

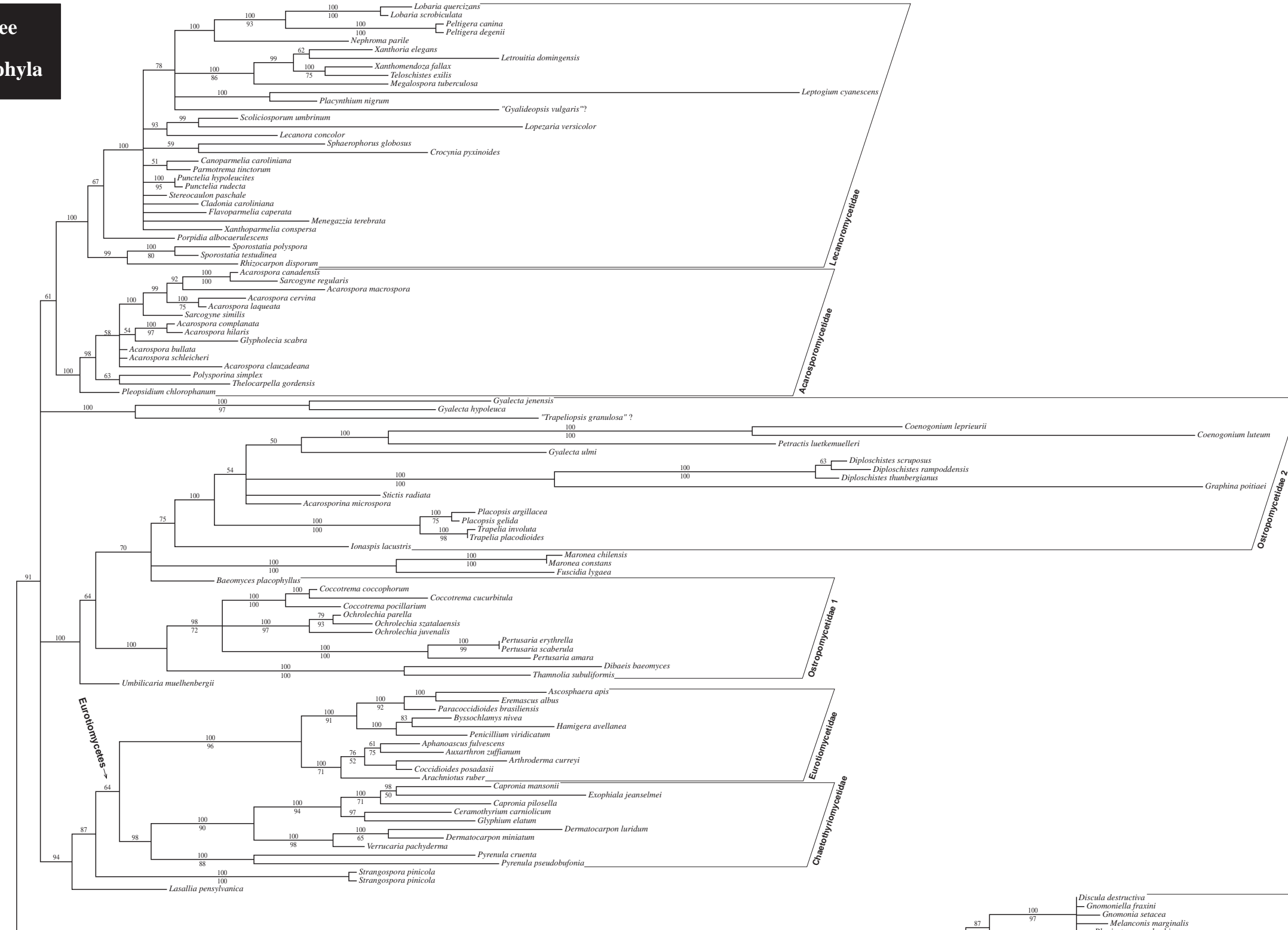


Assembling the fungal tree of life: progress, classification, and evolution of subcellular traits

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Two-locus Bayesian MCMCMC tree
nucSSU+nuLSU
558 species, 430 genera, 68 orders, 5 phyla

