

Outlineoffungi.org - Note 1461 *Sporopachydermiaceae*

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Sporopachydermiaceae M. Groenew., Hittinger, Opulente & A. Rokas

Sporopachydermiaceae was established to accommodate *Sporopachydermia* Rodr. Mir. as the type genus according to morphological characteristics, physiological features, and a concatenation single-model (LG+G4) approach on a data matrix of 1672 taxa (1644 fungi and 28 outgroups) and 290 BUSCO genes (Groenewald et al. 2023). The type species is [Sporopachydermia lactativora](#) Rodr. Mir. The new family *Sporopachydermiaceae* is classified under *Sporopachydermiales*, *Sporopachydermiomycetes*, *Saccharomycotina*, and *Ascomycota* (Groenewald et al. 2023). The family-specific protein families mentioned, OG0028621, OG0028581, OG0028722, and OG0028736, have been studied through phylogenetic analyses employing DNA sequences that encode LSU rDNA, mtSSU rDNA, and Cox2 sequences (Kurtzman & Robnett, 2007). For reproduction, the members of this family employ a method of asexual reproduction involving multilateral budding on a narrow base, with the absence of pseudohyphae and true hyphae formation noted. In terms of metabolic characteristics, glucose fermentation is either absent or weak, and nitrate assimilation is not observed. The organism assimilates myo-inositol as its sole carbon source. Additionally, it is capable of forming Coenzyme Q-9 (Groenewald et al. 2023).

References

- Groenewald M, Hittinger CT, Bensch K, Opulente DA, et al. 2023 – A genome-informed higher rank classification of the biotechnologically important fungal subphylum *Saccharomycotina*. *Studies in Mycology* 105(1), 1– 22.
- Kurtzman CP, Robnett CJ. 2007 – Multigene phylogenetic analysis of the *Trichomonascus*, *Wickerhamiella*, and *Zygoascus* yeast clades, and the proposal of *Sugiyamaella* gen. nov. and 14 new species combinations. *FEMS Yeast Research* 7, 141–151.

Entry by

Maryam Tavakol Noorabadi, Innovative Institute for Plant Health, Zhongkai University of Agriculture and Engineering, Guangzhou 510225, People's Republic of China

(Edited by **Kevin D Hyde**)

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