinus</i>)
<i>Coprinellus disseminatus</i>	AF041525	Hopple and Vilgalys, 1999 (as <i>Coprinus</i>)
<i>Coprinellus heptemerus</i>	AF041522	Hopple and Vilgalys, 1999 (as <i>Coprinus</i>)
<i>Psathyrella gracilis</i>	AF041533	Hopple and Vilgalys, 1999
<i>Psathyrella</i> sp.	AF261488	This work: (D) JMCR.119
<i>Psathyrella candolleana</i>	AF041531	Hopple and Vilgalys, 1999
<i>Psathyrella delineata</i>	AF041532	Hopple and Vilgalys, 1999
<i>Psathyrella</i> aff. <i>vanhermanii</i>	AF261487	This work: (D) JMCR.31
<i>Psathyrella camptopoda</i>	AF261489	This work: DAOM214256
<i>Lacrymaria velutina</i>	AF041534	Hopple and Vilgalys, 1999
	AF139972*	Thorn et al., 2000
<i>Crepidotus crocophyllus</i>	AF139946	Thorn et al., 2000
<i>Crepidotus nephrodes</i>	AF205670	This work: (V) MCA 189
	AF205672*	This work: (V) OKM27048
<i>Crepidotus distortus</i>	AF205671	This work: (V) MCA386
<i>Crepidotus applanatus</i> v. <i>globigera</i>	AF205673	This work: (V)MCA188
<i>Crepidotus malachius</i>	AF205674	This work: (V) MCA343
<i>Crepidotus herbarum</i>	n.a.	This work: DAOM196391
<i>Crepidotus</i> sp.	AF205675	This work: (V) MCA258
<i>Crepidotus fraxinicola</i>	AF205676	This work: (V) OKM26739
<i>Crepidotus mollis</i>	AF205677	This work: (V) OKM26279
<i>Crepidotus uber</i>	AF205702	This work: (V) MCA672
<i>Crepidotus</i> cf. <i>subaffinis</i>	AF205703	This work: (V) MCA604
<i>Crepidotus inhonestus</i>	AF205704	This work: (V) MCA638
<i>Crepidotus lundelli</i>	AF205705	This work: (V)MCA163
<i>Crepidotus amygdalosporus</i>	AF205678	This work: (V) OKM26
<i>Crepidotus versutus</i>	AF205683	This work: (V)MCA381
<i>Crepidotus</i> sp.	AF205684	This work: (V) OKM26899
<i>Crepidotus aureus</i>	AF205685	This work: (V) OKM27300
<i>Crepidotus cesatii</i>	AF205681	This work: (V) OKM26976
<i>Crepidotus sphaerosporus</i>	AF205682	This work: (V) OKM270
<i>Crepidotus cinnabarinus</i>	AF205686	This work: (V) MCA387
<i>Crepidotus</i> sp.	AF205669	This work: (V) OKM27270
<i>Crepidotus betula</i>	AF205679	This work: (V) MCA384
<i>Crepidotus antillarum</i>	AF205680	This work: (V) OKM26827
<i>Crepidotus nyssicola</i>	AF205690	This work: (V) TJB8699
<i>Simocybe</i> sp.	AF205687	This work: (V) MCA424
<i>Simocybe sumptuosa</i>	AF205688	This work: (V) OKM27046
<i>Simocybe amara</i>	AF205708	This work: (V) MCA682
<i>Simocybe americana</i>	AF205709	This work: (V) VTMH3760
<i>Simocybe centuncula</i>	AF205707	This work: (V) MCA393
<i>Simocybe</i> sp.	AF205706	This work: (V) MCA750
<i>Pleuroflammula</i> sp.	AF208533	This work: (V) OKM24609
<i>Pleuroflammula flammea</i>	AF261490	This work: DAOM194781
	AF261491*	This work: DAOM198223
<i>Tubaria furfuracea</i>	AF205710	This work: (V) MCA391
<i>Tubaria hiemalis</i>	AF205689	This work: (V) MCA385

