A revised family-level classification of the Polyporales (Basidiomycota)

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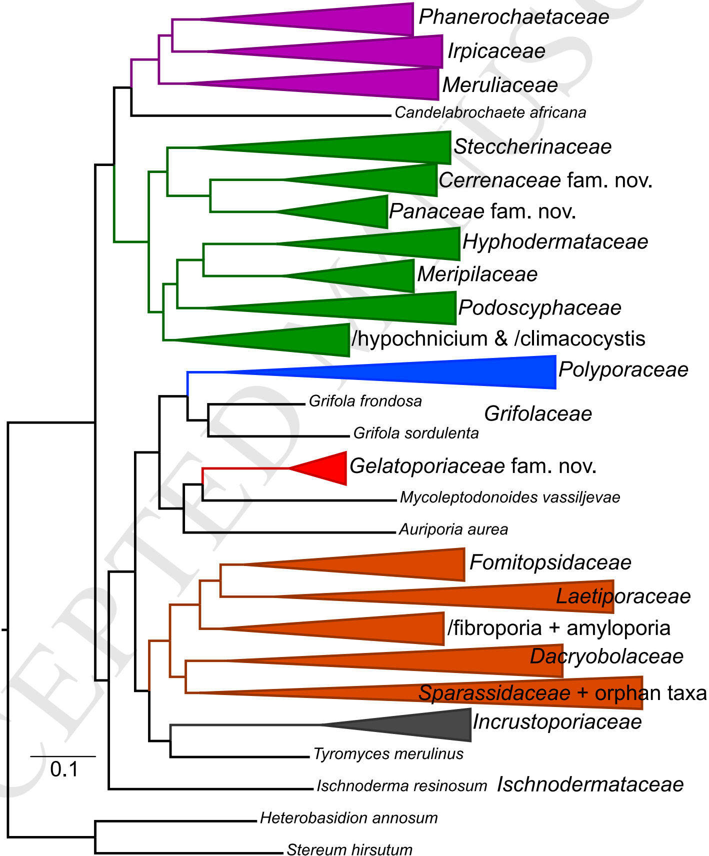
Phanerochaetaceae
Irpicaceae
Meruliaceae
Candelabrochaete africana
Steccherinaceae
Cerrenaceae fam. nov.
Panaceae fam. nov.
Hyphodermataceae
Meripilaceae
Podoscyphaceae
/hypochnicium & /climacocystis
Polyporaceae
Grifola frondosa
Grifolaceae
Grifola sordulenta
Gelatoporiaceae fam. nov.
Mycoleptodonoides vassiljevae
Auriporia aurea
Fomitopsidaceae
Laetiporaceae
/fibroporia + amyloporia
Dacryobolaceae
Sparassidaceae + orphan taxa
Incrustoporiaceae
Tyromyces merulinus
0.1
Ischnoderma resinosum
Ischnodermataceae
Heterobasidion annosum
Stereum hirsutum

Title: A revised family-level classification of the *Polyporales* (*Basidiomycota*)

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Abstract: *Polyporales* is strongly supported as a clade of *Agaricomycetes*, but the lack of a consensus higher-level classification within the group is a barrier to further taxonomic revision. We amplified nrLSU, nrITS and *rpb1* genes across the *Polyporales*, with a special focus on the latter. We combined the new sequences with molecular data generated during the PolyPEET project and performed Maximum Likelihood and Bayesian phylogenetic analyses. Analyses of our final 3-gene dataset (292 *Polyporales* taxa) provide a phylogenetic overview of the order that we translate here into a formal family-level classification. Eighteen clades are assigned a family name, including three families described as new (*Cerrenaceae* fam. nov., *Gelatoporiaceae* fam. nov., *Panaceae* fam. nov.) and fifteen others (*Dacryobolaceae*, *Fomitopsidaceae, Grifolaceae, Hyphodermataceae*, *Incrustoporiaceae*, *Irpicaceae, Ischnodermataceae, Laetiporaceae, Meripilaceae, Meruliaceae, Phanerochaetaceae*, *Podoscyphaceae*, *Polyporaceae*, *Sparassidaceae*, *Steccherinaceae*). Three clades are given informal names (/hypochnicium, /climacocystis and /fibroporia+amyloporia). Four taxa (*Candelabrochete africana*, *Mycoleptodonoides vassiljevae*, *Auriporia aurea* and *Tyromyces merulinus*) cannot be assigned to a family within the *Polyporales*. The classification proposed here provides a framework for further taxonomic revision and will facilitate communication among applied and basic scientists. A survey of morphological, anatomical, physiological and genetic traits confirms the plasticity of characters previously emphasized in taxonomy of *Polyporales*.

Key Words: *Polyporales*; *rpb1*; family-level taxonomy; phylogeny, PolyPEET

1. Introduction

Polyporales is one of the most intensively studied clades of *Fungi*. According to MycoBank, there have been 577 taxonomic proposals in *Polyporales* from 2010 to 2017, including 42 new genera and one new family, *Fragiliporiaceae* (Zhao *et al.* 2015). Over the same period, 2183 publications with the keyword “Polyporales” are recorded in PubMed. As major wood-decay fungi, species of *Polyporales* are of interest to both fungal ecologists and applied scientists. The first species of *Agaricomycotina* to have its genome sequenced, the model white rot fungus *Phanerochaete chrysosporium*, is a member of *Polyporales* (Martinez *et al.* 2004). The first brown rot genome, *Rhodonia (Postia) placenta*, was also a polypore (Martinez *et al.* 2009). At present, there are 46 genomes of *Polyporales* hosted by the Joint Genome Institute MycoCosm portal (Grigoriev *et al.* 2013), which is about 22% of all 212 *Agaricomycotina* genomes, or about 6% of all 772 fungal genomes. However, with roughly 1800 described species, *Polyporales* account for only about 1.5% of all known species of *Fungi* (Kirk *et al.* 2008).

Polyporales were sampled extensively in phylogenetic studies using ribosomal RNA (rRNA) genes (Binder *et al.* 2005; Boidin *et al.* 1998; Hibbett and Donoghue 1995; Hibbett and Vilgalys 1993; Larsson *et al.* 2004). From such analyses, four informally named clades of *Polyporales* were recognized: /antrodia, /core polyporoid, /phlebioid and /residual (the / notation is used here to denote clade names; /antrodia is read as “ (the) antrodia clade”), but support for these groups, and their interrelationships, was often lacking. Addition of protein-coding genes, including RNA polymerase II subunit 2 (*rpb2*), and translation elongation factor 1-α (*tef1*) was necessary to achieve strong support for monophyly of *Polyporales* as a whole, and many internal nodes (Matheny *et al.* 2007).

The PolyPEET project (http://wordpress.clarku.edu/polypeet/), which was active from 2010 to 2016, focused on systematics of *Polyporales*. PolyPEET supported research on taxonomy of *Trametes* (Justo & Hibbett 2010; Carlson *et al.* 2014), *Phanerochaete* (Floudas & Hibbett 2015), *Lentinus* (Seelan *et al.* 2015), and the brown-rot polypores (Ortiz-Santana *et al.* 2013; Spirin *et al.* 2013a,b), as well as comparative genomics (Binder *et al.* 2013; Ruiz-Dueñas *et al.* 2013; Riley *et al.* 2014), sapwood and foliar endophytes (which contain a surprising diversity of *Polyporales*; Martin *et al.* 2015), and bioremediation (Young *et al.* 2015).

Binder *et al.* (2013) presented the most comprehensive phylogenetic analyses for *Polyporales* so far, including analyses of a 373-species, six-gene supermatrix, containing sequences from genes encoding rRNA (nrLSU, 5.8S, and nrSSU), RNA polymerase II subunits 1 and 2 (*rpb1*, *rpb2*), and *tef1*. Binder *et al.* also analyzed ten *Polyporales* genomes, and performed phylogenetic informativeness profiling to assess the resolution afforded by individual genes. The analyses of Binder *et al.* upheld /antrodia, /core polyporoid, /phlebioid and /residual, with varying levels of support. Several lineages outside these major clades were also recovered. Phylogenetic informativeness profiling suggested that the RNA polymerase II large subunit (*rpb1*) is the most informative gene among those traditionally used in *Polyporales* systematics. Unfortunately, it also turned out to be the least represented in public databases.

Polyporales is now well accepted as a strongly supported clade of *Agaricomycetes* (Hibbett *et al.* 2014). However, further taxonomic revision and general communication about *Polyporales* is hampered by the lack of a consensus classification within the group. As reviewed by Binder *et al.* (2013), there are forty nomenclaturally valid family names in *Polyporales*, plus the new *Fragiliporiaceae*, although many names are rarely used. The present study continues where that of Binder *et al.* (2013) left off and evaluates the status of 37 of the legitimate family names available in the *Polyporales*. New molecular data were obtained from across the *Polyporales*, emphasizing *rpb1* and focusing on taxa of phylogenetic and nomenclatural relevance. The new data were combined with sequences generated during the PolyPEET project and from other resources, including genomes, yielding a dataset with 292 species. A classification with eighteen families and four informal unranked clades is proposed, and the distribution of morphological, anatomical, physiological, and genetic characters that have been emphasized in prior taxonomy of *Polyporales* is reviewed.

2. Material & Methods

2.1. Fungal isolates and DNA extraction

Culture collections and specimens were retrieved from the Center for Forest Mycology Research (USDA Forest Service, Madison, Wisconsin, U.S.A.), the Finnish Museum of Natural History at the University of Helsinki (Herbarium H), supplemented with c. 60 new collections and cultures made during the PolyPEET project. Protocols for culture growth and DNA extraction were the same ones outlined in Justo & Hibbett (2011).

2.2. PCR amplification and sequencing

The target loci for this study were nrITS, nrLSU and *rpb1*, with a special focus on *rpb1*. For nrITS the primer pair ITS-1F/ITS4 was used (White *et al.*, 1990; Gardes & Bruns, 1993). For nrLSU either the combinations LR0R/LR7 or LR0R/LR5 were used, with additional sequencing primers LR3 and LR5 (Vilgalys Lab, http://www.biology.duke.edu/fungi/mycolab/primers). The area between conserved domains A and C of *rpb1* (approx. 1400 bp) was amplified using the primer pair *rpb1*-Af and *rpb1*-Cr (Stiller & Hall, 1997; Matheny *et al.*, 2002). In some cases the primer *rpb1* -2.2f (Binder *et al.*, 2010) was used as an alternative to *rpb1* -Af, giving a slightly shorter product (approx. 1000 bp). Additional sequencing primers were: *rpb1*-2f, *rpb1*-2.1f, *rpb1*-2.2f, and *rpb1*-2.1r (Frøslev *et al.*, 2005). Expected fragment lengths and degree of primer overlap for *rpb1* are posted at http://wordpress.clarku.edu/polypeet/datasets/primer-information/. We used the same PCR protocols outlined in Justo & Hibbett (2011). The PCR products were sequenced using BigDye 3.1 terminator sequencing chemistry (Applied Biosystems, Foster City, California, U.S.A.).

Raw data were processed using Sequencher v.4.7 (GeneCodes, Ann Arbor, Michigan, U.S.A.).

2.3 Sequence alignment and phylogenetic analyses

To construct the final datasets we combined our newly generated nrITS, nrLSU and *rpb1* data with all previously generated sequences during the PolyPEET project. We then added *rpb1* sequences of *Polyporales* available in GenBank (not coming from the PolyPEET project), and retrieved additional *rpb1* data from the genomes available at MycoCosm (Grigoriev *et al.* 2013) for the following species: *Dichomitus squalens, Ganoderma sessile, Heterobasidion annosum, Phlebia brevispora, Stereum hirsutum,* *Wolfiporia cocos*. At this point we excluded all taxa without *rpb1* from further analyses. For taxa represented by multiple nrLSU + nrITS sequences in the nrDNA dataset, only one sequence set per taxon was included in the final 3-gene dataset.

The sequences were aligned using MAFFT v.7 (Katoh & Standley, 2013; http://mafft.cbrc.jp/alignment/server/). The strategy FFT-NS-i was selected for nrLSU and *rpb1*, and the strategy Q-INS-i for nrITS, as they were deemed the more appropriate given the nature and size of the datasets. The alignments were edited and manually corrected using AliView (Larsson 2014). For the combined datasets each gene was aligned separately and then concatenated. Three different datasets were assembled: *rpb1*-only, nrLSU+nrITS and a combined 3-gene dataset.

For all datasets two different analyses were performed: (i) Maximum likelihood analyses (ML) were performed with RAxML v.8.2.8 (Stamatakis, 2014), under a GTR model with one hundred rapid bootstrap replicates; (ii) Bayesian analyses (BY) were performed with MrBayes v.3.2.6 (Ronquist *et al.* 2012) for 10 million generations, under a GTR model, with four chains, and trees sampled every 100 generations. Convergence of the separate runs was confirmed by checking the average standard deviation of split frequencies (Ronquist *et al.* 2012). The initial burn-in phase was set to 2.5 million generations and after examining the graphic representation of the likelihood scores of the sampled trees, using Tracer (Drummond *et al.* 2012), this burn-in value was confirmed to be an adequate value for all datasets. A fifty percent majority-rule consensus tree was computed using the remaining trees. Both ML and BY analyses were run at the CIPRES Science Gateway (Miller *et al.* 2010; http://www.phylo.org/). In all analyses *Stereum hirsutum* and *Heterobasidion annosum* (Russulales) were used as outgroup taxa.

A search for potential conflicts between the nrDNA (LSU + ITS) dataset, and the *rpb1*-dataset was performed by comparing the resulting trees for each dataset, and looking for strongly supported positive conflict i.e., we looked for alternative topologies for the same taxon, on the different datasets, that were supported by at least 70% bootstrap and 1 posterior probability. No strongly supported topological conflicts were detected between the datasets analyzed in the present study.

Morphological, physiological, and genetic characters for each family were compiled from the monographic treatments of Bernicchia (2004), Bernicchia & Pérez-

Gorjón (2010), Eriksson & Ryvarden (1973, 1975, 1976), Eriksson *et al.* (1978, 1981, 1984), Gilbertson & Ryvarden (1986, 1987), Hjorstam et al. (1987, 1988) Rajchenberg (2011) Reid (1965), Ryvarden (1991, 2010), and Ryvarden & Melo (2014).

3. Results

3.1. New sequences and alignments

A total of 144 *rpb1*, 127 nrITS and 67 nrLSU were generated in this study. The final *rpb1*-only alignment contains 292 ingroup taxa and 1612 total characters, with 1415 variable positions (87%). The nrDNA alignment contains 310 ingroup, combined nrLSU + nrITS sequences (some taxa appear more than once), and 2276 characters, with 1482 variable positions (65%). The 3-gene dataset contains 292 ingroup taxa (no duplicated taxa), and 3888 characters, with 2897 variable positions (74%).

All newly generated sequences are deposited in GenBank (Table 1). All alignment files, and associated tree files, have been deposited in TreeBASE (http://purl.org/phylo/treebase/phylows/study/TB2:S20775).

3.2 Phylogenetic analyses

The best tree from the ML analysis of the 3-gene dataset is presented in Figures 1-9, including support values from the BY consensus tree, which did not differ significantly in topology. Support values mentioned in the text are presented as (ML/BY).

The *Polyporales* can be subdivided into two main clades (Fig.1): (i) a clade including /phlebioid, /residual and *Candelabrochaete africana* (82/1) and (ii) a clade including /core polyporoid, /antrodia and satellite lineages (73/1). *Ischnoderma resinosum* appears as sister to this second clade, but with no support.

In Fig. 2 we give an overview of the families that we recognize in the *Polyporales*. A family name is assigned to 18 clades recovered in the analyses, including 3 families described as new here. Three clades are only given informal names (/hypochnicium, /climacocystis and /fibroporia+amyloporia). *Candelabrochaete africana, Mycoleptodonoides vassiljevae*, *Auriporia aurea* and *Tyromyces merulinus* cannot be placed with certainty in any of the recognized families. Comments about the internal topology of each one of these families are given in the Taxonomy section.

Some minor topological differences exist between the trees from the analyses of the ribosomal-only and *rpb1*-only datasets with respect to the 3-gene dataset. These differences involve taxa that are particularly labile in all analyses: *Candelabrochaete africana, Caudicicola gracilis, Tyromyces merulinus, Mycoleptodonoides vassiljevae, Auriporia aurea,* and *Ischnoderma resinosum.* In all cases the different placements in the ribosomal-only and *rpb1*-only datasets are not strongly supported. The trees for the ML and BY analyses of the ribosomal-only and *rpb1*-only datasets are available at TreeBASE S20775.

4. Taxonomy

When deciding on the application of existing family names a pragmatic approach has been chosen, attaching the available names to well-defined and well-supported clades in the phylogenies. For areas of the phylogeny still in need of additional research we have chosen to use family names that are already published (e.g. *Podoscyphaceae*), acknowledging that defining their limits and composition will need further studies. In cases where no family name is available, or if they cannot be applied with certainty based on the current phylogenetic information (e.g. *Laricifomitaceae*), informal clade names are recommended until a better resolved phylogeny is available (e.g. /hypochnicium, /climadodon, /fibroporia+amyloporia).

Alternative taxonomic arrangements were considered, including adopting more broadly or narrowly defined families for all groups under study. Two representative examples of both cases are discussed in detail under *Podoscyphaceae* and *Polyporaceae*. When multiple family names with equal nomenclatural priority are available for the same clade we have chosen the name that has been more widely used.

