

Multigene Phylogeny of *Panus sensu stricto* (Polyporaceae)

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Purpose: The genus *Panus* Fr. (Polyporaceae, Basidiomycota) includes saprotrophic, lamellate, lignicolous, and wood-decaying (white rot) mushroom forming fungi. This genus is widely documented from tropical and temperate forests and is taxonomically controversial. Here, the generic concept Corner (1981) is followed for *Panus sensu stricto*.

Methods: We obtained 219 ITS, 120 nrLSU, 28 RPB2 and 20 TEF1 sequences, focusing on *Panus sensu stricto*, and performed phylogenetic analyses using maximum likelihood and Bayesian analysis.

Results and conclusions: These results showed that the ITS, LSU, RPB2 and TEF1 concatenated phylogeny suggests that the diversification of *Panus sensu stricto* has been more extensive in tropical regions. Our analyses showed that *Panus sensu stricto* comprises 12 major clades. Pegler's (1983) sections, *Panus* and *Velutini* are not monophyletic. Based on molecular data and on the size of the pseudosclerotium, *Panus fulvus* and *Panus fulvus* represent two different lineages. Species delimitation within the genus *Panus* were resolved with more informative markers like elongation factor (TEF- α 1) and RPB2 are produced herein with supported phylogeny.