Appendix A. (continued)

Taxon	GenBank Accession No.	Source: Strain No. ^a
<i>Tubaria rufo-fulva</i>	AF205712	This work: (V) OKM24681
<i>Tubaria</i> sp.	AF205711	This work: (V) OKM24351
<i>Phaeomarasmium erinaceus</i>	AF261492	This work: DAOM153741
	AF261594*	This work: (L) SV.H4 = ECV934
<i>Flammulaster rhombisporus</i>	AF261493	This work: DAOM182559
<i>Laccaria bicolor</i>	AF042588	Moncalvo et al., 2000
<i>Laccaria ochropurpurea</i>	AF261494	This work: (D) JM96/46
<i>Laccaria vulcanica</i>	AF261495	This work: (D)JMCR.127
<i>Rapacea mariae</i>	AF261496	This work: ZT4339
<i>Rozites caperatus</i>	AF261497	This work: (D) G96/3
<i>Dermocybe marylandensis</i>	AF042615	Moncalvo et al., 2000
<i>Cortinarius subbalustinus</i>	AF195592	This work: SJ940
<i>Cortinarius iodes</i>	AF042613	Moncalvo et al., 2000
<i>Cortinarius</i> sp.	AF042614	Moncalvo et al., 2000
<i>Cortinarius distans</i>	AF261595	This work: (D) SV.S6
<i>Cortinarius vibratilis</i>	AF261498	This work: DAOM209287
<i>Cortinarius violaceus</i>	AF261499	This work: DAOM216796
<i>Cortinarius traganus</i>	AF261500	This work: DAOM212213
<i>Cortinarius speciosissimus</i>	AF261501	This work: DAOM174626
<i>Thaxterogaster pingue</i>	AF261550	This work: DAOM225303
	AF261549*	This work: IB19951102
<i>Thaxterogaster porphyreum</i>	AF261551	This work: (D) HN3036
<i>Thaxterogaster violaceus</i>	AF261552	This work: DAOM198883
<i>Phaeocollybia attenuata</i>	AF261502	This work: NORVELL1981111.C2.5
<i>Phaeocollybia redheadii</i>	AF261503	This work: DAOM215609
<i>Phaeocollybia kauffmanii</i>	AF261504*	This work: NORVELL1981104.01.3
<i>Phaeocollybia dissiliens</i>	AF261505	This work: NORVELL1981111.C2.6
<i>Phaeocollybia jennyae</i>	AF261506	This work: DAOM221500
<i>Squamanita odorata</i>	AF261507	This work: DAOM225481
<i>Squamanita umbonata</i>	AF261508	This work: DAOM199323
<i>Stagnicola perplexa</i>	AF261509	This work: DAOM191293
<i>Inocybe petiginosa</i>	AF261510	This work: DAOM174733
<i>Inocybe geophylla</i> var. <i>lilacea</i>	AF042616	Moncalvo et al., 2000
<i>Inocybe</i> sp.	AF042617	Moncalvo et al., 2000
<i>Psilocybe</i> sp.	AF042618	Moncalvo et al., 2000 (as <i>P. silvatica</i>)
<i>Psilocybe phyllogena</i>	AF261596	This work: (L) v220 = CBS102746
<i>Psilocybe micropora</i>	AF261597	This work: (L) v226 = CBS101990
<i>Psilocybe inquilinus</i>	AF261598	This work: (L) v188 = CBS102740
<i>Psilocybe subviscida</i>	AF261599	This work: (D) D580
<i>Psilocybe pratensis</i>	AF261600	This work: (L) v189 = CBS101972
<i>Psilocybe xeroderma</i>	AF261601	This work: (L) v221 = CBS101989
<i>Psilocybe schoeneti</i>	AF261602	This work: (L) v200 = CBS101979
<i>Psilocybe crobula</i>	AF261603	This work: (L) v078 = CBS101835
<i>Psilocybe montana</i> v. <i>macrospora</i>	AF261604	This work: (L) v212 = CBS101983
<i>Psilocybe montana</i>	n.a.*	This work: (L) v069 = CBS101829
<i>Psilocybe chionophila</i>	AF261605	This work: c659 = CBS659.87 (type)
<i>Psilocybe</i> aff. <i>apelliculosa</i>	AF261606	This work: (L) v026 = CBS101811
<i>Psilocybe apelliculosa</i>	AF261607	This work: (L) v113 = CBS101867
<i>Melanotus phillipsii</i>	AF261608	This work: (L) v077 = CBS101833
<i>Melanotus subcuneiformis</i>	AF261511	This work: (D) RV.PR64
<i>Melanotus horizontalis</i>	AF261609	This work: (L) v208 = CBS101982
<i>Psilocybe pseudobullacea</i>	AF261610	This work: (L) v145 = CBS101873
<i>Psilocybe pseudobullacea</i>	AF261611	This work: (D) D2402 (AnnePringle)

