

Outlineoffungi.org - Note 572 [Microconidiobolus](#) – expanded note

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[Microconidiobolus](#) B. Huang & Y. Nie

[Microconidiobolus](#) was introduced by [Nie et al. \(2020\)](#), alongside [Capillidium](#), [Neoconidiobolus](#) and *Conidiobolus sensu stricto*, based on morphology and multi-locus phylogenetic analyses (nrLSU, nrSSU, mtSSU and EF-1 α) as part of a re-evaluation and delimitation of the polyphyletic genus *Conidiobolus sensu lato*. This genus contains three species, namely *M. nodosus*, [M. paulus](#) (syn. *M. undulatus*) and *M. terrestris*, and is supported by both molecular and morphological data. The clade containing [Microconidiobolus](#) species was placed as a sister group of *Conidiobolus sensu stricto*, a position confirmed using the combination of nrLSU, TEF1, mtSSU ([Cai et al., 2021b](#)) and nrLSU ([Möckel et al., 2022](#)). Species of [Microconidiobolus](#) mainly differ from *Conidiobolus* species by producing smaller primary conidia without microspores or capilliconidia. The first mitochondrial genome of the genus (GenBank accession number [MW_795365](#)) was generated by [Cai et al. \(2021a\)](#) from the mycelia of *M. nodosus*. Their phylogenetic tree constructed by maximum likelihood and based on 14 translated mitochondrial genomes placed *M. nodosus* as a sister clade of *Conidiobolus* sp., supporting its placement in *Entomophthoromycotina*. [Yang et al. \(2022\)](#) and [Nie et al. \(2021\)](#) integrated the mitogenome of *M. nodosus* in phylogenetic reconstructions based on 14 mitochondrion-encoded proteins and found a similar well-supported placement. This genus illustrates the combined use of multi-loci and wide-genome molecular markers in the identification and phylogenetic assessment of fungal taxa.

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