The list of taxa belonging to each family (or clade) is based on the results presented here (Figs. 1-9), as well as the phylogenies of Binder *et al.* (2013), Floudas & Hibbett (2015), Miettinen *et al.* (2012, 2016), Ortiz-Santana *et al.* (2013) and Sjökvist *et al.* (2012). Additional relevant references are mentioned under the comments for each family. Under “additional taxa” we list species of uncertain generic placement that have been confirmed to belong in each family. The study of the genus-level taxonomy within each family falls out of the scope of the present paper, but in some particularly problematic cases (e.g. *Phlebia* s. lato, /antrodia) some comments are given, and generic types are highlighted in the respective figures.

We provide a short morphological characterization for each family, that is intended to apply to the majority of the species included in that family, but exceptions do occur in most cases. A morphological overview of all families recognized here is given in Table 2.

4.1 *Phanerochaetaceae* Jülich 1981 (Fig. 3)

Synonym. *Hapalopilaceae* Jülich 1981

Synonym. *Bjerkanderaceae* Jülich 1981

Type genus: *Phanerochaete* P. Karst.

Mostly corticioid species; hyphal system monomitic; hyphae without clamp-connections; spores thin-walled, smooth, hyaline; cystidia often present. More rarely polypores and/or dimitic and/or clamp-connections present. Producing a white-rot.

Genera: *Bjerkandera* P. Karst, *Donkia* Pilát, *Hapalopilus* P. Karst, *Hyphodermella* J. Erikss. & Ryvarden, *Oxychaete* Miettinen, *Phaeophlebiopsis* Floudas & Hibbett, *Phanerina* Miettinen, *Phlebiopsis* Jülich (including *Castanoporus* Ryvarden, see Miettinen *et. al.* 2016), *Pirex* Hjortstam & Ryvarden, *Porostereum* Pilát, *Rhizochaete* Gresl., Nakasone & Rajchenb., *Riopa* D.A. Reid, *Terana* Adans.

Additional taxa: *Ceriporiopsis carnegieae* (D.V. Baxter) Gilb. & Ryvarden, *Phanerochaete lamprocystidiata* Sheng H. Wu, *Phanerochaete lutea* (Sheng H. Wu) Hjortstam, *Phlebia bresadolae* Parmasto, *Phlebia deflectens* (P. Karst.) Ryvarden, *Phlebia firma* J. Erikss. & Hjortstam, *Phlebia lilascens* (Bourdot) J. Erikss. & Hjortstam, *Phlebia unica* (H.S. Jacks. & Dearden) Ginns, *Phlebiopsis himalayensis* Dhingra, *Phlebiopsis roumeguerii* (Bres.) Jülich & Stalpers.

Comments: The names *Hapalopilaceae* and *Bjerkanderaceae* have equal nomenclatural priority, but are placed here as synonyms of *Phanerochaetaceae*. A comprehensive overview of the genus *Phanerochaete* and related taxa has been recently published (Floudas & Hibbett 2015), combining morphological and molecular data. Although the limits of *Phanerochaete* s. stricto are now clearly defined, many species still await proper generic placement (see additional taxa above), and generic concepts in the family are in need of additional research (Miettinen *et al.* 2016).

4.2 *Irpicaceae* Spirin & Zmitr. 2003 (Fig. 4)

Type genus: *Irpex* Fr.

Corticioid species or polypores; hyphal system monomitic; hyphae without clamp-connections; spores thin-walled, smooth, hyaline; cystidia often absent. More rarely dimitic and/or with cystidia and/or clamp-connections present. Producing a white-rot, except for one brown-rot genus (*Leptoporus*).

Genera: *Byssomerulius* Parmasto, *Ceriporia* Donk, *Cytidiella* Pouzar, *Efibula* Sheng H. Wu, *Emmia* Zmitr., Spirin & Malysheva, *Flavodon* Ryvarden, *Gloeoporus* Mont., *Hydnopolyporus* D.A. Reid, *Leptoporus* Quél., *Meruliopsis* Bondartsev, *Trametopsis* Tomšovský.

Additional taxa: *Candelabrochaete langloisii* (Pat.) Boidin, *Candelabrochaete septocystidia* (Burt) Burds., *Ceraceomyces eludens* K.H. Larss., *Ceraceomyces microsporus* K.H. Larss., *Ceraceomyces serpens* (Tode) Ginns, *Ceriporia lacerata* N. Maek., Suhara & R. Kondo, *Ceriporiopsis aneirina* (Sommerf.) Domański, *Ceriporiopsis resinascens* (Romell) Domański, *Hapalopilus ochraceolateritius* (Bondartsev) Bondartsev & Singer, *Phanerochaete allantospora* Burds. & Gilb., *Phanerochaete angustocystidiata* Sheng H. Wu, *Phanerochaete exilis* (Burt) Burds., *Phanerochaete ginnsii* Sheng H. Wu, *Phanerochaete intertexta* Sheng H. Wu, *Phanerochaete leptoderma* Sheng H. Wu, *Phanerochaete xerophila* Burds., *Phlebia albida* H. Post, *Phlebia albomellea* (Bondartsev) Nakasone, *Phlebia nitidula* (P. Karst.) Ryvarden.

Comments: *Irpicaceae* encompasses a great variation of basidiome and hymenophore types, with typical polypore and corticioid morphologies intermixing with each other. These morphological transitions have occurred repeatedly within this lineage (Floudas & Hibbett 2015; Miettinen *et al.* 2016); recognizing smaller, well-supported clades as independent families would not result in a more straightforward morphological grouping of these taxa. Microscopically, most members of the family are rather nondescript, with smooth hyaline spores, monomitic hyphal systems, non-clamped septa and lack of cystidia, however exceptions to this pattern do exist (e.g. cystidia in *Irpex*, *Emmia* and others; clamp-connections in *Gloeoporus* and others), and this combination of characters occurs also outside the *Irpicaceae*.

4.3 *Meruliaceae* Rea 1922 (Fig. 5)

Synonym. *Climacodontaceae* Jülich 1981

Synonym. *Phlebiaceae* Jülich 1981

Type genus: *Merulius* Fr.

Corticioid species or polypores, commonly with a waxy appearance when dry; hyphal system monomitic and tightly arranged; hyphae with clamp-connections; spores thin-walled, smooth, hyaline; cystidia often present. More rarely dimitic and/or without cystidia and/or without clamp-connections. Producing a white-rot.

Genera: *Aurantiopileus* Ginns, D.L. Lindner & T.J. Baroni, *Aurantiporus* Murrill, *Climacodon* P. Karst., *Crustodontia* Hjortstam & Ryvarden, *Hydnophlebia* Parmasto, *Lilaceophlebia* (Parmasto) Spirin & Zmitr., *Luteoporia* F. Wu, Jia J. Chen & S.H. He, *Mycoacia* Donk, *Mycoaciella* J. Erikss. & Ryvarden, *Phlebia* Fr., *Phlebiporia* Jia J. Chen, B.K. Cui & Y.C. Dai, *Sarcodontia* Schulzer, *Scopuloides* (Massee) Höhn. & Litsch.

Additional taxa: *Ceriporia alachuana* (Murrill) Hallenb., *Ceriporiopsis gilvescens* (Bres.) Domański, *Ceriporiopsis guidella* Bernicchia & Ryvarden, *Ceriporiopsis pseudoplacenta* Vlasák & Ryvarden, *Phanerochaete odontoidea* Sheng H. Wu, *Phanerochaete subglobosa* Sheng H. Wu, *Phanerochaete subodontoidea* Sheng H. Wu, *Phlebia acanthocystis* Gilb. & Nakasone, *Phlebia aurea* (Fr.) Nakasone, *Phlebia centrifuga* P. Karst., *Phlebia coccineofulva* Schwein., *Phlebia fascicularis* (Rick) Nakasone & Burds., *Phlebia hydnoidea* Schwein., *Phlebia ludoviciana* (Burt) Nakasone & Burds., *Phlebia nantahaliensis* Nakasone & Burds., *Phlebia subochracea* (Bres.) J. Erikss. & Ryvarden, *Phlebia uda* (Fr.) Nakasone, *Scopuloides hydnoides* (Cooke & Massee) Hjortstam & Ryvarden.

Comments: Species currently classified in *Phlebia* can be found in three different families: *Phanerochaetaceae, Irpicaceae* and *Meruliaceae*. The proposed synonymy of *Phlebia* and *Merulius* (Nakasone & Burdsall 1984) needs to be re-evaluated. A generic concept of *Phlebia* that includes *Merulius* would also need to include *Aurantiporus*, *Aurantiopileus* and *Ceriporiopsis pseudoplacenta*, based on the current phylogenetic results. The proposed synonymies of *Mycoacia* (Nakasone 1997) and *Mycoaciella* (Nakasone 2002) with *Phlebia* also need further attention. The generic type of *Mycoacia* appears in a more inclusive clade with *Ceriporiopsis gilvescens*, *Lilaceophlebia livida* and several *Phlebia* species, not related to the *Phlebia/Merulius* clade (Fig. 5). The genus *Mycoaciella* appears in an unsupported position together with *Phlebia uda* and *Crustodontia chrysocreas* in the analyses of Binder *et al.* (2013). Additional available generic names for *Phlebia* s.lato include *Crustodontia, Sarcodontia* and *Lilaceophlebia*. Extensive molecular sampling is essential to establish sound generic concepts in *Phlebia* s. lato. A representative example of the current inadequacy of generic concepts is the genus *Lilaceophlebia*. Of the 16 species recombined in this genus (Spirin & Zmitrovich 2004), only one, *Phlebia tuberculata*, has been shown to be close to the type of *Lilaceophlebia*, and the two species that do appear close to the type in the phylogenies, *Phlebia fascicularis* and *Phlebia aurea* (Fig. 5), were never included in *Lilaceophlebia*.

4.4 *Steccherinaceae* Parmasto 1968 (Fig. 6)

Synonym. *Mycorraphiacaeae* Jülich 1981

Type genus: *Steccherinum* Gray

Polypores or species with hydnoid hymenophores; hyphael system dimitic; hyphae with clamp-connections; spores mostly thin-walled and rather small, smooth, hyaline; cystidia often present. More rarely monomitic and/or without clamp-connections. Producing a white-rot.

Genera: *Antella* Miettinen, *Antrodiella* Ryvarden & I. Johans., *Atraporiella* Ryvarden, *Austeria* Miettinen, *Butyrea* Miettinen, *Cabalodontia* M. Piątek, *Caudicicola* Miettinen, Kotir. & Kulju, *Citripora* Miettinen, *Chaetoporus* P. Karst., *Etheirodon* Banker, *Flabellophora* G. Cunn., *Flaviporus* Murrill, *Frantisekia* Spirin & Zmitr., *Junghuhnia* Corda, *Lamelloporus* Ryvarden, *Loweomyces* (Kotl. & Pouzar) Jülich, *Metuloidea* G. Cunn., *Mycorrhaphium* Maas Geest., *Niemelaea* Zmitr., Ezhov et Khimich., *Nigroporus* Murrill, *Trulla* Miettinen & Ryvarden, *Xanthoporus* Audet.

Additional taxa: *Antrodiella perennis* B.K. Cui & Y.C. Dai, *Fibricium subceraceum* (Hallenb.) Bernicchia, *Junghuhnia micropora* Spirin, Zmitr. & Malysheva, "*Mellipora constricta*" nom. prov., *Mycoacia columellifera* (G. Cunn.) Hjortstam, *Skeletocutis novaezelandiae* (G. Cunn.) P.K. Buchanan & Ryvarden, *Steccherinum aridum* Svrček, *Steccherinum laeticolor* (Berk. & M.A. Curtis) Banker, *Steccherinum litschaueri* (Bourdot & Galzin) J. Erikss., *Steccherinum oreophilum* Lindsey & Gilb., *Steccherinum robustius* (J. Erikss. & S. Lundell) J. Erikss., *Steccherinum straminellum* (Bres.) Melo.

Comments: For a detailed discussion of the taxa in this family see Miettinen *et al.* (2012) and Miettinen & Ryvarden (2016). The recently described *Caudicicola* (Kotiranta *et al.* 2017) appears as sister to all other members of the *Steccherinaceae* (Fig. 6).

4.5 *Cerrenaceae* Miettinen, Justo & Hibbett, fam. nov. (Fig. 6)

Mycobank 820826

Diagnosis. Basidiomes resupinate, effused-reflexed or pileate. Hymenophore poroid, daedaleoid or hydnoid. Hyphal system mono- or dimitic, rarely trimitic. Clamp-connections usually present. Spores hyaline, smooth, non-amyloid, non-dextrinoid, thin- or thick-walled. Thin-walled hymenial cystidia (gloeocystidia) present, also thick-walled encrusted cystidia in one genus. Mating system heterothallic, bi- or tetrapolar. Nuclear behavior heterocytic or astatocoenocytic (as far as is known). Producing a white-rot, also parasitic.

Type genus: *Cerrena* Gray, A natural arrangement of British plants 1: 649, 1821.

Genera: *Irpiciporus* Murrill, *Pseudolagarobasidium* J.C. Jang & T. Chen, *Radulodon* Ryvarden

Additional taxa: *Rigidoporus vinctus* (Berk.) Ryvarden, *Spongipellis delectans* (Peck) Murrill, *Spongipellis litschaueri* Lohwag, *Spongipellis pachyodon* (Pers.) Kotl. & Pouzar, *Spongipellis unicolor* (Schwein.) Murrill

Comments: *Spongipellis spumea* (Sowerby) Pat., the type species of *Spongipellis*, appears in an isolated position within /residual (Binder *et al.* 2013; Tomšovský 2012), not related to other species of the genus. The genus *Rigidoporus* is also polyphyletic, with the species-complex around *R. vinctus* placed in the *Cerrenaceae* and the type species, *R. lineatus*, and related taxa in the *Meripilaceae*. The *Cerrenaceae* is strongly supported as the sister group to the *Panaceae* (Fig. 6). Both *Cerrena* (Enebak & Blanchette 1989) and

Pseudolagarobasidium (Hallenberg *et al.* 2008) have demonstrated abilities to act as parasites of living plants.

4.6 *Panaceae* Miettinen, Justo & Hibbett, fam. nov. (Fig. 6)

Mycobank 820827

Diagnosis. Basidiomes pileate-stipitate. Hymenophore lamellate or smooth. Hyphal system dimitic. Clamp-connections present. Spores hyaline, smooth, non-amyloid, non-dextrinoid, thin-walled. Cystidia present as gloeocystidia or thick-walled cystidia. Mating system heterothallic and tetrapolar. Producing a white-rot.

Type genus: *Panus* Fr., Epicrisis Systematis Mycologici: 396, 1838.

Genera: *Cymatoderma* Jungh.

Comments: The phylogenies of Sjökvist *et al.* (2012) recovered a polyphyletic *Cymatoderma*, with some species closely related to *Podoscypha*, and a second group, including the type *C. elegans,* on a distant position within /residual. The species of *Cymatoderma* sampled in our analyses is closely related to *C. elegans* and *C. caperatum,* based on nrLSU and nrITS sequences (data not shown), indicating that *Cymatoderma* s. stricto belongs in the *Panaceae*. The genus *Panus* represents an independent origin of the agaricoid habit in the *Polyporales*, the others being *Lentinus* and *Neofavolus* in the *Polyporaceae* (Seelan *et al.* 2015).

4.7 *Hyphodermataceae* Jülich 1981 (Fig. 6)

Type genus: *Hyphoderma* Fr.

Corticiod species; hyphal system monomitic; hyphae with clamp-connections; spores thin-walled, smooth, hyaline; cystidia present in most species. Producing a white-rot.

Genera: *Hyphoderma*

Comments: The genus *Hyphoderma* as traditionally defined is polyphyletic, with c. 20 species now classified in *Peniophorella* in the *Hymenochaetales* (Larsson 2007). The genera *Hypochnicium* and *Bulbillomyces* are consistently recovered as separate from *Hyphoderma* in our analyses: 3-gene (Fig. 6), ribosomal-only and rpb1-only (TreeBASE

S20775). Alternative topologies for these genera have been recovered in the study of Larsson (2007).

4.8 *Meripilaceae* Jülich 1981(Fig. 6)

Synonym. *Rigidoporaceae* Jülich 1981

Type genus: *Meripilus* P. Karst.

Polypores; hyphal system monomitic or dimitic; hyphae without clamp-connections; spores thin-walled to slightly thick-walled, often subglobose, smooth, hyaline; cystdia often present. Producing a white-rot.

Genera: *Physisporinus* P. Karst., *Rigidoporus* Murrill

Comments: Additional species of *Rigidoporus* are placed in the *Cerrenaceae*. The names *Meripilaceae* and *Rigidoporaceae* have equal nomenclatural priority; the former is chosen here.

4.9 *Podoscyphaceae* D.A. Reid 1965 (Fig. 6)

Type genus: *Podoscypha* Pat.

Pileate species with smooth, ridged, or poroid hymenophore; hyphal system dimitic or trimitic; hyphae with clamp-connections; spores thin-walled, smooth, hyaline; cystidia often present. Producing a white-rot. In the broad sense adopted here (see comments) it also includes corticioid species, with monomitc hyphal systems, no clamp-connections and thick-walled, ornamented spores.

Genera: *Abortiporus* Murrill, *Pouzaroporia* Vampola

Additional taxa: *Cymatoderma dendriticum* (Pers.) D.A. Reid, *Cymatoderma pallens* Berthet & Boidin, *Hypochnicium punctulatum* (Cooke) J. Erikss., *Hypochnicium sphaerosporum* (Höhn. & Litsch.) J. Erikss., *Hypochnicium wakefieldiae* (Bres.) J. Erikss.