Appendix A. (continued)

Taxon	GenBank Accession No.	Source: Strain No. ^a
<i>Psilocybe coprophila</i>	AF139971	Thorn et al., 2000
	AF261612*	This work: (L) v254 = CBS101998
<i>Psilocybe merdaria</i>	AF261613	This work: (L) v121 = CBS101859
<i>Psilocybe moelleri</i>	AF261614	This work: (L) v120 = CBS101858
<i>Psilocybe subcoprophila</i>	AF261615	This work: (L) v135
<i>Phaeogalera stagnina</i>	AF261512	This work: DAOM187559
<i>Kuehneromyces mutabilis</i>	AF042619	This work: (S) DSM1684
<i>Psilocybe stuntzii</i>	AF042567	This work: (V)VT 1263
	U11917*	Chapela et al., 1994
<i>Psilocybe semilanceata</i>	AF261616	This work: (L) v112 = CBS101853
<i>Psilocybe fimetaria</i>	AF261617	This work: (L) v051 = CBS101814
<i>Psilocybe liniformans</i>	AF261618	This work: (L) v185
<i>Psilocybe cubensis</i>	AF261619	This work: (L) v141
<i>Psilocybe cyanescens</i>	AF261620	This work: (L) v199 = CBS10197
<i>Psilocybe subaeruginosa</i>	AF261621	This work: (D) RV95/502 (= HN2883)
	AF261622*	This work: (D) RV95/448 (= HN3408)
<i>Pachylepyrium funariophilum</i>	AF261513	This work: (T) TENN6030
Unidentified agaric	AF261623	This work: (L) SV.S2
<i>Hebeloma</i> sp.	AF261514	This work: AANEN540
<i>Hebeloma crustuliniforme</i>	U11918	Chapela et al., 1994
<i>Hebeloma longicaudum</i>	AF261515	This work: DAOM176597
cf. <i>Pholiota lignicola</i>	AF195594	This work: SJ90025
<i>Flammula alnicola</i>	AF195588	This work: SJ86071
<i>Naucoria escharoides</i>	AF261516	This work: AANEN-M29
	AF261517*	This work: DAOM174734
<i>Stropharia semiglobata</i>	AF261624	This work: (L) v253
	AF261625*	This work: (L) v166 = CBS102729
<i>Stropharia umbonatescens</i>	AF261626	This work: (D) D602
cf. <i>Stropharia</i>	AF261518	This work: (D) JMCR.99
<i>Pholiota subochracea</i>	AF195598	This work: SJ85066
<i>Phaeonematoloma myosotis</i>	AF195599	This work: SJ97002
<i>Hypholoma udum</i>	AF261627	This work: (L) v038 (as <i>Psilocybe uda</i>)
<i>Hypholoma ericaeum</i>	AF261628	This work: (L) H16(HB7) = CB6321
<i>Hypholoma subericaeum</i>	AF261629	This work: (L) H15(HB8) = GHP996
<i>Hypholoma fasciculare</i>	AF261630	This work: CBS810.87
<i>Hypholoma subviride</i>	AF042570	Moncalvo et al., 2000
	AF261631*	This work: (L) SV.S4
<i>Hypholoma capnoides</i>	AF195595	This work: SJ84170
<i>Hypholoma sublateritium</i>	AF042569	Moncalvo et al., 2000
<i>Stropharia rugosoannulata</i>	AF041544	Hopple and Vilgalys, 1999
	AF139976	Thorn et al., 2000
	AF261632	This work: (L) v001 = CBS101784
<i>Hypholoma aurantiacum</i>	AF261633	This work: (L) H17(HB5) = Daams
<i>Stropharia magnivelaris</i>	AF195600	This work: SJ85098
<i>Leratiomyces similis</i>	AF042009	Binder et al., 1997
<i>Weraroa erythrocephala</i>	AF261634	This work: (D) RV95/656 = HN3037
<i>Stropharia coronilla</i>	AF261635	This work: (L) v073
	AF059232*	Mitchell and Bresinsky, 1999
<i>Stropharia hardii</i>	AF261636	This work: (L) SV.S3
	AF261637*	This work: (L) SV.S7
<i>Stropharia aeruginosa</i>	AF195597	This work: SJ76247
<i>Stropharia hornemannii</i>	AF195596	This work: SJ92047
	AF261638*	This work: CBS838.87

