

Phylogenetic relationships and morphological evolution in *Lentinus*, *Polyporellus* and *Neofavolus*, emphasizing southeastern Asian taxa

Abstrak

The genus *Lentinus* (Polyporaceae, Basidiomycota) is widely documented from tropical and temperate forests and is taxonomically controversial. Here we studied the relationships between *Lentinus* subg. *Lentinus* sensu Pegler (i.e. sections *Lentinus*, *Tigrini*, *Dicholamellatae*, *Rigidi*, *Lentodiellum* and *Pleuroti* and polypores that share similar morphological characters). We generated sequences of internal transcribed spacers (ITS) and partial 28S regions of nuc rDNA and genes encoding the largest subunit of RNA polymerase II (RPB1), focusing on *Lentinus* subg. *Lentinus* sensu Pegler and the *Neofavolus* group, combined these data with sequences from GenBank (including RPB2 gene sequences) and performed phylogenetic analyses with maximum likelihood and Bayesian methods. We also evaluated the transition in hymenophore morphology between *Lentinus*, *Neofavolus* and related polypores with ancestral state reconstruction. Single-gene phylogenies and phylogenies combining ITS and 28S with RPB1 and RPB2 genes all support existence of a *Lentinus*/*Polyporellus* clade and a separate *Neofavolus* clade. *Polyporellus* (represented by *P. arcularius*, *P. ciliatus*, *P. brumalis*) forms a clade with species representing *Lentinus* subg. *Lentinus* sensu Pegler (1983), excluding *L. suavissimus*. *Lentinus tigrinus* appears as the sister group of *Polyporellus* in the fourgene phylogeny, but this placement was weakly supported. All three multigene analyses and the single-gene analysis using ITS strongly supported *Polyporus tricholoma* as the sister group of the *Lentinus*/*Polyporellus* clade; only the 28S rRNA phylogeny failed to support this placement. Under parsimony the ancestral hymenophoral configuration for the *Lentinus*/*Polyporellus* clade is estimated to be circular pores, with independent transitions to angular pores and lamellae. The ancestral state for the *Neofavolus* clade is estimated to be angular pores, with a single transition to lamellae in *L. suavissimus*. We propose that *Lentinus suavissimus* (section *Pleuroti*) should be reclassified as *Neofavolus suavissimus* comb. nov