Comments: The limits and composition of *Podoscyphaceae* need further study. As accepted here the family receives moderate to high support in the 3-gene analyses (73/1). In the ribosomal-only analyses the same topology is recovered but without strong support. In the *rpb1*-only analyses a similar topology is recovered, again without strong support, and *Pouzaroporia* is placed outside the family (TreeBASE S20775). The species of *Hypochnicium* included in the *Podoscyphaceae* do not appear closely related to the type species *H. bombycinum*.

The name *Podoscyphaceae* could be adopted to include all families in /residual (Fig. 6) but the morphological characterization of such a group would be even more problematic than the individual definition of each of the families recognized here. The extreme morphological variation within the *Steccherinaceae* (Miettinen *et al.* 2002) makes it very difficult to characterize the family by means other than phylogeny and a certain predominance of morphological characters. However, recognizing the *Steccherinaceae* as a discrete group allows us to recognize several smaller families in /residual that are relatively easier to characterize in terms of morphology.

4.10 Additional /residual lineages (Fig. 6)

Genera: *Bulbillomyces* Jülich, *Climacocystis* Kotl. & Pouzar, *Diplomitoporus* Domański, *Hypochnicium* J. Erikss., *Rickiopora* Westphalen, Tomšovský & Rajchenb.

Additional taxa: *Phlebia bresadolae* Parmasto

Comments: Two well-supported clades, /hypochnicium (*Hypochnicium*, *Bulbillomyces*) and /climacocystis (*Climacocystis*, *Diplomitoporus*), appear as sister-taxa but without strong support (Fig. 6). The relative position of these two clades is never well supported in the ribosomal-only, *rpb1*-only or 3-gene analyses, therefore we refrain from proposing any formal family-level placement at this time. Based on the results of Binder *et al.* (2013) *Phlebia bresadolae* belongs in /climacocystis. The recently described genus *Rickiopora* is probably related to *Climacocystis* (Westphalen *et al.* 2016).

4.11 *Polyporaceae* Corda 1939 (Fig. 7)

Synonym. *Ganodermataceae* (Donk) Donk 1948
Synonym. *Coriolaceae* Singer 1961
Synonym. *Cryptoporaceae* Jülich 1981
Synonym. *Echinochaetaceae* Jülich 1981
Synonym. *Fomitaceae* Jülich 1981
Synonym. *Grammotheleaceae* Jülich 1981
Synonym. *Haddowiaceae* Jülich 1981

Synonym. *Microporaceae* Jülich 1981

Synonym. *Pachykytosporaceae* Jülich 1981

Synonym. *Perenniporiaceae* Jülich 1981

Synonym. *Sparsitubaceae* Jülich 1981

Synonym. *Lophariaceae* Boidin, Mugnier & Canales 1998

Synonym. *Trametaceae* Boidin, Mugnier & Canales 1998

Type genus: *Polyporus* P. Micheli ex Adans.

Polypores, rarely corticioid species; hyphal system mostly dimitic or trimitic, some monomitic species also present, and those usually with dendroid hyphal elements in the hymenium; hyphae with clamp-connections, exceptionally simple-septate; spores thin- to thick-walled, smooth to ornamented, relatively big for *Polyporales*, hyaline to brown; cystidia mostly absent. Producing a white-rot.

Genera: *Abundisporus* Ryvarden, *Amauroderma* Murrill, *Cerarioporia* F. Wu, L.W. Zhou & J. Si, *Colospora* Miettinen & Spirin, *Cryptoporus* (Peck) Shear, *Datronia* Donk, *Datroniella* B.K. Cui, Hai J. Li & Y.C. Dai, *Dendrodontia* Hjortstam & Ryvarden, *Dentocorticium* (Parmasto) M.J. Larsen & Gilb., *Dichomitus* D.A. Reid, *Donkioporia* Kotl. & Pouzar, *Earliella* Murrill, *Echinochaete* D.A. Reid, *Epithele* (Pat.) Pat., *Favolus* P. Beauv., *Fomes* (Fr.) Fr., *Fomitella* Murrill, *Ganoderma* P. Karst., *Grammothele* Berk. & M.A. Curtis, *Grammothelopsis* Jülich, *Hexagonia* Fr., *Haploporus* Bondartsev & Singer ex Singer, *Hornodermoporus* Teixeira, *Lentinus* Fr., *Lignosus* Lloyd ex Torrend, *Lopharia* Kalchbr. & MacOwan, *Megasporia* B.K. Cui, Y.C. Dai & Hai J. Li, *Megasporoporia* Ryvarden & J.E. Wright, *Melanoderma* B.K. Cui & Y.C. Dai, *Microporellus* Murrill, *Microporus* P. Beauv., *Neodatronia* B.K. Cui, Hai J. Li & Y.C. Dai, *Neofavolus* Sotome & T. Hatt., *Pachykytospora* Kotl. & Pouzar, *Perenniporia* Murrill, *Perenniporiella* Decock & Ryvarden, *Pseudofavolus* Pat., *Pyrofomes* Kotl. & Pouzar, *Tinctoporellus* Ryvarden, *Tomophagus* Murrill, *Trametes* Fr., *Truncospora* Pilát ex Pilát, *Vanderbylia* D.A. Reid, *Yuchengia* B.K. Cui & Steffen.

Additional taxa: *Coriolopsis byrsina* (Mont.) Ryvarden, *Coriolopsis caperata* (Berk.) Murrill, *Coriolopsis gallica* (Fr.) Ryvarden, *Coriolopsis glabro-rigens* (Lloyd) Núñez & Ryvarden, *Coriolopsis rigida* (Berk. & Mont.) Murrill, *Coriolopsis sanguinaria* (Klotzsch) Teng, *Coriolopsis strumosa* (Fr.) Ryvarden, *Coriolopsis trogii* (Berk.)

Domański, *Diplomitoporus overholtsii* (Pilát) Gilb. & Ryvarden, *Funalia subgallica* Hai J. Li & S.H. He.

Comments: A central, unresolved, problem for the generic-level taxonomy of the *Polyporaceae* is the typification of *Polyporus*. Krueger & Gargas (2004) made a convincing case as to why *Polyporus brumalis* should be considered the type of *Polyporus,* instead of *Polyporus tuberaster,* as has been accepted by most modern authors (Ryvarden 1991; Sotome *et al.* 2008). That creates a nomenclatural problem for the delimitation of the *P. brumalis* group (*Polyporellus*) and *Lentinus*. Sotome *et al.* (2008) published the first large phylogeny of *Polyporus,* and they acknowledged the problems with the typification of the genus, but for practical purposes considered *P. tuberaster* as the type species, and mentioned that the typification of *Polyporus* would be addressed in a future paper. Zmitrovich & Kovalenko (2016) gave a phylogenetic overview of the polyporoid and lentinoid genera, and recognized seven genera to accommodate these taxa in the *Polyporaceae*. However, these authors assume that *P. tuberaster* is the type of *Polyporus,* which is not correct under Article 9 of the *International Code of Nomenclature for Algae, Fungi and Plants* (McNeill *et al.* 2012). *Polyporus*, as traditionally defined, is polyphyletic so name changes are bound to happen one way or the other. However, it is our opinion that strict application of the nomenclature rules here will result in disadvantageous changes, as *Polyporus* and *Lentinus*, two names with long established usages and central to the taxonomic arrangement of the *Polyporaceae*, will be in direct conflict. We suggest that the best way to move forward is to formally propose the conservation of *Polyporus* with a conserved type, as allowed by Article 14. 9 (McNeill *et al.* 2012), preferably not *P. brumalis* to avoid conflict with *Lentinus*.

The genus *Trametes* is accepted in the sense of Justo & Hibbett (2011), including the type of *Coriolopsis* Murrill. This leaves the majority of species formerly placed in *Coriolopsis* in need of new generic placements. The genus *Funalia* Pat. could accommodate some of these species, as proposed by Li *et al.* (2016), but molecular data from the type species *Funalia mons-veneris* (Jungh.) Pat., are still lacking. Suitable modern collections of this species should be sequenced to settle the status of *Funalia*.

Alternative taxonomic arrangements of the *Polyporaceae* were considered. Taking the approach of narrowly defining a family, because of its unique set of morphological characters, can lead to a more problematic taxonomic scenario. The *Ganodermataceae* stands out morphologically because of the yellow, ornamented spores with a double spore-wall. However, recognizing the *Ganodermataceae* as an independent taxon would create a cascading effect in the *Polyporaceae*, and at least four additional families would have to be adopted to accommodate the taxa currently placed in the *Polyporaceae* (Fig. 7). In this scenario, considering the results presented here and those of Binder *et al.* (2013) the following families would be recognized: *Grammothelaceae, Fomitaceae/Microporaceae, Lophariaceae, Polyporaceae* and *Coriolaceae*. The number of families would only increase as additional taxa are sampled for *rpb1* data. These segregated families would all be distinct from the *Ganodermataceae* on morphological grounds, but for the most part indistinguishable from each other.

4.12 *Fomitopsidaceae* Jülich 1981 (Fig. 8)

Synonym. *Daedaleaceae* Jülich 1981

Synonym. *Piptoporaceae* Jülich 1981

Polypores; hyphal system dimitic or trimitic, more rarely monomitic; hyphae with clamp-connections; spores thin-walled, smooth, hyaline; cystidia absent, sometimes skeletal hyphal ends protruding into the hymenium. Producing a brown-rot.

Type genus: *Fomitopsis* P. Karst. (including *Piptoporus* P. Karst.)

Genera: *Anthoporia* Karasiński & Niemelä, *Antrodia* P. Karst., *Buglossoporus* Kotl. & Pouzar, *Cartilosoma* Teixeira, *Daedalea* Pers., *Fragifomes* B.K. Cui, M.L. Han & Y.C. Dai, *Melanoporia* Murrill, *Neolentiporus* Rajchenb., *Niveoporofomes* B.K. Cui, M.L. Han & Y.C. Dai, *Rhodofomes* Kotl. & Pouzar, *Rhodofomitopsis* B.K. Cui, M.L. Han & Y.C. Dai, *Rubellofomes* B.K. Cui, M.L. Han & Y.C. Dai, *Ungulidaedalea* B.K. Cui, M.L. Han & Y.C. Dai

Additional taxa: *Antrodia hyalina* Spirin, Miettinen & Kotir., *Antrodia juniperina* (Murrill) Niemelä & Ryvarden, *Antrodia macrospora* Bernicchia & De Domincis, *Antrodia malicola* (Berk. & M.A. Curtis) Donk, *Antrodia mellita* Niemelä & Penttilä, *Antrodia minuta* Spirin, *Antrodia oleracea* (R.W. Davidson & Lombard) Ryvarden, *Antrodia pulvinascens* (Pilát) Niemelä, *Antrodia serialiformis* Kout̕ & Vlasák, *Antrodia* *serialis* (Fr.) Donk, *Antrodia taxa* T.T. Chang & W.N. Chou, *Antrodia variiformis* (Peck) Donk.

Comments: The names *Daedaleaceae* and *Piptoporaceae*, with equal nomenclatural priority, are considered here as synonyms of *Fomitopsidaceae*. The recent studies of Ortiz-Santana *et al.* (2013) and Spirin *et al.* (2013a,b) have defined the limits of *Antrodia*, but many species traditionally classified in *Antrodia* still await proper generic placement (see additional taxa above).

Fomitopsis, as traditionally defined, is polyphyletic and has been the subject of a recent study by Han *et al.* (2016). These authors have proposed to subsume *Piptoporus* into *Fomitopsis* sensu stricto, while they place other *Fomitopsis* species in the genera *Fragifomes*, *Niveoporofomes*, *Rhodofomes*, *Rhodofomitopsis*, *Rubellofomes* and *Ungulidaedalea*. The genus *Piptoporellus*, also introduced by Han *et al.* (2016), falls outside the *Fomitopsidaceae*, and its relations with other members of /antrodia remain unresolved.

4.13 *Laetiporaceae* Jülich 1981 (Fig. 8)

Synonym. *Phaeolaceae* Jülich 1981

Type genus: *Laetiporus* Murrill

Polypores; hyphal system dimitic, more rarely monomitic; hyphae without clamp-connections; spores thin-walled, smooth, hyaline; cystidia mostly absent. More rarely monomitic and cystidia present. Producing a brown-rot.

Genera: *Phaeolus* (Pat.) Pat., *Wolfiporia* Ryvarden & Gilb.

Comments: Based on the phylogenies of Ortiz-Santana *et al.* (2013), Binder *et al.* (2013) and Han *et al.* (2016) *Phaeolus* is closely related to *Laetiporus* and *Wolfiporia*, therefore the name *Phaeolaceae* is placed here in synonymy with *Laetiporaceae*. Mycobank cites *Laetiporaceae* Jülich as an invalid name, but after consulting the original publication (Jülich 1981) we have found no reasons to consider the name invalid. The delimitation of *Laetiporus* vs. *Wolfiporia* needs further study.

4.14 /fibroporia+amyloporia (Fig. 8)

Polypores, almost all resupinate; hyphal system mostly dimitic; hyphae with clamp-connections; spores thin- to slightly thick-walled, smooth, hyaline; cystidia mostly absent. Producing a brown-rot.

Genera: *Amyloporia* Bondartsev & Singer ex Singer, *Fibroporia* Parmasto, *Rhodonia* Niemelä

Comments: The results presented here place *Amyloporia* and *Fibroporia* outside the *Fomitopsidaceae*, but the relations to each other and to the rest of /antrodia are not fully resolved at the moment. In previous studies different topologies have been recovered for both genera: (i) *Fibroporia* as sister to most of /antrodia, and *Amyloporia* included in the *Fomitopsidaceae* (Ortiz-Santana *et al.* 2013); (ii) *Fibroporia* and *Amyloporia* as sister-taxa, and grouped with *Laricifomes* Kotl. & Pouzar and *Antrodia albobrunnea* (Binder *et al.* 2013); (iii) *Amyloporia*, together with *Laricifomes*, *Ryvardenia* Rajchenb. and *Gilbertsonia* Parmasto in an unsupported position as sister to *Fomitopsidaceae,* and *Fibroporia* as sister to *Piptoporellus* (Han *et al.* 2016, nuclear ribosomal + *rpb2* dataset); (iv) *Amyloporia* and *Fibroporia* together with species of *Postia* s. lato (Han *et al.* 2016, nuclear ribosomal + mitochondrial ribosomal + *rpb2* + *tef1* dataset). For the time being we refrain from proposing any family-level placement for *Amyloporia, Fibroporia, Laricifomes, Ryvardenia, Gilbertsonia* and *Piptoporellus*. The name *Laricifomitaceae* Jülich, typified by *Laricifomes*, is available. The type species of *Rhodonia* (*R. placenta*) appears nested within *Amyloporia* s. lato, but at the moment it is not clear what is the best taxonomic solution for this group (one or multiple genera).

4.15 *Dacryobolaceae* Jülich 1981 (Fig. 8)

Type genus: *Dacryobolus* Fr.

Polypores or corticoid species; hyphal system monomitic, more rarely di- or trimitic; hyphae with clamp-connections; spores thin- to thick-walled, smooth or rarely ornamented, hyaline; cystidia present or absent. Producing a brown-rot.

Genera: *Amylocystis* Bondartsev & Singer ex Singer, *Jahnoporus* Nuss, *Oligoporus* Bref., *Postia* Fr., *Spongiporus* Murrill

Comments: In the phylogenies presented by Ortiz-Santana *et al.* (2013) and Binder *et al.* (2013) the genera *Auriporia* Ryvarden, *Sarcoporia* P. Karst., and

Taiwanofungus Sheng H. Wu, Z.H. Yu, Y.C. Dai & C.H. Su, appear sometimes related to the genera here accepted as part of the *Dacryobolaceae*. In the present study *Auriporia* appears outside /antrodia (Fig. 9) and *Sarcoporia* does not appear as closely related to the *Dacryobolaceae* (Fig. 8). The placement of these genera and *Taiwanofungus*, not sampled here, needs further study.

4.16 *Sparassidaceae* Jülich 1981 (Fig. 8)

Type genus: *Sparassis* Fr.

Basidiomes consist of branched flabellae arising from a central core; hyphal system monomitic, with gloeoplerous hyphae; hyphae with scattered clamp-connections; spores thin- to slightly thick-walled, smooth, hyaline; cystidia mostly absent. Producing a brown-rot.

Comments: The genus *Sparassis* appears as sister to the *Laetiporaceae* in the analyses of Ortiz-Santana *et al.* (2013) and Binder *et al.* (2013), while in our analyses it appears in a more inclusive clade as sister to the *Dacryobolaceae* (Fig. 8), but neither placement is strongly supported. The genera *Crustoderma* Parmasto, *Pycnoporellus* Murrill and *Sarcoporia* appear in our analysis in the same clade as *Sparassis*, but without strong support, and their placement in or out the *Sparassidaceae* needs to be confirmed in future studies.

4.17 *Grifolaceae* Jülich 1981 (Fig. 9)

Type genus: *Grifola* Fr.

Polypores (stipitate-imbricate); hyphal system monomitic; hyphae with scattered clamp-connections; spores thin-walled, smooth, hyaline; cystidia absent. Producing a white-rot and acting as root parasites.

Comments: *Grifola* consistently appears as sister to the *Polyporaceae*, although without strong support (Justo & Hibbett 2011, Binder *et al.* 2013). The name *Grifolaceae* is accepted here to accommodate this genus.

4.18 *Gelatoporiaceae* Miettinen, Justo & Hibbett, fam. nov. (Fig. 9)

Mycobank 820828

Diagnosis. Basidiomes resupinate. Hymenophore poroid. Hyphal system monomitc, rarely dimitic. Clamp-connections present. Spores hyaline, smooth, non-amyloid, non-dextrinoid, thin-walled, rarely slightly thick-walled. Cystidia absent, but characteristic cystidioles may be present. Mating system heterothallic, bi- or tetrapolar. Nuclear behavior astatocoenocytic (as far as is known). Producing a white-rot.