Appendix A. (continued)

Taxon	GenBank Accession No.	Source: Strain No. ^a
<i>Weraroa virescens</i>	AF042013	Binder et al., 1997
	AF261639*	This work: (D) RV95/669 = HN3050
<i>Pholiota squarrosoides</i>	AF042568	Moncalvo et al., 2000
	AF261641*	This work: (L) SV.S1
<i>Pholiota squarrosa</i>	AF261642	This work: (L) H24(HB17) = MEN
<i>Pholiota lenta</i>	AF195608	This work: SJ12894
	AF261643*	This work: CBS185.53
<i>Pholiota mixta</i>	AF195609	This work: SJ96022
<i>Pholiota highlandensis</i>	AF261644	This work: (L) v027
<i>Pholiota henningsii</i>	AF261645	This work: CBS710.84
<i>Pholiota lundbergii</i>	AF195607	This work: (E) LL950724
<i>Pholiota limonella</i>	AF195602	This work: (E) NH9200
<i>Pholiota aurivella</i>	AF195603	This work: SJ84131
<i>Pholiota jahnii</i>	AF195604	This work: SJ83118
<i>Pholiota gummosa</i>	AF195605	This work: SJ84095
<i>Pholiota conissans</i>	AF195606	This work: SJ96017
<i>Pholiota flammans</i>	AF195601	This work: SJ86074
<i>Hemipholiota lucifera</i>	AF261646	This work: (L) H26(HB12) = GHP1817
<i>Hemipholiota destruens</i>	AF261647	This work: (L) H18(HB16) = CB
<i>Hemipholiota populnea</i>	AF195593	This work: SJ94086
<i>Agrocybe praecox</i>	AF042644	Moncalvo et al., 2000
	AF041545*	Hopple and Vilgalys, 1999
	AF139941*	Thorn et al., 2000
<i>Agrocybe semiorbicularis</i>	AF139942	Thorn et al., 2000
<i>Agrocybe dura</i>	AF261648	This work: (L) v228
<i>Gastrocybe lateritia</i>	AF261519	This work: DAOM167564
<i>Bolbitius vitellinus</i>	U11913	Chapela et al., 1994
	AF041543*	Hopple and Vilgalys, 1999
<i>Bolbitius demangei</i>	AF261520	This work: (D) JMCR.137
<i>Conocybe rickenii</i>	AF041546	Hopple and Vilgalys, 1999
<i>Pholiotina subnuda</i>	AF261521	This work: DAOM208660
<i>Naucoria bohemica</i>	AF261522	This work: DAOM174734
<i>Descolea gunnii</i>	AF261523	This work: (D) DUKE3001
<i>Leratiomyces smaragdina</i>	AF042011	Binder et al., 1997
<i>Galerina marginata</i>	AF195590	This work: (E) RM3225
<i>Galerina nana</i>	AF261524	This work: DAOM208552
<i>Panaeolina foenicicii</i>	U11924	Chapela et al., 1994
	AF041537*	Hopple and Vilgalys, 1999
<i>Panaeolus acuminatus</i>	AF041535	Hopple and Vilgalys, 1999
<i>Panaeolus</i> sp.	AF261525	This work: (D) JM98/6
<i>Panaeolus semiovatus</i>	AF041536	Hopple and Vilgalys, 1999
<i>Copelandia cyanescens</i>	AF261526	This work: (D) JM98/10
<i>Pholiota oedipus</i>	AF261649	This work: (L) H19(HB6) = GHP1469
<i>Stropharia albocrenulata</i>	AF195589	This work: (E) KGN94
<i>Pholiota tuberculosa</i>	AF195587	This work: SJ86019
<i>Ripartites metrodii</i>	AF042012	Binder et al., 1997
<i>Gymnopilus aeruginosus</i>	AF261650	This work: CBS296.36
<i>Gymnopilus spectabilis</i>	AF261651	This work: CBS489.90
<i>Gymnopilus junonius</i>	AF195591	This work: SJ84074
<i>Gymnopilus penetrans</i>	AF261652	This work: CBS168.79
<i>Hebelomina neerlandica</i>	AF261527	This work: CBS169.79
<i>Galerina paludosa</i>	AF261528	This work: DAOM197244
	AF261653*	This work: CBS388.88