Bayesian posterior probability
NJ bootstrap proportion
0.1 substitutions/site



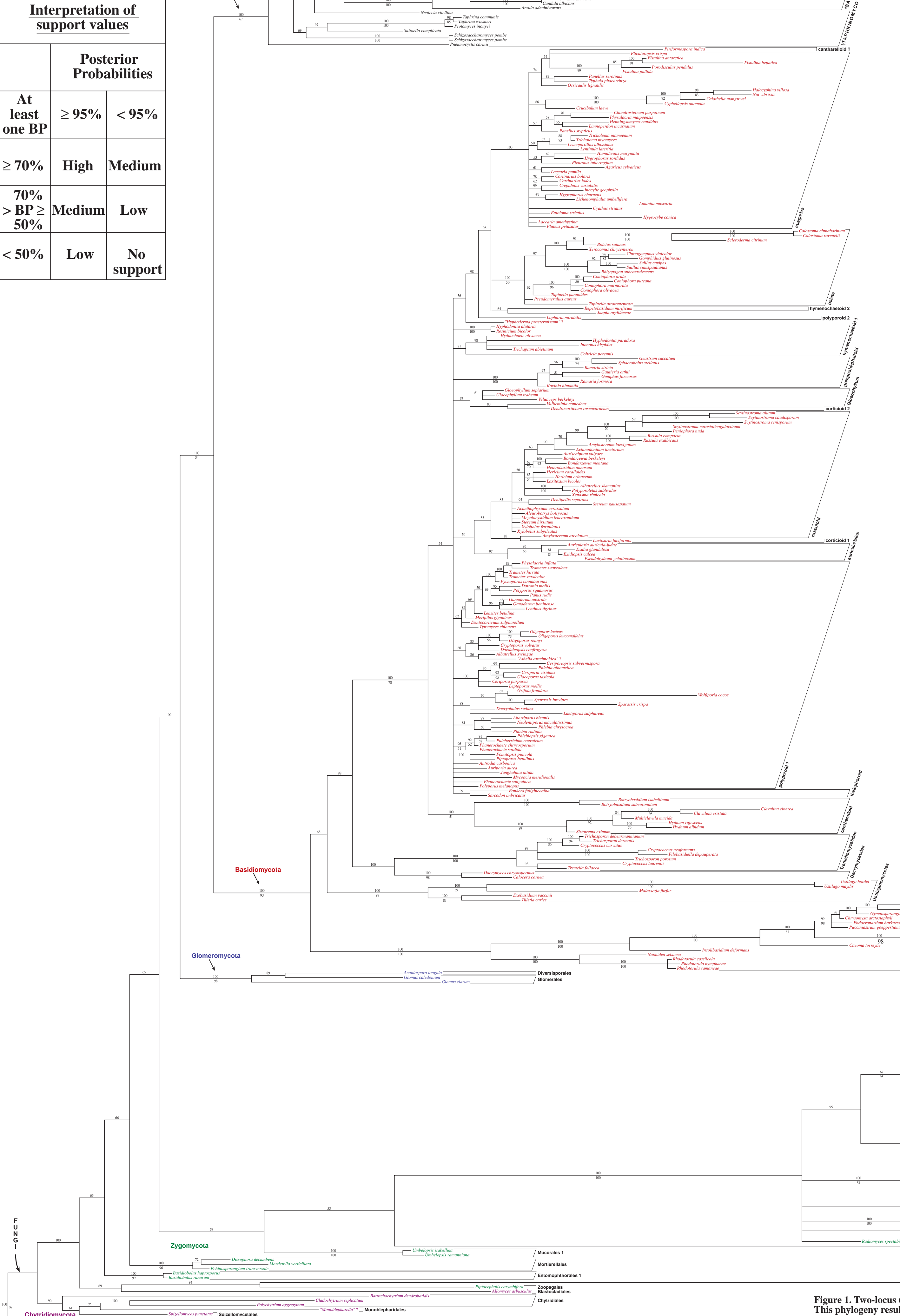
Acknowledgment
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Introduction and objectives
Despite the numerous technological advancements available to fungal systematists, progress in understanding the deepest nodes in the fungal tree of life will be limited without a new approach to conducting large-scale multilocus phylogenetic studies and phenotype-based comparative studies on fungi. This novel approach will require concerted data acquisition by focusing sequencing efforts on specific loci and fungal taxa, by conducting phenotypic studies on specific fungal traits, by improving interaction among fungal systematists, and by the automation of data acquisition and analysis coupled with data bases accessible through the World Wide Web. These goals form the framework of the Assembling the Fungal Tree of Life Project (AFTOL), which seeks to infer the phylogenetic relationships among 1500 species representing all fungal phyla based on eight loci (=10 kb). Here, we report phylogenetic studies for the maximal number of species across all known fungal phyla for which DNA sequence data from two, three, and four loci are available. The resulting phylogenetic trees are based on sequences available in GenBank and unpublished sequences generated by various laboratories or by the AFTOL project. This study provides a phylogenetic synthesis for the Fungi and a framework for future phylogenetic studies on fungi.