Type genus: *Gelatoporia* Niemelä, Karstenia 25: 22, 1985.

Genera: *Cinereomyces* Jülich, *Obba* Miettinen & Rajchenb., *Sebipora* Miettinen

Comments: Miettinen & Rajchenberg (2012) introduced the name "*Cinereomyces* clade" to accommodate a small group of white-rot polypores of uncertain position within the *Polyporales*. Further analyses by Binder *et al.* (2013) and the data presented here confirm that this clade represents a separate lineage from the *Polyporaceae*, which is formally described here as the family *Gelatoporiacae*. For a detailed study of the genera in this family see Miettinen & Rajchenberg (2012).

In our analyses *Mycoleptodonoides vassiljevae* and *Auriporia aurea* appear close to the *Gelatoporiaceae* but without strong support. If the position of *Auriporia* is confirmed in future studies it would represent a third independent origin of brown-rot in the *Polyporales*, other than /antrodia and *Leptoporus* in the *Irpicaceae*.

4.19 *Incrustoporiaceae* Jülich 1981 (Fig. 9)

Type genus: *Incrustoporia* Domański

Polyporoid species; hyphal system dimitic, more rarely monomitic; hyphae with clamp-connections, rarely simple-septate; spores thin-walled, smooth, hyaline, relatively small; cystidia usually absent, but tips of generative hyphae at tube mouths commonly with rose-thorn encrustation. Producing a white-rot.

Genera: *Piloporia* Niemelä, *Skeletocutis* Kotl. & Pouzar, *Tyromyces* P. Karst.

Comments: The generic limits of *Incrustoporia*, *Skeletocutis* and *Tyromyces* are not currently settled, and additional sampling of this clade is needed before a taxonomic arrangement can be put forward. *Tyromyces merulinus* (Berk.) G. Cunn. appears as sister to the *Incrustoporiaceae*, but this position only receives support in the Bayesian analyses and alternative placements for this species have been recovered.

4.20 *Ischnodermataceae* Jülich 1981 (Fig. 9)

Type genus: *Ischnoderma* P. Karst.

Polypores; hyphal system dimitic, with hyphae tightly arranged; hyphae with clamp-connections; spores thin-walled, smooth, hyaline; cystidia absent. Producing a white-rot.

Comments: Our analyses confirm the rather isolated position of the genus *Ischnoderma* within the *Polyporales* recovered in previous phylogenies (Binder *et al.* 2013). The monotypic family *Ischodermataceae* is adopted here for this genus.

4.21 Additional family names putatively belonging in the *Polyporales*

Diachanthodaceae Jülich, 1981. No molecular data are available for the type species of the type genus, *Diacanthodes novo-guineensis* (Hennings) O. Fidalgo.

Fragiliporiaceae Y.C. Dai, B.K. Cui & C.L. Zhao, 2015. This family was recently introduced (Zhao *et al.* 2015) to accommodate the newly described genus *Fragiliporia.* The molecular phylogenies of these authors recover *Fragiliporia* in an isolated position within the *Polyporales*, possibly related to /phlebioid and /residual, but not included in either clade. We performed an analysis on an alternate version of our ribosomal-only dataset to include *Fragiliporia*, and it was recovered in an isolated, unsupported position as sister to *Candelabrochaete africana* (tree available at TreeBASE S20775). *Fragiliporia* is characterized by resupinate basidiomes; tubes being very soft when fresh, becoming brittle when dry (become almost powdery when bruised); monomitic hyphal system; common clamp-connections; and thin-walled, hyaline basidiospores (Zhao *et al.* 2015). Future studies should include *rpb1* data to address the relations of *Fragiliporia* with *Candelabrochaete africana* and its position within the *Polyporales*.

Hymenogrammaceae Jülich, 1981. The corticioid/poroid type species, *Hymenogramme javensis* Mont. & Berk., has few distinct morphological characters and has not been sequenced, leaving placement of this family as uncertain.

Nigrofomitaceae Jülich, 1981. Currently there is only one nrITS sequence available (GenBank KT156704.1) for the type species of the type genus, *Nigrofomes melanoporus* (Mont.) Murrill. A BLAST search of this sequence does not yield any close relative in the *Polyporales*. Additional *Nigrofomes* sequences from Southeast Asia (Miettinen, unpublished data) indicate that this family belongs in the *Hymenochaetales*.

Phaeotrametaceae Popoff ex Piątek, 2005. No molecular data are available for the type species of the type genus, *Phaeotrametes decipiens* (Berk.) J.E. Wright.

5. Discussion

The classification of *Polyporales* presented here integrates results from prior analyses by members of the PolyPEET consortium (Floudas & Hibbett 2015, Justo & Hibbett 2011, Miettinen *et al.* 2012, 2016; Ortiz-Santana *et al.* 2013) with those of many other research groups (Han *et al*. 2016; Krüger and Gargas 2004; Li *et al.* 2016; Sotome *et al.* 2008; Spirin and Zmitrovich 2004; Zhao *et al*. 2015). The combination of *rpb1* and ribosomal RNA genes provides robust resolution of many clades, including eighteen that are recognized here as families, but some nodes remain weakly supported and numerous taxa have yet to be sampled. In future studies addressing the family-level organization of the *Polyporales*, data for protein-coding genes, especially *rpb1*, should be routinely included. The classification proposed here provides a nomenclatural as well as phylogenetic framework that will facilitate further revision at all taxonomic levels within *Polyporales*, following the principles elucidated by Vellinga *et al.* (2015).

Increased genome sampling will be necessary to resolve many nodes in *Polyporales*. It is hoped that this classification will help guide such efforts, such as the 1000 Fungal Genomes Project, which aims to sample at least two representatives of all families of fungi (Grigoriev *et al.* 2013). Leaving aside the non-equivalence of taxa classified at the same rank, it is clear that genome sampling in *Polyporales* to date has not maximized phylogenetic diversity; the 46 *Polyporales* genomes currently available on the JGI MycoCosm portal represent only ten of the 18 families recognized here and three unplaced clades (Table 3). Nine families or clades are represented by only one or two genomes, while the *Polyporaceae* is represented by 22 genomes (16 species).

In developing this classification, an effort has been made to name clades that can be recognized or described easily. However, many of the characters emphasized in prior taxonomy exhibit homoplasy and are poor predictors of higher-level evolutionary relationships within the *Polyporales* (Table 2). Macromorphology of fruiting bodies, which was coded with three states for basidiomes form (pileate, stipitate or resupinate) and with four states for hymenophore configuration (poroid, daedaleoid/lamellate, smooth, or hydnoid), is particularly variable. Fourteen families have two or three different basidiome types, with twelve containing both pileate (sessile) and resupinate forms. Fifteen families contain species with poroid hymenophores, which is the most common configuration, whereas daedaleoid/lamellate and smooth hymenophores each occur in nine families; twelve families have at least two different hymenophore types. Similar variation is evident in the diversity of hyphal systems (monomitc, dimitic, or trimitic), which affect the consistency and longevity of fruiting bodies. Fifteen families contain dimitic or trimitic hyphal systems, which confer tough, resilient fruiting bodies, but fifteen families contain monomitic forms, and eleven families have at least two kinds of hyphal systems. The fruiting bodies of *Polyporales* may be massive or minute, ephemeral or perennial, and they can be produced in diverse locations, including the tops, sides, or bottoms of fallen logs, on standing tree trunks, small woody debris, or soil. The diversity of macromorphology and hyphal construction in *Polyporales* reflects a dynamic history of morphological evolution, as lineages have adapted to the challenges of spore dispersal under different environmental conditions and on diverse substrates.

Decay mode is one of the most stable characters in *Polyporales*, and has been used as the basis for segregating genera (Gilbertson and Ryvarden 1986; Ryvarden 1991). The majority of *Polyporales* produce a white rot, which is the plesiomorphic condition for the group (Floudas *et al.* 2012), with only two confirmed transitions to a brown-rot (/antrodia and *Leptoporus*), and a possible third represented by *Auriporia* (Fig. 9). The eight brown rot genomes currently available all represent members of /antrodia. It will be interesting to see if the dramatic reduction in the lignocellulolytic apparatus observed in *Rhodonia (Postia) placenta* and other brown rot members of /antrodia also occurs in *Leptoporus* and *Auriporia*.

Rot type can be inferred from direct examination of wood substrates or from cultural tests, and it is regularly reported for species of *Polyporales* and other wood decay fungi (Gilbertson and Ryvarden 1986; Nobles 1971). In contrast, determination of mating systems requires laborious crossing experiments using single-spore isolates, and this character is not nearly as well documented as decay mode. Nevertheless, even with limited taxon sampling, mating type appears to be highly labile; nine or ten families include bipolar species, ten or eleven families contain tetrapolar species, and two or three families have both modes represented (Table 2). James *et al.* (2013) described the genetic architecture underlying tetrapolar and bipolar mating systems based on a sample of ten *Polyporales* genomes representing seven of the eighteen families recognized here. Expanded genome sampling will make it possible to test the generality of their conclusions, including the putative irreversibility of transitions from tetrapolar to bipolar mating systems.

Nuclear behavior in the *Polyporales* has been analyzed in detail by Rajchenberg (2011), and it includes the number of nuclei present in a fungus at different phases of its life cycle, the production of basidiospores, the production of germinating basidiospores, production of the hyphal cells of the primary (monosporic) mycelium, production of the hyphal cells of the secondary (polyspore or tissue) mycelium and the variation in number of nuclei under different oxygen pressures. Other characters that have been discussed in the context of *Polyporales* taxonomy include features of spores (staining, pigmentation, wall thickness, and ornamentation), cystidia and clamp connections (Table 2). The genetic bases and selective significance of these characters are obscure.

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Figure captions

Figure 1. Overview of the major clades of *Polyporales*, based on the ML tree from the 3-gene dataset. Support values are given as ML/BY.

Figure 2. Overview of the families and clades recognized here, based on the ML tree from the 3-gene dataset. Support values are given as ML/BY.

Figure 3. *Phanerochaetaceae*, based on the ML tree from the 3-gene dataset. Support values are given as ML/BY. Stars indicate the type genus of a family.

Figure 4. *Irpicaceae*, based on the ML tree from the 3-gene dataset. Support values are given as ML/BY. Stars indicate the type genus of a family.

Figure 5. *Meruliaceae*, based on the ML tree from the 3-gene dataset. Support values are given as ML/BY. Stars indicate the type genus of a family. Circles indicate the type species of a genus.

Figure 6. Families in /residual, based on the ML tree from the 3-gene dataset. Support values are given as ML/BY. Stars indicate the type genus of a family. Bars indicate the limits of each family.

Figure 7. *Polyporaceae*, based on the ML tree from the 3-gene dataset. Support values are given as ML/BY. Stars indicate the type genus of a family.

Figure 8. Families in /antrodia, based on the ML tree from the 3-gene dataset. Support values are given as ML/BY. Stars indicate the type genus of a family. Circles indicate the type species of a genus. Bars indicate the limits of each family.

Figure 9. *Grifolaceae, Gelatoporiaceae, Incrustoporiaceae, Ischnodermataceae,* and un-assigned taxa, based on the ML tree from the 3-gene dataset. Support values are given as ML/BY. Bars indicate the limits of each family.

Table 1. Sequences used in this study. (*) Indicates sequences generated in this study

Taxon	**Collection**	***rpb1***	**nrLSU**	**nrITS**
Abortiporus biennis	FD-319	KP134783	KP135195	KP135300
Amylocystis lapponica	FP-105131	KY948973*	KY948879*	KY948805*
Amyloporia carbonica	Zabel-40GLN	KY949013*	KC585065	KC585243
Amyloporia cf. stratosa	GatesFF-461	KY949014*	KY948881*	KY948806*
Amyloporia sinuosa	FP-105386	KY949018*	KC585066	KC585244
Amyloporia xantha	DAOM-16570	KY949016*	KC585076	KC585254
Amyloporia xantha	HHB-8673	KY949017*	KC585084	KC585261
Antella americana	HHB-4100-Sp	KP134885	KP135196	KP135316
Anthoporia albobrunnea	S-4665	KY949020*	KY948880*	KY948808*
Antrodia favescens	FP-103723	KY949009*	KC585092	KC585269
Antrodia heteromorpha	Kosolapov VIII-2003	KY949011*	KC543145	KC543145
Antrodia hyalina	Kotiranta-19668	KY949008*	JQ700284	JQ700284
Antrodia juniperina	SRM-403	KY948991*	KC585109	KC585285
Antrodia malicola	LE208476	KY948992*	JQ700282	JQ700282
Antrodia mellita	Spirin-3315	KY948994*	KC543139	KC543139
Antrodia minuta	Spirin-2680	KY948993*	KC595898	KC595898
Antrodia oleracea	HHB-5988	KY948987*	KC585117	KC585293
Antrodia pulvinascens	Pennanen-1532	KY948995*	JQ700286	JQ700286
Antrodia ramentacea	Spirin-2540	KY949002*	KC595903	KC595903
Antrodia serialiformis	FP-105717	KY949000*	KC585126	KC585302
Antrodia serialis	FP-133692	KY948998*	KC585127	KC585303
Antrodia serpens	Vampola-X-1989	KY949012*	KC543143	KC543143
Antrodia variiformis	FP-104442	KY948997*	KC585134	KC585309
Antrodiella stipitata	FD-136	KP134886	KP135197	KP135314
Aurantiporus albidus	CIEFAP-117	KY948925*	KY948848*	KY948739*
Aurantiporus croceus	Miettinen-16483	KY948927*	KY948901*	KY948745*
Aurantiporus fissilis	HHB-9530-sp	KY948922*	-	KY948774*
Aurantiporus fissilis	Voucher-814	-	HQ729001	-
Auriporia aurea	FP-98524	KY948984*	KC585141	KC585316
Bjerkandera adusta	HHB-12826-Sp	KP134784	KP135198	KP134983
Bjerkandera aff. centroamericana	L-13104-sp	KY948936*	KY948855*	KY948791*
Bulbillomyces farinosus	FP-100488-T	KY948929*	-	KY948802*
Bulbillomyces farinosus	NH-9933	-	DQ681201	-

Taxon	**Collection**	***rpb1***	**nrLSU**	**nrITS**
Butyrea luteoalba	FP-105786-Sp	KP134887	KP135226	KP135320
Byssomerulius corium	FP-102382	KP134802	KP135230	KP135007
Byssomerulius sp.	OMC-1195	KY948962*	-	KY948746*
Candelabrochaete africana	FP-102987-Sp	KP134872	KP135199	KP135294
Candelabrochaete langloisii	FP-110343-sp	KY948981*	KY948886*	KY948793*
Candelabrochaete septocystidia	AS-95	-	EU118609	-
Candelabrochaete septocystidia	RMJ-119-sp	KY948959*	-	KY948783*
Caudicicola gracilis	X-3081	KY415972*	KY415962*	KY415962*
Ceraceomyces serpens	HHB-15692-Sp	KP134785	KP135200	KP135031
Ceraceomyces sp.	Miettinen-16854.3	KY948964*	KY948890*	KY948742*
Ceriporia alachuana	FP-103881-Sp	KP134845	KP135201	KP135341
Ceriporia lacerata	FP-55521-T	KP134805	KP135202	KP135024
Ceriporia purpurea	KKN-223-Sp	KP134788	KP135203	KP135044
Ceriporia reticulata	RLG-11354-Sp	KP134794	KP135204	KP135041
Ceriporia sp.	FP-134993	KP134792	-	KP135048
Ceriporia sp.	HHB-12714	KP134790	-	KP135046
Ceriporia sp.	L-8020	KP134789	-	KP135050
Ceriporia sp.	OMC-1333	KY948958*	KY948887*	KY948779*
Ceriporia spissa	FD-352	KP134793	KP135206	-
Ceriporiopsis aneirina	HHB-15629-Sp	KP134795	KP135207	KP135023
Ceriporiopsis carnegieae	RLG-7277-T	KY948935*	KY948854*	KY948792*
Ceriporiopsis gilvescens	L-3519-sp	KY948919*	-	KY948761*
Ceriporiopsis gilvescens	Niemelä-5516	-	HQ659222	-
Ceriporiopsis pseudoplacenta	Miettinen-18997	KY948926*	KY948902*	KY948744*
Cerrena unicolor	FD-299	KP134874	KP135209	KP135304
Climacocystis borealis	FD-31	KP134882	KP135210	KP135308
Climacodon septentrionalis	AFTOL-767	AY864873	AY684165	AY854082
Coriolopsis cf. byrsina	FP-105050-sp	JN164838	JN164788	JN165001
Coriolopsis cf. caperata	CR-22	JN164837	JN164789	JN164999
Coriolopsis gallica	RLG-7630-sp	JN164821	JN164814	JN165013
Coriolopsis trogii	RLG-4286-sp	JN164820	JN164808	JN164993
Crustoderma corneum	HHB-5685	KY949037*	KC585143	KC585318
Crustoderma flavescens	HHB-9359	KY949038*	KC585150	KC585325