Appendix A. (continued)

Taxon	GenBank Accession No.	Source: Strain No. ^a
<i>Cantharocybe gruberi</i>	AF261529	This work: DAOM225482
	AF261530*	This work: DED6609
<i>Volvariella volvacea</i>	AF261531	This work: (D) JMleg.SRL
<i>Volvariella hypopithys</i>	AF261532	This work: (D) JMleg.AIME
<i>Schizophyllum commune</i>	AF261587	This work: (D) TYJ.Belize1
<i>Schizophyllum radiatum</i>	AF261588	This work: CBS301.32
<i>Schizophyllum fasciatum</i>	AF261589	This work: CBS267.60.
<i>Schizophyllum umbrinum</i>	AF261590	This work: (D) FL02.1
<i>Schizophyllum amplum</i>	AF261591	This work: (D) RGT-970618/01
<i>Fistulina hepatica</i>	AF261592	This work: (D) DSH93-183
<i>Porodisculus pendulus</i>	AF261593	This work: DAOM198417
<i>Phylloporus rhodoxanthus</i>	U11925	Chapela et al., 1994
<i>Boletus retipes</i>	U11914	Chapela et al., 1994
<i>Suillus luteus</i>	AF042622	Moncalvo et al., 2000
<i>Hygrophoropsis aurantiaca</i>	AF042007	Binder et al., 1997
<i>Boletus satanas</i>	AF042015	Binder et al., 1997
<i>Scleroderma columnare</i>	AF261533	This work: (D) JMCR.77
<i>Russula earlei</i>	AF042571	Moncalvo et al., 2000
<i>Russula mairei</i>	U11926	Chapela et al., 1994
<i>Russula virescens</i>	AF041548	Hopple and Vilgalys, 1999
<i>Russula romagnesii</i>	AF042572	Moncalvo et al., 2000
<i>Lactarius corrugis</i>	U11919	Chapela et al., 1994
<i>Lactarius piperatus</i>	AF042573	Moncalvo et al., 2000
<i>Lactarius</i> sp.	AF042574	Moncalvo et al., 2000 (as <i>L. volemus</i>)
<i>Bondarzewia mesenterica</i>	AF042646	Moncalvo et al., 2000
<i>Heterobasidion annosum</i>	AF139949	Thorn et al., 2000
<i>Auriscalpium vulgare</i>	AF261281	This work: (E) F799
<i>Faerberia carbonaria</i>	AF139947	Thorn et al., 2000
<i>Neolentinus dactyloides</i>	AF135174	Thorn et al., 2000
<i>Podoscypha parvula</i>	AF261534	This work: DAOM171399
<i>Beenakia</i> sp.	AF261535	This work: (D) PR10 june 97
<i>Ganoderma lucidum</i> gr.	X78776	Moncalvo et al., 1995
<i>Ganoderma australe</i> gr.	X78780	Moncalvo et al., 1995
<i>Amauroderma omphalodes</i>	n.a.	This work: (D) MUCL4027
<i>Pycnoporus cinnabarinus</i>	AF261536	This work: DAOM72065
<i>Lentinus tigrinus</i>	AF135173	Thorn et al., 2000
<i>Lentinus squarrosulus</i>	AF261563	This work: (D) Neda C500
<i>Panus</i> sp.	AF261564	This work: (D) E.Kay88/65
<i>Panus</i> sp.	AF261565	This work: (D) RV95/37
<i>Trametes suaveolens</i>	AF261537	This work: (H) DAOM196328
<i>Fomes fomentarius</i>	AF261538	This work: (H) DAOM129034
<i>Polyporus squamosus</i>	AF135181	Thorn et al., 2000
<i>Dentocorticium sulphurellum</i>	AF261539	This work: (H) FPL11801
<i>Polyporus varius</i>	AF261540	This work: (H) DSH93/195
<i>Datronia mollis</i>	AF261541	This work: (H) DAOM211792
<i>Daedaleopsis confragosa</i>	AF261542	This work: (H) DAOM180 496
<i>Lenzites betulina</i>	AF261543	This work: (H) DAOM180504
<i>Polyporus tuberaster</i>	AF261544	This work: (H) DAOM79978
<i>Polyporus melanopus</i>	AF261545	This work: (H) DAOM212269
<i>Gloeophyllum trabeum</i>	AF139948	Thorn et al., 2000
<i>Irpex lacteus</i>	AF139961	Thorn et al., 2000
<i>Phanerochaete chrysorhiza</i>	AF139967	Thorn et al., 2000
<i>Phanerochaete chrysosporium</i>	AF139966	Thorn et al., 2000

Appendix A. (continued)

