Outlineoffungi.org - Note 859 *Guizhoumyces*

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Guizhoumyces Wei, T.P & Y.L. Jiang

Guizhoumyces was introduced by Wei et al. (2022) to accommodate *G. aciculaea* as the type species, based on morphological characteristics and phylogenetic analysis of combined ITS, LSU, *rpb*2, *tef*1α, and *tub*2 sequence data. *Guizhoumyces aciculaea* was collected from the soil and leaf litter in China. Based on the multi-gene phylogenetic analysis, *Guizhoumyces* formed a monophyletic lineage sister to *Veronaeopsis* within *Sympoventuriaceae*, and closely related to *Bellamyces*, *Helicopsis*, *Sympoventuria*, *Troposporella*, and *Pseudosigmoidea*. Also, *Guizhoumyces* shares some morphological characteristics with *Pseudosigmoidea* and *Sigmoidea*. Conidiophores are simple, branched and subcylindrical, with polyphialidic and integrated conidiogenous cells. Conidia are enteroblastic, and acicular to obclavate or cylindrical. Chlamydospores were not seen and the sexual morph is unknown. The taxonomic placement of *Guizhoumyces* is in *Sympoventuriaceae*, *Venturiales*, *Pleosporomycetidae*, *Dothideomycetes*, *Pezizomycotina*, and *Ascomycota*.

Reference

Wei TP, Zhang H, Zeng XY, Crous PW et al. 2022 – Re-evaluation of *Sympoventuriaceae*. Persoonia-Molecular Phylogeny and Evolution of Fungi 48(1), 219–260. https://doi.org/10.3767/persoonia.2022.48.07

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