

Ascomycetes in Yunnan, China

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Purpose: Yunnan is one of the world's richest biodiversity hotspots, maintaining an extremely high diversity of microfungi. However, the studies of microfungi in this province are still poorly documented. In this study, we attempt to improve an accurate species number of microfungi in Yunnan Province, China based on morphological characteristics and multigene phylogenetic analyses.

Methods: Saprobic and pathogenic ascomycetes were collected from various plants (e.g. *Acer*, *Artemisia*, *Caragana*, *Cirsium*, *Cycas*, *Liriope*, *Lonicera*, *Mangifera*, *Pinus*, *Thysanolaena*, *Zea* as well as many fern species) in both aquatic and terrestrial habitats. The samples were collected from Baoshan, Honghe, Kunming, Lijiang and Xishuangbanna during April to December 2015-2017 and returned to the laboratory for examination. Multigene phylogenetic analyses of a concatenated LSU, SSU, TEF1- α , RPB2 and ITS sequence dataset were carried out based on maximum likelihood and Bayesian inference criteria.

Results and conclusions: Based on multigene phylogenetic analyses, 38 taxa distributed in ten orders and 18 families were described and illustrated in "Fungal diversity notes 929-1035: taxonomic and phylogenetic contributions on genera and species of fungi". Six new genera and 25 new species are introduced in this study. A reference specimen for *Tamsiniella labiosa* is designated and the sexual-aseexual morph connection of *Plenodomus sinensis* is reported. In addition, new host records and distributions in Yunnan are reported for *Amarenomyces dactylidis*, *Muyocopron lithocarpi*, *Periconia cortaderiae*, *Phragmocamarosporium hederiae* and *Sphaerellopsis paraphysata* .