Taxon	**Collection**	***rpb1***	**nrLSU**	**nrITS**
Cymatoderma sp.	OMC-1427	KY948971*	KY948872*	KY948826*
Dacryobolus karstenii	Miettinen-18685	KY948955*	KY948900*	KY948743*
Daedalea quercina	FP-56429	KY948989*	KY948883*	KY948809*
Datronia mollis	RLG-6304-sp	JN164818	JN164791	JN165002
Datronia scutellata	RLG-9584-T	JN164817	JN164792	JN165004
Dendrodontia bicolor	FP-150666	KY948983*	KY948878*	KY948710*
Dentocorticium sulphurellum	FP-11801	JN164841	-	-
Dentocorticium sulphurellum	T-609	-	JN164815	JN165015
Dichomitus squalens	LE258894	-	KM411471	KM411455
Dichomitus squalens	LYAD-421 SS1	genome	-	-
Diplomitoporus crustulinus	FD-137	KP134883	KP135211	KP135299
Diplomitoporus overholtsii	HHB-9450-sp	KY948911*	KY948876*	KY948712*
Donkia pulcherrima	OMC-1428	KY948939*	KY948856*	KY948784*
Earliella scabrosa	PR-1209	JN164819	JN164793	JN165009
Efibula americana	FP-102165	KP134808	KP135256	KP135016
Efibula clarkii	FD-228	KP134803	-	KP135019
Efibula gracilis	FD-455	KP134804	-	KP135027
Efibula tuberculata	OM-6707	KP134807	-	KP135017
Epithele macarangae	FP-150881	KY948909*	KY948843*	KY948713*
Etheirodon aff. fimbriatum	FP-102075	KY948950*	KY948864*	KY948821*
Fibroporia gossypium	MR-11443	KY949029*	KY948897*	KY948811*
Fibroporia pseudorennyi	Rivoire 3914	KY949032*	KC595927	KC595927
Fibroporia radiculosa	L-11659	KY949034*	KC585166	KC585341
Fibroporia vaillantii	FP-90877	KY949035*	KC585170	KC585345
Fomitella supina	OMC-1405	KY948910*	KY948841*	KY948711*
Fomitopsis ostreiformis	Miettinen-14311	KY949006*	KC595920	KC595920
Fomitopsis pinicola	AFTOL-770	AY864874	AY684164	AY854083
Fomitopsis rosea	RLG-6954	KY949003*	KC585181	KC585353
Ganoderma boninense	RS	-	X78777	-
Ganoderma boninense	WD-2028 (FFPRI)	KJ143944	-	KJ143905
Ganoderma curtisii	CBS-100131	KJ143946	-	JQ781848
Ganoderma lingzhi	Cui-9166 (BJFC)	JX029982	-	KJ143907
Ganoderma lucidum	Cui-9207 (BJFC)	KJ143949	-	KJ143910

Taxon	**Collection**	***rpb1***	**nrLSU**	**nrITS**
Ganoderma multipileum	Dai-9447 (IFP)	KJ143953	-	KJ143914
Ganoderma oregonense	CBS-265.88	KJ143954	-	JQ781875
Ganoderma resinaceum	CBS-194.76	KJ143956	-	KJ143916
Ganoderma sessile	10597-SS1	genomic	-	-
Ganoderma sessile	JV-1209/9	-	-	KJ143918
Ganoderma tsugae	Dai-12751b (BJFC)	KJ143960	-	-
Ganoderma tsugae	UBC-F23891	-	KJ146707	KJ146707
Ganoderma zonatum	FL-02 (TNM)	KJ143962	-	KJ143921
Gelatoporia subvermispora	FD-354	KP134879	KP135212	KP135312
Gloeoporus dichrous	FP-151129	KP134866	KP135213	KP135058
Gloeoporus pannocinctus	L-15726-Sp	KP134867	KP135214	KP135060
Grammothele aff. *fuligo*	FP-150657	KY948908*	KY948840*	KY948716*
Grammothele sp.	FP-150285	KY948907*	KY948839*	KY948729*
Grammothele sp.	FP-150289	KY948904*	KY948836*	KY948717*
Grifola frondosa	AFTOL-701	AY864876	AY629318	AY854084
Grifola sordulenta	AFTOL-562	AY864879	AY645050	AY854085
Hapalopilus nidulans	FD-512	KP134809	-	KP135419
Hapalopilus ochraceolateritius	Miettinen-16992.1	KY948965*	KY948891*	KY948741*
Heterobasidion annosum	DAOM-73191	-	AF287866	-
Heterobasidion annosum	TC-32-1	genome	-	-
Heterobasidion annosum	VL-296	-	-	JF440572
Hexagonia tenuis	Niemelä-9032	KY949042*	KY948842*	KY948738*
Hydnophlebia chrysorhiza	FD-282	KP134848	KP135217	KP135338
Hydnophlebia omnivora I	KKN-112	KP134846	KP135216	KP135334
Hydnophlebia omnivora II	ME-497	KP134847	KP135218	KP135332
Hyphoderma litschaueri	FP-101740-Sp	KP134868	KP135219	KP135295
Hyphoderma medioburiense	FD-335	KP134869	KP135220	KP135298
Hyphoderma mutatum	HHB-15479-Sp	KP134870	KP135221	KP135296
Hyphoderma setigerum	FD-312	KP134871	KP135222	KP135297
Hyphodermella rosae	FP-150552	KP134823	KP135223	KP134978
Hypochnicium bombycinum	HHB-12631-sp	KY948930*	-	KY948801*
Hypochnicium karstenii	HHB-9373-sp	KY948931*	-	KY948799*
Hypochnicium karstenii	NH-10924	-	DQ677510	-

Taxon	**Collection**	***rpb1***	**nrLSU**	**nrITS**
Hypochnicium punctulatum	FP-101698-sp	KY948932*	KY948860*	KY948827*
Hypochnicium sp.	FP-110227-sp	KY948944*	KY948862*	KY948804*
Hypochnicium sphaerosporum	RLG-15138-sp	KY948940*	KY948861*	KY948803*
Hypochnicium wakefieldiae	KJM-271-sp	KY948933*	-	KY948828*
Hypochnicium wakefieldiae	NH 11232	-	DQ677512	-
Irpex lacteus	FD-9	KP134806	KP135224	KP135026
Ischnoderma resinosum	FD-328	KP134884	KP135225	KP135303
Jahnoporus hirtus	Spinosa 10-X-2014 (H)	KY949044*		KU165784
Jahnoporus hirtus	Vlasák-1108/1		KU165782	-
Laetiporus conifericola	CA-8	KY949024*	EU402523	EU402575
Laetiporus persicinus	HHB-9564	KY949027*	EU402513	EU402579
Laetiporus sulphureus	CT-1	KY949025*	EU402532	EU402565
Lentinus badius	JS-0094	KP325691	KP283512	KP283478
Lentinus crinitus	DSH-9243C	KP325687	KP283523	KP283495
Lentinus sajor-caju	FRI-62056	KP325677	KP283509	KP283492
Lentinus squarrosulus	CUI-6513	KP325680	KP283516	KP283482
Lentinus tigrinus	DSH-92D787	KP325689	-	KP283488
Lentinus tigrinus	LE-214778	-	KM411475	-
Leptoporus mollis I (AZ)	RLG-7163	KY948956*	-	KY948794*
Leptoporus mollis II (WA)	TJV-93-174-T	KY948957*	EU402510	KY948795*
Lilaceophlebia livida	FP-135046-sp	KY948917*	KY948850*	KY948758*
Lopharia cinerascens	FP-105043-sp	JN164840	JN164813	JN165019
Meripilus giganteus	FP-135344-Sp	KP134873	KP135228	KP135307
Meruliopsis albostramineus	HHB-10729	KP134787	KP135229	KP135051
Meruliopsis sp.	FD-278	KP134796	KP135205	KP135057
Meruliopsis sp.	FD-497	KP134786	-	KP135054
Merulius tremellosus	FD-323	KP134856	KP135231	-
Mycoacia fuscoatra	HHB-10782-Sp	KP134857	KP135265	KP135365
Mycoacia nothofagi	HHB-4273-Sp	KP134858	KP135266	KP135369
Mycoleptodonoides vassiljevae	Spirin-8033	KY948970*	KY948877*	KY948737*
Neofavolus sp.	MA-672	KP325696	KP283524	KP283506
Neofavolus suavissimus	ADD-7	KP325694	KP283527	KP283501

Taxon	**Collection**	***rpb1***	**nrLSU**	**nrITS**
Obba rivulosa	FP-135416-Sp	KP134878	KP135208	KP135309
Oligoporus balsameus	FP-135372	KY948974*	KC585187	KC585358
Oligoporus sericeomollis	L-15571	KY948977*	KC585192	KC585363
Oxychaete cervinogilvus	Schigel-5216	KX752626*	KX752596*	KX752596*
Panus fragilis	HHB-11042-Sp	KP134877	KP135233	KP135328
Phaeophlebiopsis caribbeana	HHB-6990	KP134810	KP135243	KP135415
Phaeophlebiopsis ignerii	FD-425	KP134811	-	KP135418
Phaeophlebiopsis peniophoroides	FP-150577	KP134813	KP135273	KP135417
Phaeophlebiopsis sp.	HHB-6542-Sp	KP134812	KP135248	KP135413
Phanerochaete "krikophora"	HHB-5796-Sp	KP134837	KP135268	KP135164
Phanerochaete allantospora	KKN-111	KP134791	KP135238	KP135038
Phanerochaete arizonica	RLG-10248-Sp	KP134830	KP135239	KP135170
Phanerochaete australis	HHB-7105-Sp	KP134840	KP135240	KP135081
Phanerochaete carnosa	HHB-9195-Sp	KP134831	KP135242	KP135129
Phanerochaete cf. *calotriha*	Vanhanen-382	KP134826	-	KP135107
Phanerochaete chrysosporium I	AFTOL-776	AY864880	-	AY854086
Phanerochaete chrysosporium II	HHB-6251-Sp	KP134842	KP135246	KP135094
Phanerochaete citrinosanguinea	FP-105385	KP134824	KP135234	KP135100
Phanerochaete ericina	HHB-2288	KP134834	KP135247	KP135167
Phanerochaete exilis	HHB-6988	KP134799	KP135236	KP135001
Phanerochaete laevis	HHB-15519-Sp	KP134836	KP135249	KP135149
Phanerochaete magnoliae	HHB-9829-Sp	KP134838	KP135237	KP135089
Phanerochaete pseudomagnoliae	PP-25	KP135091	KP135250	KP135091
Phanerochaete pseudosanguinea	FD-244	KP134827	KP135251	KP135098
Phanerochaete rhodellum	FD-18	KP135187	KP135258	KP135187
Phanerochaete sanguinea	HHB-7524	KP135101	KP135244	KP135101
Phanerochaete sordida I	FD-241	KP135136	KP135252	KP135136
Phanerochaete sordida II	FD-106	KP135070	KP135253	KP135070
Phanerochaete sp.	HHB-11463	KP134797	KP135235	KP134994

Taxon	**Collection**	***rpb1***	**nrLSU**	**nrITS**
Phanerochaete sp.	HHB-18104	KP134798	KP135254	KP135003
Phanerochaete sp.	RLG-13408-Sp	KP134801	KP135257	KP135020
Phanerochaete subceracea	FP-105974-R	KP134835	KP135255	KP135162
Phanerochaete xerophila	HHB-8509-Sp	KP134800	KP135259	KP134996
Phlebia albida	GB-1833	KY948960*	KY948889*	KY948748*
Phlebia aurea	NH-14434	-	AY586691	-
Phlebia aurea	RLG-5075-sp	KY948918*	-	KY948759*
Phlebia brevispora	FBCC1463	-	LN611135	LN611135
Phlebia brevispora	HHB-7030	genome	-	-
Phlebia centrifuga	HHB-9239-Sp	KP134844	KP135262	KP135380
Phlebia cf. griseoflavescens	MR-4310	KY948963*	KY948888*	KY948797*
Phlebia chrysocreas	HHB-6333-Sp	KP134861	KP135263	KP135358
Phlebia coccineofulva	HHB-11466-sp	KY948915*	KY948851*	KY948766*
Phlebia floridensis	HHB-9905	KP134863	KP135264	KP135383
Phlebia hydnoidea	HHB-1993-sp	KY948921*	KY948853*	KY948778*
Phlebia lindtneri	GB-501	KY948923*	KY948847*	KY948772*
Phlebia lividina	HHB-4160-sp	KY948916*	KY948849*	KY948755*
Phlebia ludoviciana	FD-427	KP134849	-	KP135342
Phlebia nantahaliensis	HHB-2816-sp	KY948920*	KY948852*	KY948777*
Phlebia nitidula	Nystroem-020830	-	EU118655	-
Phlebia nitidula	T-407	KY948961*	-	KY948747*
Phlebia radiata	AFTOL-484	AY864881	AF287885	AY854087
Phlebia setulosa	HHB-6891-Sp	KP134864	KP135267	KP135382
Phlebia sp.	HHB-17984	KP134860	KP135261	KP135359
Phlebia sp.	HHB-18295	KP134814	KP135269	KP135405
Phlebia sp.	RLG-10795-sp	KY948937*	KY948857*	KY948785*
Phlebia subochracea I	HHB-8715-sp	KY948913*	KY948846*	KY948770*
Phlebia subochracea II	HHB-8494-sp	KY948912*	KY948845*	KY948768*
Phlebia uda	FP-101544-Sp	KP134859	KP135232	KP135361
Phlebiopsis castanea	Spirin-5295	KX752629*	KX752610*	KX752610*
Phlebiopsis crassa	KKN-86-Sp	KP134820	KP135215	KP135394
Phlebiopsis flavidoalba	FD-263	KP134819	KP135271	KP135402
Phlebiopsis galochroa	FP-102937	KP134822	KP135270	KP135391
Phlebiopsis gigantea	FP-70857-Sp	KP134821	KP135272	KP135390
Phlebiopsis ravenelii	FP-110129	KP134850	KP135274	KP135362

Taxon	**Collection**	***rpb1***	**nrLSU**	**nrITS**
Physisporinus sp.	Miettinen-15239	KY948946*	KY948867*	KY948732*
Physisporinus sp.	Miettinen-16699	KY948947*	KY948863*	KY948733*
Piptoporus betulinus	L-15603	KY949005*	KC585202	KC585373
Pirex concentricus	OSC-41587	KP134843	KP135275	KP134984
Podoscypha parvula	CBS 331.66	-	JN649361	JN649361
Podoscypha parvula	Niemelä-7690	KY948934*	-	-
Polyporellus arcularius	DSH92-132	KP325686	KP283522	KP283489
Polyporus brumalis	PB-4 (EP4)	KP325685	KP283519	KP283490
Polyporus squamosus	AFTOL-704	DQ831023	AY629320	DQ267123
Porogramme albocincta	PR-1478-T	KY948906*	KY948838*	KY948725*
Postia caesia	Kinnunen-5087	KY948978*	KY948885*	KY948814*
Postia lactea	Kotiranta-20058	KY948979*	KC595939	KC595939
Postia lowei	Pennanen-1254	KY948980*	KC595941	KC595941
Pouzaroporia subrufa	Miettinen-14343	KY948972*	KY948896*	KY948736*
Pycnoporellus alboluteus	FP-105074	KY949039*	KC585214	KC585381
Pycnoporellus fulgens	CA-20	KY949040*	KC585218	KC585385
Radulodon casearius	HHB-9567-sp	KY948943*	KY948871*	KY948752*
Rhizochaete americana	FP-102188	KP134815	KP135277	KP135409
Rhizochaete belizensis	FP-150712	KP134817	KP135280	KP135408
Rhizochaete filamentosa	HHB-3169-Sp	KP134818	KP135278	KP135410
Rhizochaete fouqueriae	KKN-121-sp	KY948938*	KY948858*	KY948786*
Rhizochaete radicata	FD-123	KP134816	KP135279	KP135407
Rhodonia placenta	Dietz-7E	KY949028*	KC585223	KC585390
Rigidoporus undatus	Miettinen-13591	KY948945*	KY948870*	KY948731*
Rigidoporus vinctus	ECS-194-R	KY948953*	KY948873*	KY948734*
Rigidoporus vinctus	Miettinen-16136	KY953212*	-	KY953211*
Rigidoporus vinctus	Miettinen-17916	KY948954*	KY948874*	KY948735*
Sarcodontia crocea	OMC-1488	KY948928*	KY948903*	KY948798*
Sarcoporia polyspora	L-14910	KY949022*	KC585226	KC585393
Scopuloides rimosa I	RLG-5104	KP134852	KP135283	KP135351
Scopuloides rimosa II	HHB-7042	KP135350	KP135282	KP135350
Scopuloides rimosa III	HHB-15484	KP134851	KP135281	KP135352
Scopuloides sp.	FP-102935	KP134855	KP135285	KP135353
Scopuloides sp.	FP-150473	KP134854	KP135284	KP135355
Skeletocutis chrysella	L-15957-sp	KY948982*	-	-