Taxon	GenBank Accession No.	Source: Strain No. ^a
<i>Ceraceomyces serpens</i>	AF090882	Larsson and Larsson, 1998
<i>Ceraceomyces microsporus</i>	AF090874	Larsson and Larsson, 1998
<i>Ceraceomyces eludens</i>	AF090881	Larsson and Larsson, 1998
<i>Phlebia lilascens</i> GR.2	AF141621	Hallenberg and Parmasto (GenBank)
<i>Phlebia nitidula</i>	AF141625	Hallenberg and Parmasto (GenBank)
<i>Phlebia centrifuga</i>	AF141618	Hallenberg and Parmasto (GenBank)
<i>Phlebia acerina</i>	AF141615	Hallenberg and Parmasto (GenBank)
<i>Phlebia lindtneri</i>	AF141623	Hallenberg and Parmasto (GenBank)
<i>Phlebia livida</i>	AF141624	Hallenberg and Parmasto (GenBank)
<i>Pseudotomentella ochracea</i>	AF092847	Hallenberg and Parmasto (GenBank)
<i>Phlebiopsis gigantea</i>	AF141634	Hallenberg and Parmasto (GenBank)
<i>Gelatoporia pannocincta</i>	AF141612	Hallenberg and Parmasto (GenBank)
<i>Hyphodontia radula</i>	AF141613	Hallenberg and Parmasto (GenBank)
<i>Phlebia bresadolae</i>	AF141617	Hallenberg and Parmasto (GenBank)
<i>Phlebia deflectens</i>	AF141619	Hallenberg and Parmasto (GenBank)
<i>Phlebia griseoflavescens</i>	AF141620	Hallenberg and Parmasto (GenBank)
<i>Phlebia lilascens</i> GR.3	AF141622	Hallenberg and Parmasto (GenBank)
<i>Phlebia queletii</i>	AF141626	Hallenberg and Parmasto (GenBank)
<i>Phlebia radiata</i>	AF141627	Hallenberg and Parmasto (GenBank)
<i>Phlebia rufa</i>	AF141628	Hallenberg and Parmasto (GenBank)
<i>Phlebia subochracea</i>	AF141630	Hallenberg and Parmasto (GenBank)
<i>Phlebia subserialis</i>	AF141631	Hallenberg and Parmasto (GenBank)
<i>Phlebia tremellosa</i>	AF141632	Hallenberg and Parmasto (GenBank)
<i>Phlebia tristis</i>	AF141633	Hallenberg and Parmasto (GenBank)
<i>Phlebia uda</i>	AF141614	Hallenberg and Parmasto (GenBank)
<i>Resinicium bicolor</i>	AF141635	Hallenberg and Parmasto (GenBank)
<i>Trichaptum abietinum</i>	AF141636	Hallenberg and Parmasto (GenBank)