- Other presentations at this meeting associated with this poster:**
- 1) Valerie Hofstetter, J. Miadlikowska, C. Gueidan, V. Reeb, A. E. Arnold, F. Kauff, C. Cox, R. Yahr & F. Lutzoni. What do protein-coding genes (ATP6, EF 1-alpha and RNA polymerase II) bring to molecular systematics of lichens? Tuesday August 17, Poster Session 1: Systematics and Evolution, 18:00-19:00.
 - 2) Frank Kauff, Cymon Cox & François Lutzoni. Bioinformatics of AFTOL (Assembling the Fungal Tree of Life). Tuesday August 17, Poster Session 1: Systematics and Evolution, 18:00-19:00.
 - 3) Cymon Cox & Frank Kauff. A data management framework for the AFTOL project. Saturday, August 21, Discussion session 3: Phylogenetic methods 15:00-17:50.
 - 4) François Lutzoni et al. Where are we in assembling the fungal tree of life, classifying the Fungi and understanding the evolution of their subcellular traits? Saturday, August 21, Discussion session 3: Phylogenetic methods 15:00-17:50.

Interpretation of support values

Posterior Probabilities		
At least one BP	≥ 95%	< 95%
≥ 70%	High	Medium
70% > BP ≥ 50%	Medium	Low
< 50%	Low	No support



Three-locus Bayesian MCMCMC tree
nucSSU+nuLSU+RPB2
157 species, 134 genera, 34 orders, 2 phyla

Bayesian posterior probability
NJ bootstrap proportion / MP bootstrap proportion
0.1 substitutions/site