Taxon	**Collection**	***rpb1***	**nrLSU**	**nrITS**
Skeletocutis chrysella	X-319	-	FN907916	FN907916
Skeletocutis lilacina	HHB-10522-sp	KY948967*	KY948894*	KY948834*
Skeletocutis nivea	Miettinen-9950	KY953143	KY953045	KY953045
Skeletocutis odora	L-13763-sp	KY949046*	KY948893*	KY948830*
Skeletocutis sp.	L-3291-R	KY948968*	KY948968*	KY948835*
Sparassis radicata	OKM-4756	KY949023*	KF053407	KC987580
Spongipellis delectans	HHB-10489-Sp	KP134876	KP135287	KP135301
Spongipellis pachyodon	FD-314	KP134875	KP135288	KP135302
Spongipellis unicolor	RLG-7638-sp	KY948942*	-	KY948751*
Spongipellis unicolor	RLG-7701-T	-	HQ729016	-
Spongiporus leucospongia	OKM-4335	KY948975*	KC585228	KC585395
Steccherinaceae sp.	OMC-1192	KY949047*	KY948865*	KY948816*
Steccherinum bourdotii	HHB-9743-sp	KY949043*	-	KY948818*
Steccherinum bourdotii	Saarenoksa-10195	-	JN710584	-
Steccherinum laeticolor	FP-102480-sp	KY948948*	KY948868*	KY948823*
Steccherinum nitidum	FP-105195-Sp	KP134888	KP135227	KP135323
Steccherinum oreophilum	HHB-13202-sp	KY948949*	-	KY948824*
Steccherinum oreophilum	Niemelä-7691	-	JN710548	-
Steccherinum sp.	FD-26	KP134889	KP135289	KP135322
Steccherinum sp.	FP-8695	KY948952*	KY948869*	KY948819*
Steccherinum tenue	FP-102082-sp	KY948951*	-	KY948817*
Steccherinum tenue	KHL 12316	-	JN710598	-
Stereum hirsutum	FP-91666	genome		
Stereum hirsutum	FPL-8805	-	AF393078	AY854063
Terana caerulea	FP-104073	KP134865	KP135276	KP134980
Tinctoporellus epimiltinus	CRM-55	KY948905*	KY948837*	KY948720*
Tomophagus cattienensis (as T. colossus in Genbank)	TC-02 (TNM)	KJ143963	-	KJ143923
Trametes aesculi	FP-105679-sp	JN164833	JN164799	JN164944
Trametes betulina	HHB-9942-sp	JN164822	JN164794	JN164983
Trametes cinnabarina	AFTOL-772	JN164843	AY684160	DQ411525
Trametes conchifer	FP-106793-sp	JN164823	JN164797	JN164924
Trametes cubensis	TJV-93-213-sp	JN164834	JN164798	JN164923
Trametes ectypa	FP-106037-T	JN164824	JN164803	JN164929
Trametes gibbosa	L-11664-sp	JN164831	JN164800	JN164943

Taxon	**Collection**	***rpb1***	**nrLSU**	**nrITS**
Trametes hirsuta	RLG-5133-T	JN164829	JN164801	JN164941
Trametes maxima	OH-189-sp	JN164816	JN164804	JN164957
Trametes membranacea	PRSC-82	JN164832	JN164805	JN164945
Trametes meyenii	FPRI-401	JN164836	JN164802	JN164933
Trametes ochracea	HHB-13445-sp	JN164826	JN164812	JN164954
Trametes pavonia	FP-103050-sp	JN164835	JN164806	JN164958
Trametes polyzona	BKW-004	JN164844/ JN164846	JN164790	JN164978
Trametes pubescens	FP-101414-sp	JN164827	JN164811	JN164963
Trametes sanguinea	PRSC-95	JN164842	JN164795	JN164982
Trametes suaveolens	FP-102529-sp	JN164828	JN164807	JN164966
Trametes versicolor	FP-135156-sp	JN164825	JN164809	JN164919
Trametes villosa	FP-71974-R	JN164830	JN164810	JN164969
Trametopsis cervina	AJ-185	JN164839	JN164796	JN165020
Tyromyces chioneus	FD-4	KP134891	KP135291	KP135311
Tyromyces galactinus	L-15951-sp	KY948966*	KY948892*	KY948829*
Tyromyces merulinus	CIEFAP-204	KY949045*	KY948875*	KY948740*
Wolfiporia cocos	18176	-	KC585233	-
Wolfiporia cocos	MD-104 SS10	genomic	-	-
Wolfiporia cocos	unknown	-	-	AY728272
Wolfiporia dilatohypha	CS-635913	KY949026*	KC585234	KC585400

Table 2. Overview of morphological, anatomical, physiological, and genetic characters of the families of *Polyporales*. Symbols: + indicates the character is common in the family, but not necessarily present in all species; (+) indicates the characters is present in only a few species.

	Basidiome			**Hymenophore**				**Type or rot**	
Taxon	**Pileate**	**Stipitate**	**Resupinate**	**Poroid**[1]	**Daedaleoid /Lamellate**[2]	**Smooth**[3]	**Hydnoid**[4]	**White**	**Brown**
Cerrenaceae	+		+	+	(+)		+	+	
Dacryobolaceae	+	(+)	+	+		(+)	(+)		+
Fomitopsidaceae	+		+	+	(+)				+
Gelatoporiaceae			+	+				+	
Grifolaceae	+	+		+				+	
Hyphodermataceae			+			+	(+)	+	
Incrustoporiaceae	+		+	+				+	
Irpicaceae	(+)		+	+	(+)	+	(+)	+	(+)
Ischnodermataceae	+			+				+	
Laetiporaceae	+	+	(+)	+	(+)				+
Meripilaceae	+	+	+	+				+	
Meruliaceae	(+)		+	+		+	+	+	
Panaceae	+	+			+	+		+	
Phanerochaetaceae	(+)		+	(+)	(+)	+	(+)	+	
Podoscyphaceae	+	+	+	(+)	(+)	+		+	
Polyporaceae	+	+	+	+	+	(+)	(+)	+	
Sparassidaceae	spathulate					+			+
Steccherinaceae	+	(+)	+	+	(+)		+	+	
Character present in "n" families	15	8	14	15	9	9	8	14	5

[1] Regular round to angular pores
[2] Irregular, sinuous, daedaleoid pores or lamellae
[3] Surface smooth or with small grains, rounded projections, folds, wrinkles
[4] Surface with tooh-like projections, aculei, rigid hairs, spine-like structures

	Spores					Cystidia		
Taxon	**Amyloid**	**Dextrinoid**	**Ornamented**	**Pigmented**	**Thick-walled**	**Smooth**	**Ornamented**	**Thick-walled**
Cerrenaceae					(+)	+	(+)	(+)
Dacryobolaceae	(+)		(+)		(+)	+	(+)	(+)
Fomitopsidaceae				(+)				
Gelatoporiaceae								
Grifolaceae								
Hyphodermataceae						+	(+)	(+)
Incrustoporiaceae					(+)		(+)	
Irpicaceae						(+)	(+)	(+)
Ischnodermataceae								
Laetiporaceae						(+)		
Meripilaceae					+		+	+
Meruliaceae					(+)	+	+	+
Panaceae						+	(+)	+
Phanerochaetaceae						+	+	+
Podoscyphaceae			(+)		(+)	+	(+)	+
Polyporaceae		(+)	(+)	(+)	+	(+)	(+)	(+)
Sparassidaceae						(+)		
Steccherinaceae						(+)	+	+
Character present in “n” families	1	1	3	2	7	12	12	11

	Hyphae	Hyphal system			Mating system		
Taxon	**Clamps**	**Monomitic**	**Dimitic**	**Trimitic**	**Homothallic**	**Bipolar**	**Tetrapolar**
Cerrenaceae	+	+	+	(+)		+	+
Dacryobolaceae	+	+	+	(+)			+
Fomitopsidaceae	+	(+)	+	+	+	+	
Gelatoporiaceae	+	+	(+)			+	+
Grifolaceae	+		+				+
Hyphodermataceae	+	+				+	
Incrustoporiaceae	+	(+)	+				+
Irpicaceae	+	+	(+)		(+)?		(+)
Ischnodermataceae	+		+			+	
Laetiporaceae		(+)	+			+	
Meripilaceae		+	(+)		?	?	?
Meruliaceae	+	+	(+)			+	
Panaceae	+		+				+
Phanerochaetaceae	(+)	+				+	
Podoscyphaceae	+	+	+	(+)			+
Polyporaceae	+	(+)	+	+			+
Sparassidaceae	(+)	+				+	
Steccherinaceae	+	+	+				+
Character present in “n” families	16	15	15	5	1-3	9-10	10-11

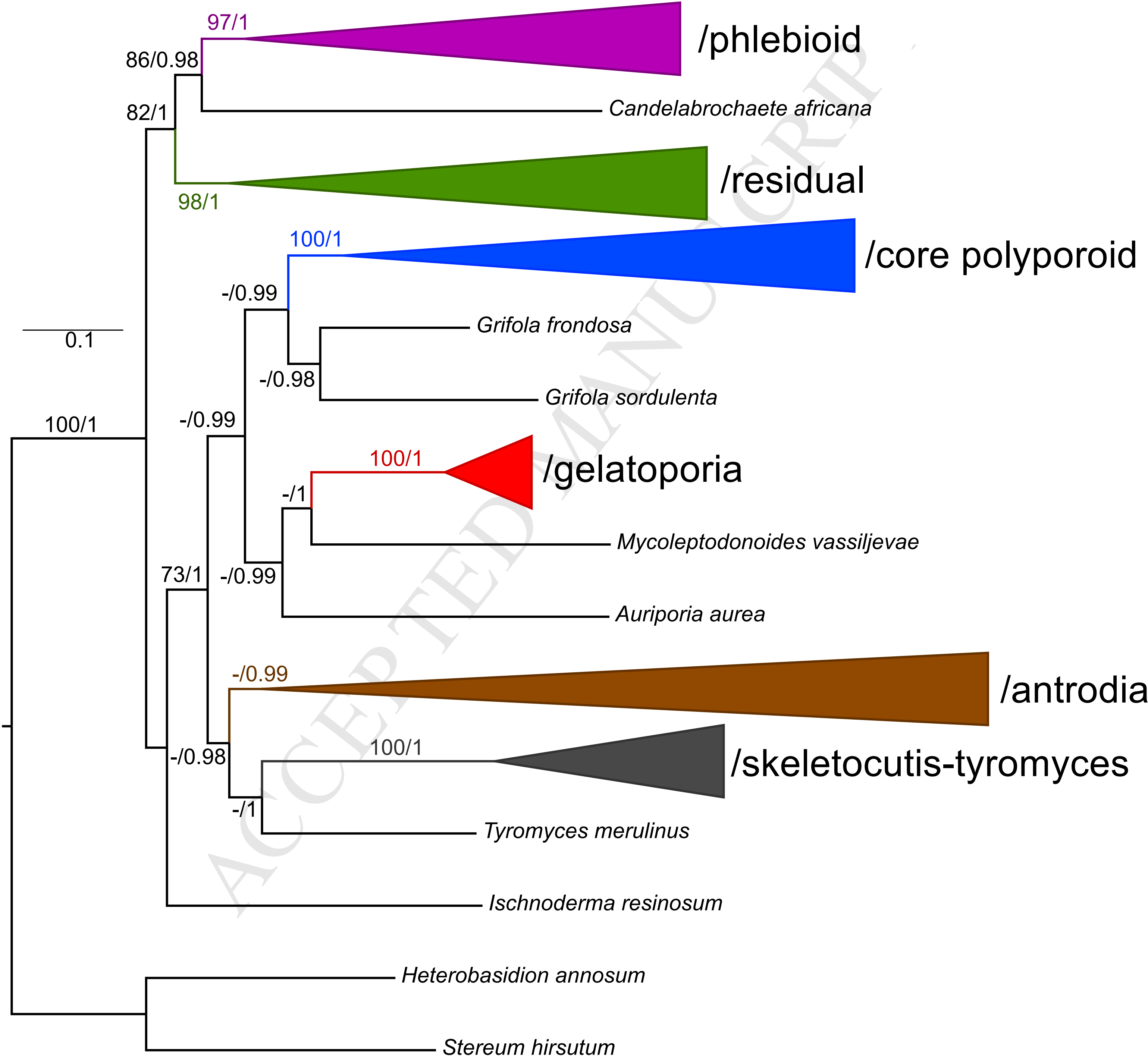
	Nuclear Behavior			
Taxon	**Normal**	**Heterocytic**	**Astatocoenocytic**	**Holocoenocytic**
Cerrenaceae		+	+	
Dacryobolaceae	+			
Fomitopsidaceae	+		(+)	
Gelatoporiaceae			+	
Grifolaceae	?	?	?	?
Hyphodermataceae	?	?	?	?
Incrustoporiaceae		+	+	
Irpicaceae		+		+
Ischnodermataceae			+	
Latetiporaceae				+
Meripilaceae	?	?	?	?
Meruliaceae	?	?	?	?
Panaceae	?	?	?	?
Phanerochaetaceae		+	(+)	
Podoscyphaceae	+			
Polyporaceae	+	(+)	(+)	
Sparassidaceae	?	?	?	?
Steccherinaceae	+			
Character present in “n” families	5-11	5-11	7-13	2-8

Table 3. Genome sampling of Polyporales in MycoCosm[1] as of April, 2017.

clade	family/clade	genomes (one/species unless noted)
/phlebioid	*Irpicaceae*	*Cytidiella melzeri* *Hydnopolyporus fimbriatus* *Irpex lacteus* *Trametopsis cervina*
	Meruliaceae	*Phlebia brevispora* *Phlebia centrifuga*
	Phanerochaetaceae	*Bjerkandera adusta* *Phanerochaete carnosa* *Phanerochaete chrysosporium* *Phlebiopsis gigantea*
/residual	*Cerrenaceae*	*Cerrena unicolor*
	Hyphodermataceae	none
	Meripilaceae	none
	Panaceae	*Panus rudis*
	Podoscyphaceae	none
	Steccherinaceae	none
	/climacocystis	*Climacocystis borealis*
	/hypochnicium	none
/core polyporoid	*Polyporaceae*	*Artolenzites elegans* (2) *Dichomitus squalens* (4) *Ganoderma sp.* *Leiotrametes sp* *Lentinus tigrinus* (3) *Polyporus arcularius* *Polyporus brumalis* *Pycnoporus cinnabarinus* *Pycnoporus coccineus* *Pycnoporus puniceus* *Pycnoporus sanguineus* *Trametes cingulata* *Trametes gibbosa* *Trametes ljubarskyi* *Trametes pubescens* *Trametes versicolor*
inc. sed. near /core polyporoid	*Gelatoporiaceae*	*Gelatoporia (Ceriporiopsis) subvermispora* *Obba rivulosa*

	Grifolaceae	none
/antrodia	*Dacryobolaceae*	none
	Fomitopsidaceae	*Daedalea quercina* *Fomitopsis pinicola*
	Laetiporaceae	*Laetiporus sulphureus* *Wolfiporia cocos*
	Sparassidaceae	*Sparassis latifolia*
	/amyloporia	*Antrodia sinuosa* *Rhodonia (Postia) placenta*
	/fibroporia	*Fibroporia radiculosa*
inc. sed. near /antrodia	*Incrustoporiaceae*	none
	Ischnodermataceae	none

[1] http://genome.jgi.doe.gov/programs/fungi/index.jsf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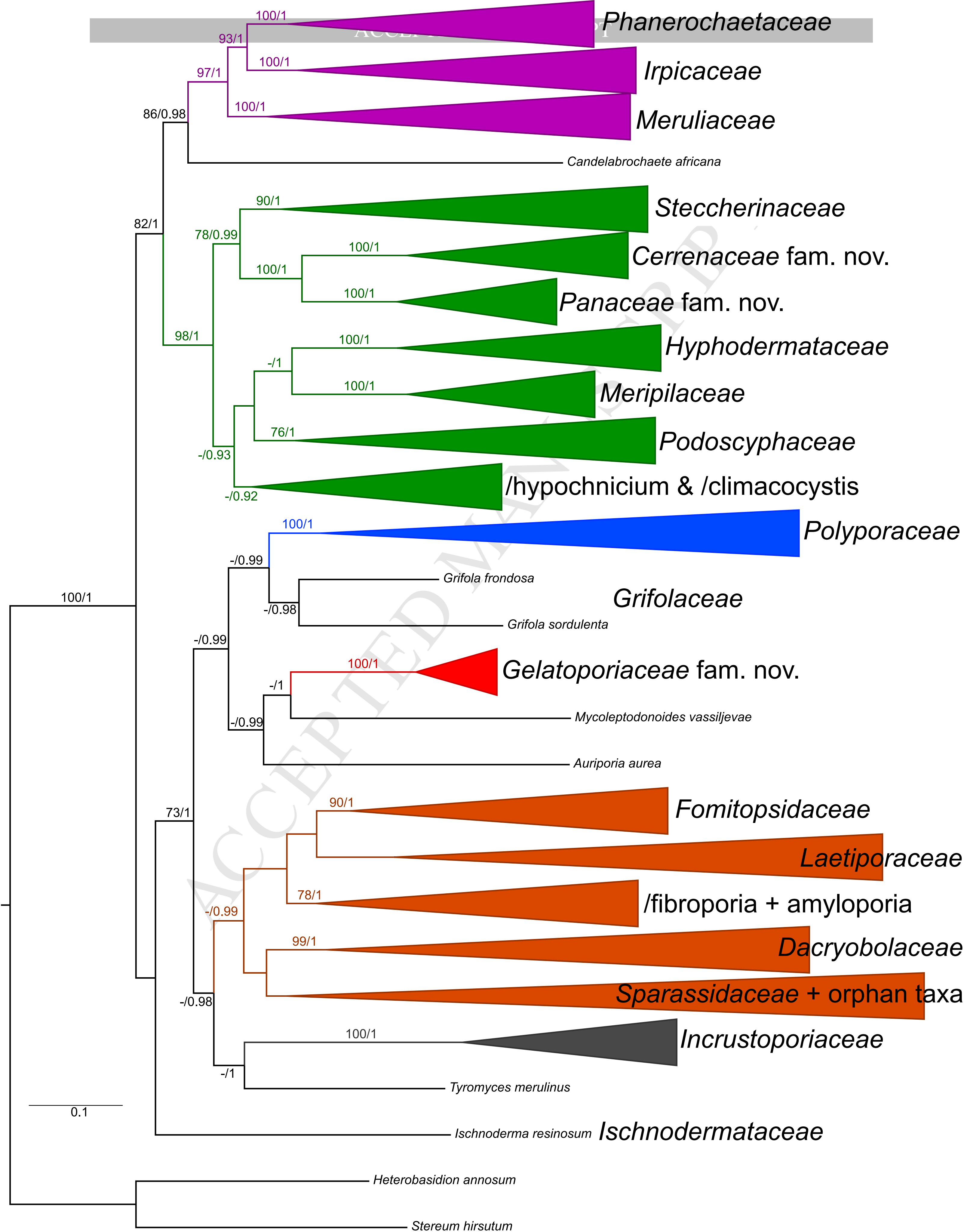
86/0.98
Candelabrochaete africana
82/1
/residual
98/1
100/1
/core polyporoid
-/0.99
0.1
Grifola frondosa
-/0.98
Grifola sordulenta
-/0.99
100/1
100/1
/gelatoporia
-/1
Mycoleptodonoides vassiljevae
73/1
-/0.99
Auriporia aurea
-/0.99
/antrodia
100/1
/skeletocutis-tyromyces
-/0.98
-/1
Tyromyces merulinus
Ischnoderma resinosum
Heterobasidion annosum
Stereum hirsutum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93/1
100/1
Irpicaceae
97/1
100/1
Meruliaceae
86/0.98
Candelabrochaete africana
90/1
Steccherinaceae
82/1
78/0.99
100/1
Cerrenaceae fam. nov.
100/1
100/1
Panaceae fam. nov.
98/1
100/1
Hyphodermataceae
-/1
100/1
Meripilaceae
76/1
Podoscyphaceae
-/0.93
/hypochnicium & /climacocystis
-/0.92
100/1
Polyporaceae
-/0.99
Grifola frondosa
Grifolaceae
100/1
-/0.98
Grifola sordulenta
-/0.99
100/1
Gelatoporiaceae fam. nov.
-/1
-/0.99
Mycoleptodonoides vassiljevae
Auriporia aurea
90/1
Fomitopsidaceae
73/1
Laetiporaceae
78/1
/fibroporia + amyloporia
-/0.99
99/1
Dacryobolaceae
Sparassidaceae + orphan taxa
-/0.98
100/1
Incrustoporiaceae
-/1
Tyromyces merulinus
0.1
Ischnoderma resinosum
Ischnodermataceae
Heterobasidion annosum
Stereum hirsutum