<i>Postia placenta</i>	AF139970	Thorn et al., 2000
<i>Lentaria michneri</i>	AF261546	This work: (D) RV98/147
<i>Ramaria eumorpha</i>	AF139973	This work: (G) T798
<i>Gomphus novaezelandia</i>	AF261547	This work: ZT68-657
<i>Gloeocantharellus okapaensis</i>	AF261548	This work: ZT7135
<i>Protuberia</i> sp.	AF261555/233	This work: (D) JM98/351
<i>Aseroe arachnoidea</i>	AF139943	This work: (G) TMI50070
<i>Multiclavula vernalis</i>	U66439	Lutzoni, 1997
<i>Multiclavula corynoides</i>	U66440	Lutzoni, 1997
<i>Clavulina cristata</i>	AF261553	This work: (D) RV98/144
<i>Serpula lacrimans</i>	AF139974	Thorn et al., 2000
<i>Sphaerobolus stellatus</i>	AF139975	This work: (G) T800
<i>Auricularia polytricha</i>	AF261554	This work: (D) HN4076

^aOrigin of material as follows: AANEN, Duur Aanen, Netherlands; (B), Jean Bérubé, Canada; BSI, Béatrice Senn-Irlet, Switzerland; (C), SUNY Cortland, U.S.A.; CALLAC, Philippe Callac, France; CBS, Centraalbureau voor Schimmelcultures, Netherlands; (D), Duke University, U.S.A.; DAOM, National Mycological Herbarium, Canada; DED, Dennis Desjardin, San Francisco State University, U.S.A.; (E), Ellen Larsson; (G), Greg Thorn; G. Platas, sequence provided by Gonzala Platas, MERK, Spain; (H), DNA provided by David Hibbett, Clark University, U.S.A.; HAL-LING, Roy Halling, New York Botanical Garden, U.S.A.; HHB, Hal Burdsall, U.S.A.; IB, University of Innsbruck, Austria; IFO, Institute for fermentation, Japan; (J), James Johnson; JLPR, Jean Lodge, Puerto Rico; (L), University of Leiden, Netherlands; NORVELL, Lorelei Norvell, Portland, U.S.A.; (S), University of Lausanne, Switzerland; SJ, Stig Jacobsson; (T), University of Tennessee, U.S.A.; UPS, Uppsala Herbarium Sweden; (V), Virginia Tech, U.S.A.; ZT, ETH Zürich, Switzerland.

* Strain not used in the final analysis (cluster with the taxon listed above in preliminary analyses).

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