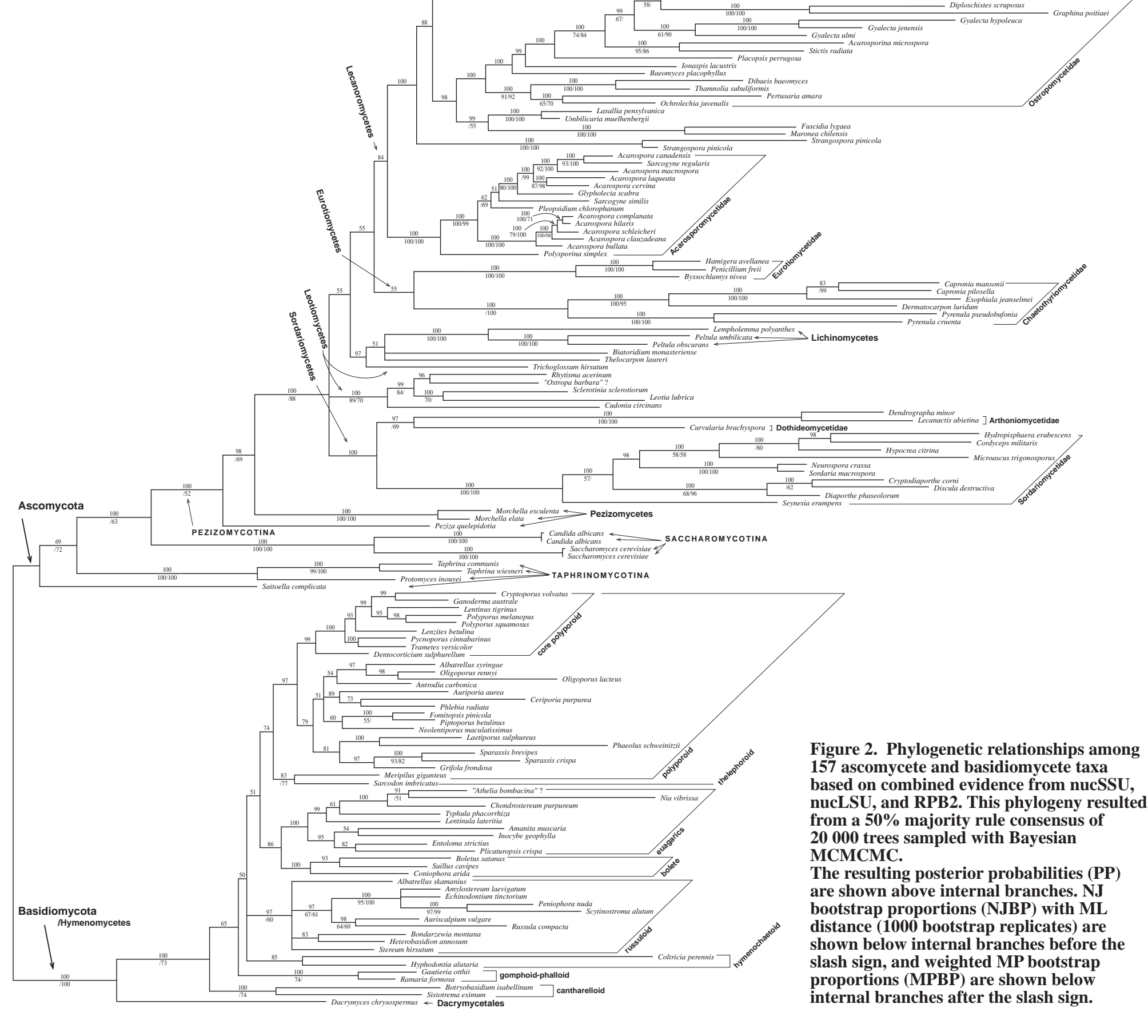


Figure 2. Phylogenetic relationships among 157 ascomycete and basidiomycete taxa based on combined evidence from nucSSU, nuLSU, and RPB2. This phylogeny resulted from a 50% majority rule consensus of 20 000 trees sampled with Bayesian MCMCMC. The resulting posterior probabilities (PP) are shown above internal branches, NJ bootstrap proportions (NBP) with ML distance (1000 bootstrap replicates) are shown below internal branches before the slash sign, and weighted MP bootstrap proportions (MPBP) are shown below internal branches after the slash sign.

Four-locus Bayesian MCMCMC tree
nucSSU+nuLSU+miSSU+RPB2
103 species, 94 genera, 30 orders, 2 phyla

Bayesian posterior probability/Bayesian bootstrap proportion
NJ bootstrap proportion/MP bootstrap proportion
0.1 substitutions/site



Figure 3. Phylogenetic relationships among 103 ascomycete and basidiomycete species based on combined evidence from nucSSU, nuLSU, miSSU rDNA, and RPB2. This phylogeny resulted from a 50% majority rule consensus of 69 000 trees sampled with Bayesian MCMCMC. The resulting posterior probabilities (PP) are shown above internal branches before the slash sign. One hundred Bayesian MCMCMC analyses were conducted on bootstrapped versions of this four-locus data set. Bayesian bootstrap proportions (BBP) ≥ 50% are presented above internal branches after the slash sign. NJ bootstrap proportions (NBP) with ML distance (1000 bootstrap replicates) are shown below internal branches before the slash sign. Weighted MP bootstrap proportions (MPBP) are shown below branches after the slash sign.

Figure 1. Two-locus (nucSSU + nuLSU) Bayesian MCMCMC fungal tree of life depicting phylogenetic relationships among 558 taxa in 430 genera, 68 orders and five phyla. This phylogeny resulted from a 50% majority rule consensus of 24 000 trees sampled with Bayesian MCMCMC. The resulting posterior probabilities (PP) are shown above internal branches. NJ bootstrap proportions (NBP) with ML distances (1000 bootstrap replicates) are shown below internal branches. Species names are colored according to their respective phylum.