Phanerochaetaceae
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71/0.98
Phanerochaete citrinosanguinea
92/1
Phanerochaete sanguinea
72/1
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Phanerochaete burtii
100/1
Phanerochaete sanguineocarnosa
100/1
Phanerochaete carnosa
Phanerochaete sordida I
Phanerochaete rhodella
Phanerochaetaceae
Phanerochaete arizonica
71/1
100/1
Phanerochaete magnoliae
96/1
Phanerochaete pseudomagnoliae
Phanerochaete australis
100/1
Phanerochaete sordida II
-/0.95
84/1
100/1
Phanerochaete chrysosporium I
Phanerochaete chrysosporium II
100/1
Phanerochaete subceracea
100/1
Phanerochaete ericina
100/1
Phanerochaete laevis
93/1
Phanerochaete "krikophora"
-/1
Oxychaete cervinogilva
Pirex concentricus
Hyphodermella rosae
77/1
Donkia pulcherrima
100/1
Phaeophlebiopsis sp. HHB6542
90/1
Phaeophlebiopsis peniophoroides
100/1
Phaeophlebiopsis ignerii
Phaeophlebiopsis caribbeana
-/1
78/1
Hapalopilus nidulans
Hapalopilaceae
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100/1
100/1
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90/1
Rhizochaete belizensis
Rhizochaete fouqueriae
88/1
Rhizochaete filamentosa
100/1
77/0.94
Rhizochaete americana
100/1
Phlebiopsis crassa
100/1
Phlebiopsis gigantea
100/1
Phlebiopsis galochroa
71/0.92
Phlebiopsis flavidoalba
100/1
Phlebiopsis castanea (= Castanoporus castaneus)
100/1
Phlebia sp. RLG10795sp
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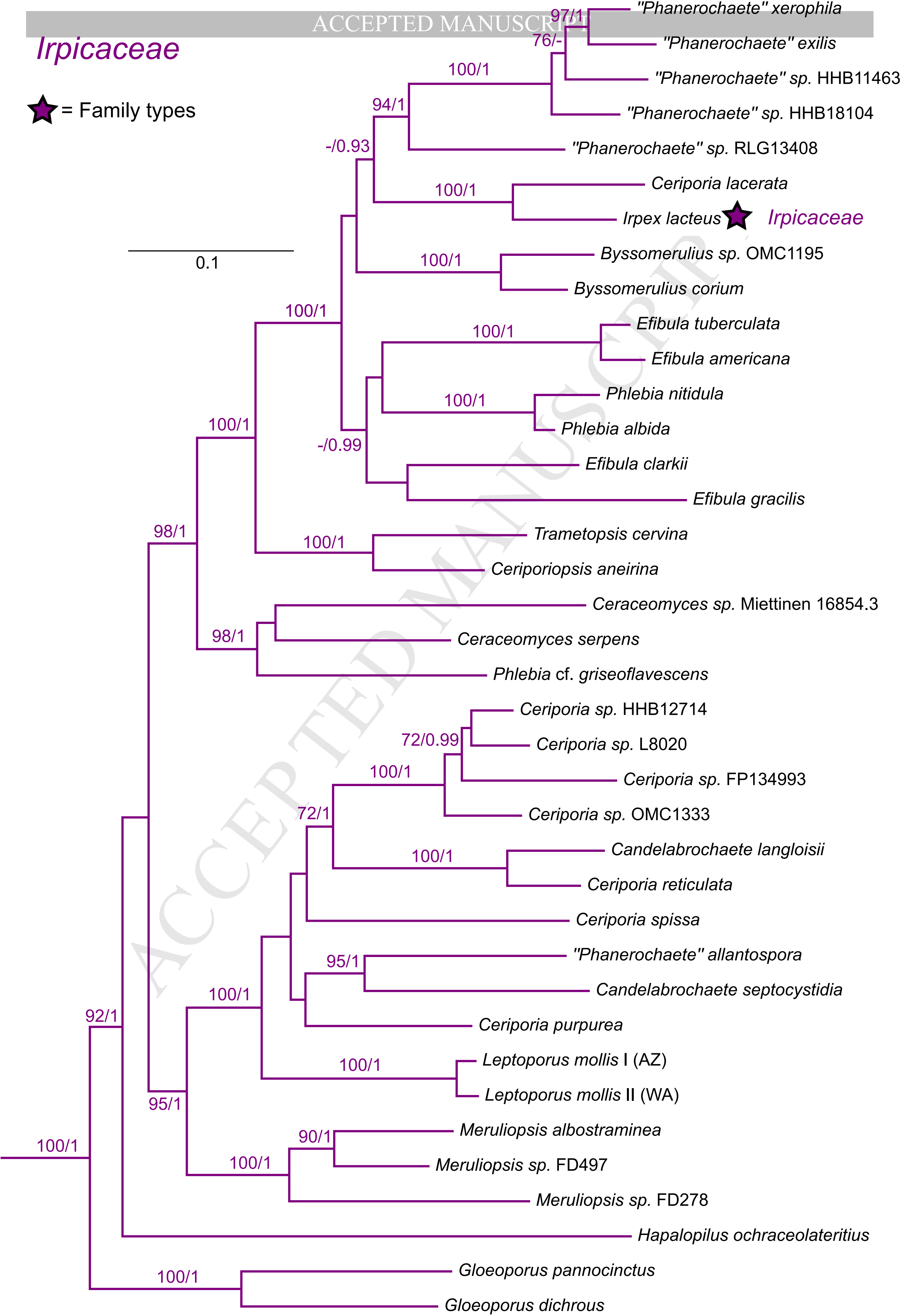
Bjerkanderaceae
100/1
Bjerkandera aff. centroamericana
Ceriporiopsis carnegieae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"Phanerochaete" sp. RLG13408
Ceriporia lacerata
Irpex lacteus
Irpicaceae
Byssomerulius sp. OMC1195
Byssomerulius corium
Efibula tuberculata
Efibula americana
Phlebia nitidula
Phlebia albida
Efibula clarkii
Efibula gracilis
Trametopsis cervina
Ceriporiopsis aneirina
Ceraceomyces sp. Miettinen 16854.3
Ceraceomyces serpens
Phlebia cf. griseoflavescens
Ceriporia sp. HHB12714
Ceriporia sp. L8020
Ceriporia sp. FP134993
Ceriporia sp. OMC1333
Candelabrochaete langloisii
Ceriporia reticulata
Ceriporia spissa
"Phanerochaete" allantospora
Candelabrochaete septocystidia
Ceriporia purpurea
Leptoporus mollis I (AZ)
Leptoporus mollis II (WA)
Meruliopsis albostraminea
Meruliopsis sp. FD497
Meruliopsis sp. FD278
Hapalopilus ochraceolateritius
Gloeoporus pannocinctus
Gloeoporus dichrous
97/1
76/-
100/1
94/1
-/0.93
100/1
100/1
100/1
100/1
100/1
-/0.99
100/1
100/1
98/1
98/1
72/0.99
100/1
72/1
100/1
95/1
100/1
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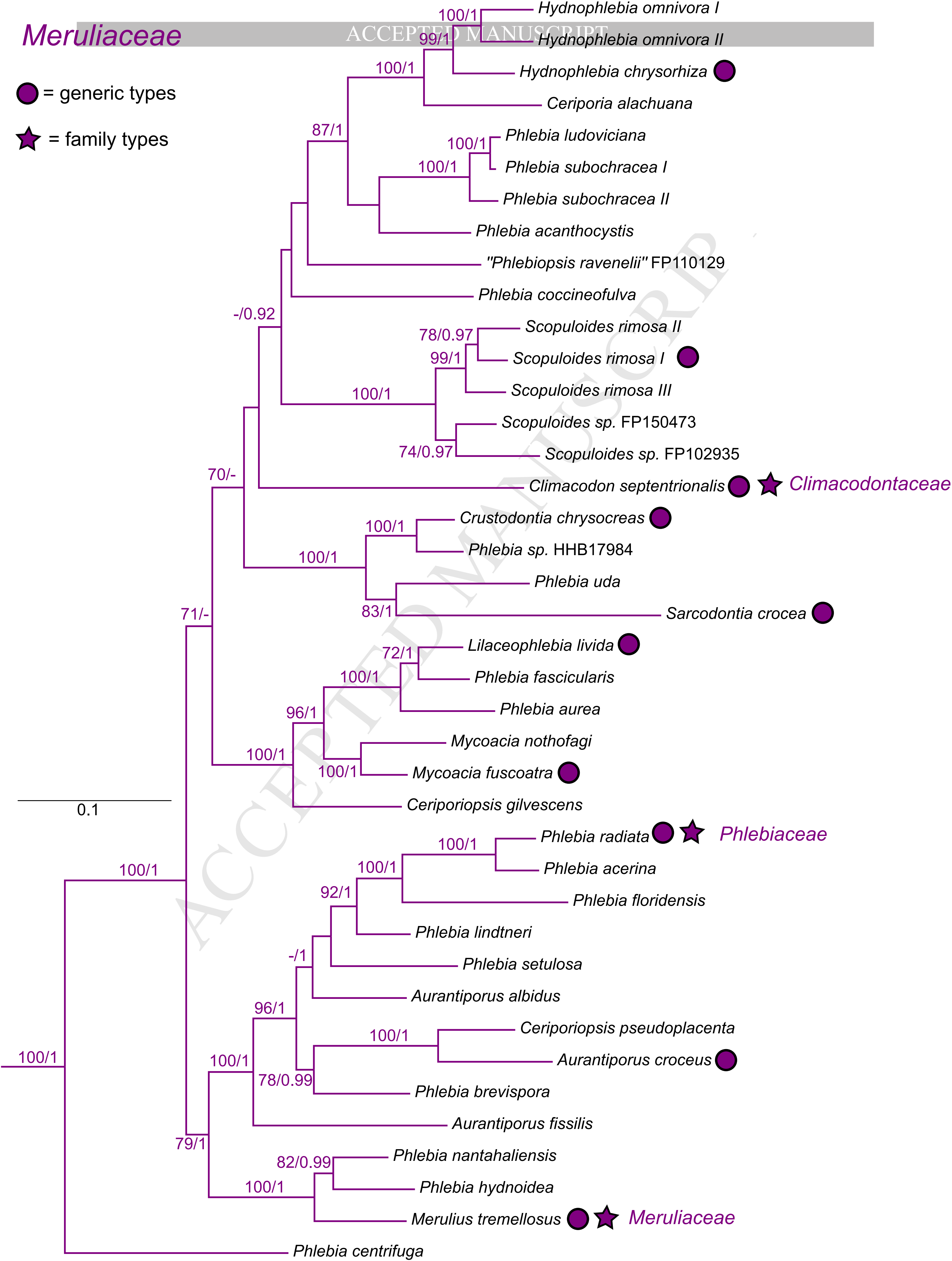
95/1
90/1
100/1
92/1
100/1
100/1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★ = family types
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Hydnophlebia chrysorhiza
Ceriporia alachuana
Phlebia ludoviciana
Phlebia subochracea I
Phlebia subochracea II
Phlebia acanthocystis
"Phlebiopsis ravenelii" FP110129
Phlebia coccineofulva
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Scopuloides rimosa III
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Phlebia sp. HHB17984
Phlebia uda
Sarcodontia crocea
Lilaceophlebia livida
Phlebia fascicularis
Phlebia aurea
Mycoacia nothofagi
Mycoacia fuscoatra
Ceriporiopsis gilvescens
Phlebia radiata
Phlebiaceae
Phlebia acerina
Phlebia floridensis
Phlebia lindtneri
Phlebia setulosa
Aurantiporus albidus
Ceriporiopsis pseudoplacenta
Aurantiporus croceus
Phlebia brevispora
Aurantiporus fissilis
Phlebia nantahaliensis
Phlebia hydnoidea
Merulius tremellosus
Meruliaceae
Phlebia centrifuga
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100/1
87/1
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99/1
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100/1
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83/1
71/-
72/1
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96/1
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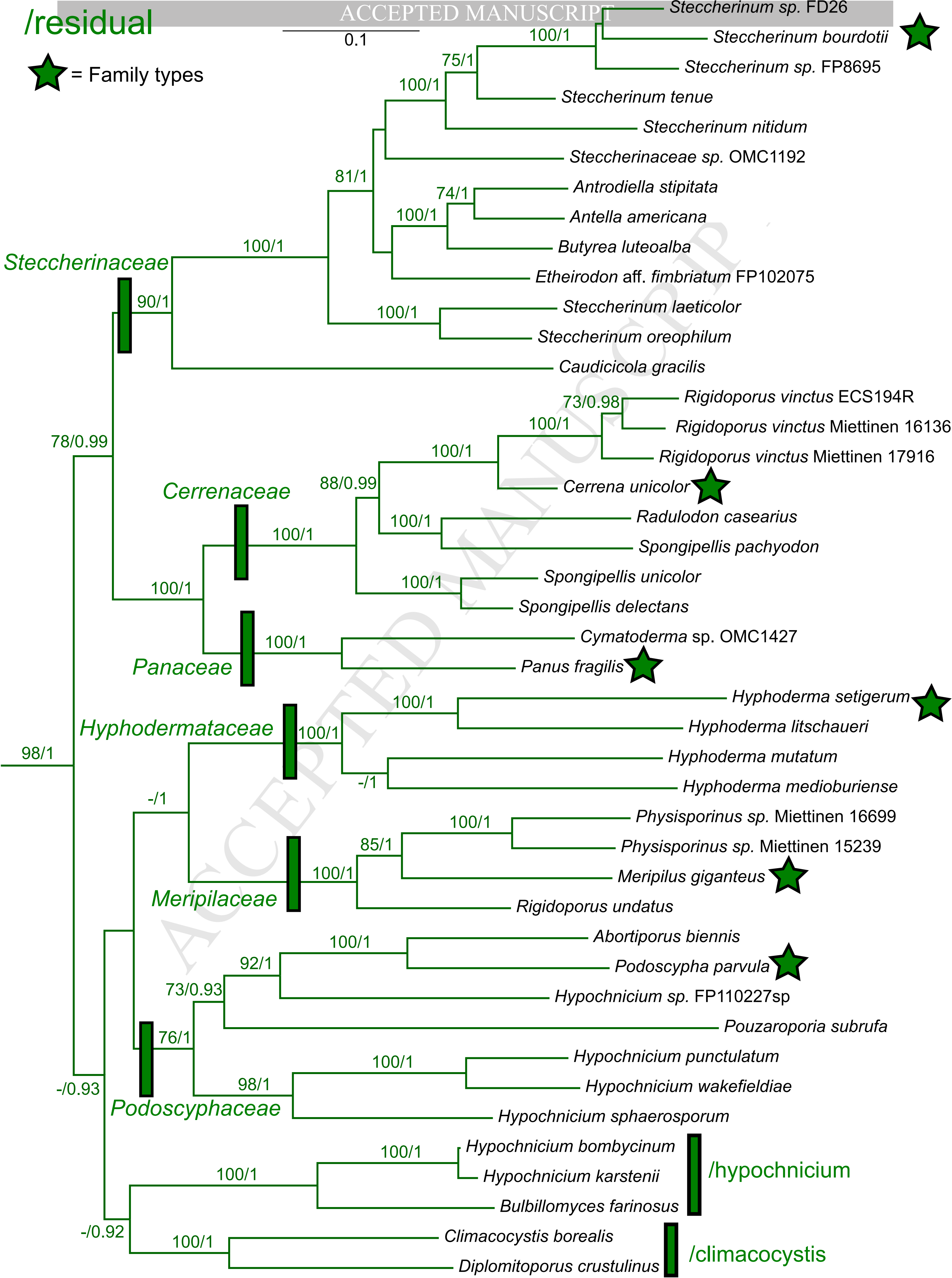
100/1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Antella americana
Butyrea luteoalba
Etheirodon aff. fimbriatum FP102075
Steccherinum laeticolor
Steccherinum oreophilum
Caudicicola gracilis
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100/1
81/1
74/1
100/1
100/1
100/1
90/1
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Rigidoporus vinctus Miettinen 16136
Rigidoporus vinctus Miettinen 17916
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Radulodon casearius
Spongipellis pachyodon
Spongipellis unicolor
Spongipellis delectans
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100/1
100/1
88/0.99
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100/1
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Panaceae
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Hyphoderma litschaueri
Hyphoderma mutatum
Hyphoderma medioburiense
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100/1
-/1
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Physisporinus sp. Miettinen 15239
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Rigidoporus undatus
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100/1
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Podoscypha parvula
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Pouzaroporia subrufa
Hypochnicium punctulatum
Hypochnicium wakefieldiae
Hypochnicium sphaerosporum
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73/0.93
76/1
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98/1
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Hypochnicium karstenii
Bulbillomyces farinosus
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/hypochnicium
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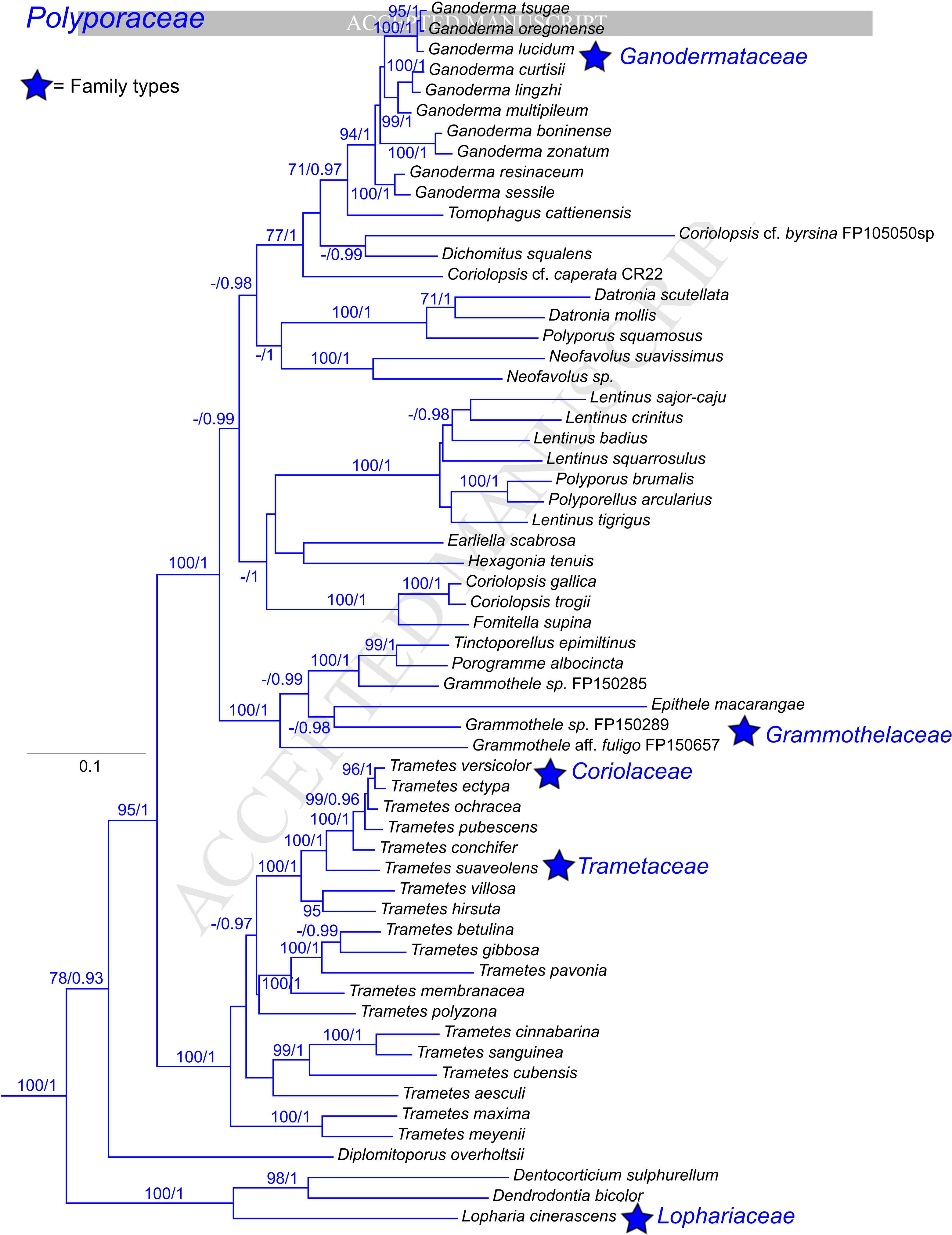
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Ganoderma lingzhi
Ganoderma multipileum
99/1
94/1
Ganoderma boninense
100/1 Ganoderma zonatum
71/0.97
Ganoderma resinaceum
100/1 Ganoderma sessile
Tomophagus cattienensis
77/1
Coriolopsis cf. byrsina FP105050sp
-/0.99 Dichomitus squalens
Coriolopsis cf. caperata CR22
-/0.98
71/1 Datronia scutellata
100/1
Datronia mollis
Polyporus squamosus
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Neofavolus sp.
Lentinus sajor-caju
-/0.98 Lentinus crinitus
-/0.99
Lentinus badius
Lentinus squarrosulus
100/1
100/1 Polyporus brumalis
Polyporellus arcularius
Lentinus tigrigus
Earliella scabrosa
100/1
Hexagonia tenuis
-/1
100/1 Coriolopsis gallica
100/1 Coriolopsis trogii
Fomitella supina
99/1 Tinctoporellus epimiltinus
100/1 Porogramme albocincta
-/0.99
Grammothele sp. FP150285
100/1
Epithele macarangae
-/0.98 Grammothele sp. FP150289
Grammothele aff. fuligo FP150657
Grammothelaceae
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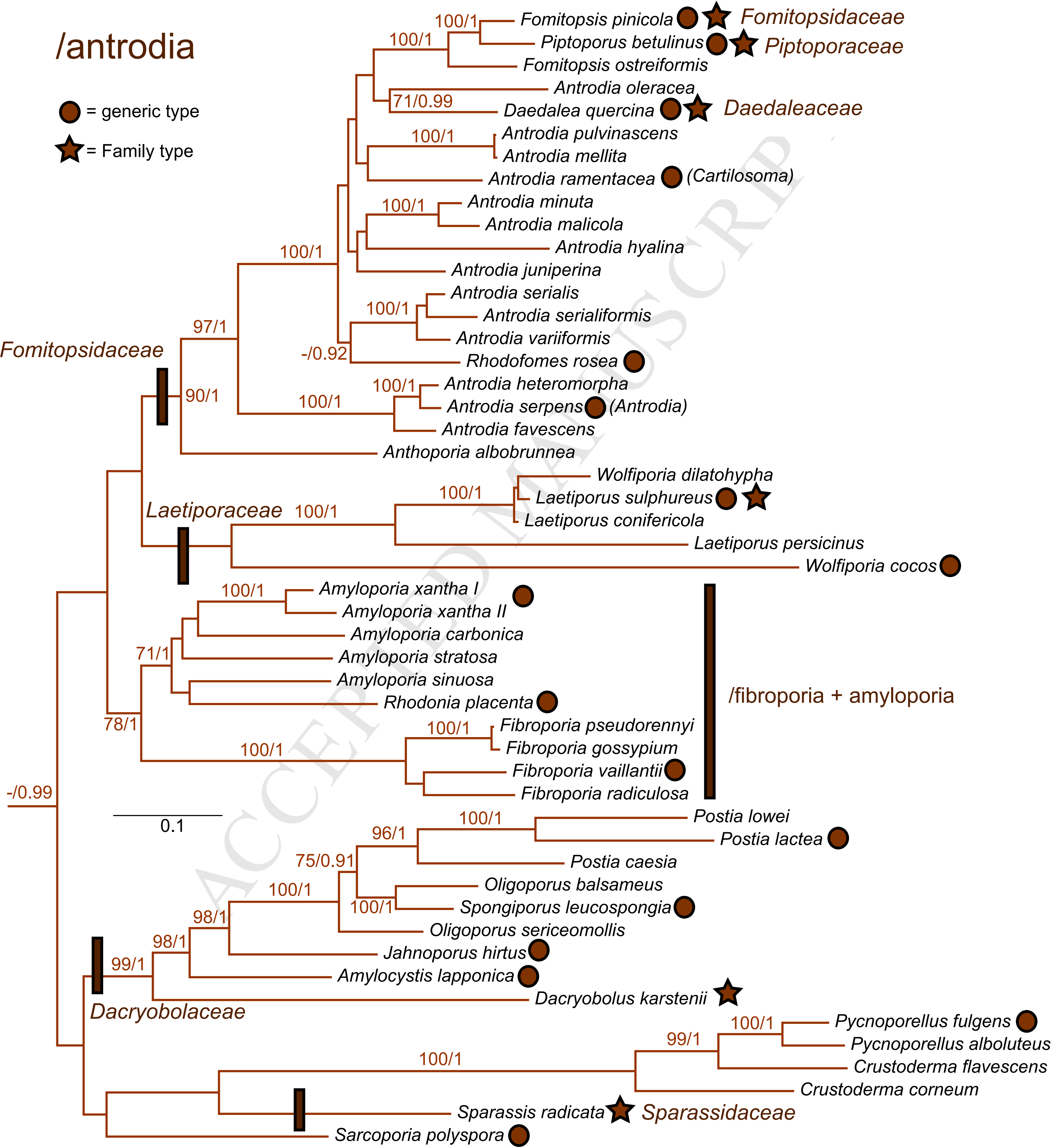
96/1 Trametes versicolor
Coriolaceae
Trametes ectypa
99/0.96 Trametes ochracea
100/1
Trametes pubescens
95/1
100/1 Trametes conchifer
100/1
Trametes suaveolens
Trametaceae
Trametes villosa
95 Trametes hirsuta
-/0.97
-/0.99 Trametes betulina
100/1
Trametes gibbosa
Trametes pavonia
78/0.93
100/1
Trametes membranacea
Trametes polyzona
100/1 Trametes cinnabarina
99/1 Trametes sanguinea
100/1
Trametes cubensis
100/1
Trametes aesculi
100/1 Trametes maxima
Trametes meyenii
Diplomitoporus overholtsii
98/1 Dentocorticium sulphurellum
100/1 Dendrodontia bicolor
Lopharia cinerascens
Lophariaceae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● = generic type
★ = Family type
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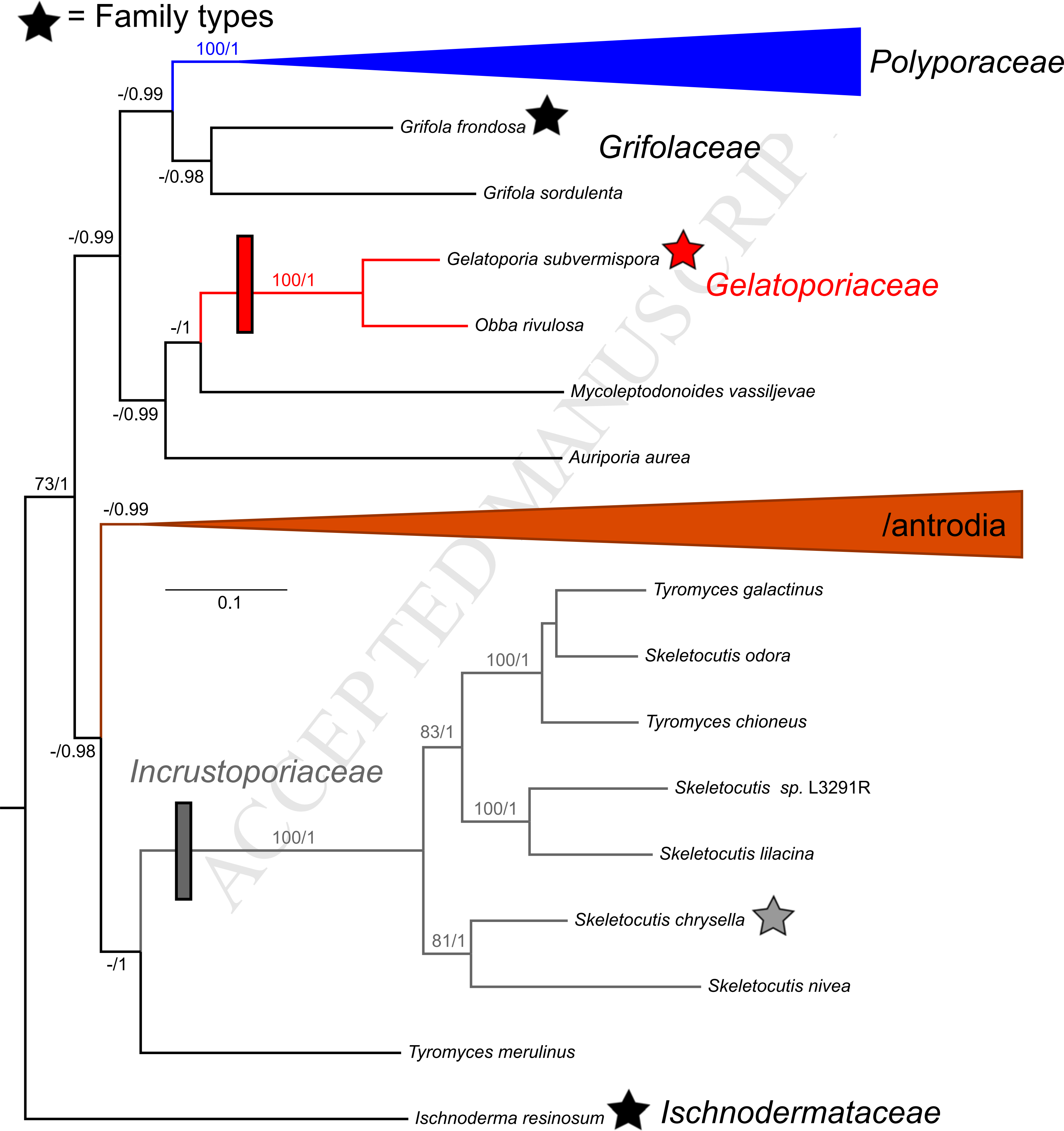
Fomitopsidaceae
100/1
Piptoporus betulinus
Piptoporaceae
Fomitopsis ostreiformis
Antrodia oleracea
71/0.99
Daedalea quercina
Daedaleaceae
100/1
Antrodia pulvinascens
Antrodia mellita
Antrodia ramentacea
(Cartilosoma)
100/1
Antrodia minuta
Antrodia malicola
Antrodia hyalina
100/1
Antrodia juniperina
Antrodia serialis
100/1
Antrodia serialiformis
97/1
Antrodia variiformis
Fomitopsidaceae
-/0.92
Rhodofomes rosea
100/1
Antrodia heteromorpha
90/1
100/1
Antrodia serpens
(Antrodia)
Antrodia favescens
Anthoporia albobrunnea
Wolfiporia dilatohypha
100/1
Laetiporus sulphureus
Laetiporaceae
100/1
Laetiporus conifericola
Laetiporus persicinus
Wolfiporia cocos
100/1
Amyloporia xantha I
Amyloporia xantha II
Amyloporia carbonica
71/1
Amyloporia stratosa
Amyloporia sinuosa
Rhodonia placenta
/fibroporia + amyloporia
78/1
100/1
Fibroporia pseudorennyi
100/1
Fibroporia gossypium
Fibroporia vaillantii
Fibroporia radiculosa
-/0.99
0.1
100/1
Postia lowei
96/1
Postia lactea
75/0.91
Postia caesia
Oligoporus balsameus
100/1
100/1
Spongiporus leucospongia
98/1
Oligoporus sericeomollis
98/1
Jahnoporus hirtus
99/1
Amylocystis lapponica
Dacryobolus karstenii
Dacryobolaceae
100/1
Pycnoporellus fulgens
99/1
Pycnoporellus alboluteus
100/1
Crustoderma flavescens
Crustoderma corneum
Sparassis radicata
Sparassidaceae
Sarcoporia polyspora



★ = Family types
100/1
Polyporaceae
-/0.99
Grifola frondosa
Grifolaceae
-/0.98
Grifola sordulenta
-/0.99
Gelatoporia subvermispora
100/1
Gelatoporiaceae
Obba rivulosa
-/1
Mycoleptodonoides vassiljevae
-/0.99
Auriporia aurea
73/1
-/0.99
/antrodia
0.1
Tyromyces galactinus
Skeletocutis odora
100/1
Tyromyces chioneus
83/1
-/0.98
Incrustoporiaceae
Skeletocutis sp. L3291R
100/1
Skeletocutis lilacina
100/1
Skeletocutis chrysella
81/1
Skeletocutis nivea
-/1
Tyromyces merulinus
Ischnoderma resinosum
Ischnodermataceae

Research Highlights:

We generated *rpb1*, nrLSU and nrITS sequences across the *Polyporales*

We performed Maximum Likelihood and Bayesian analyses for three dataset combinations

We recognize 18 families in the *Polyporales,* including 3 described as new

Three small clades and four species cannot be placed in any recognized family

We recommend the use of *rbp1* data for future family-level studies in the *Polyporales*