

Outlineoffungi.org - Note 1529 *Pachysolenaceae*

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Pachysolenaceae M. Groenew., Hittinger, Ofulente & A. Rokas

Pachysolenaceae was established to accommodate *Pachysolen* Boidin & Adzet as the type genus and *Pachysolen tannophilus* Boidin & Adzet as the type species based on morphological characters, 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). Family-specific protein family OG0016373 is characterized by a unique trait where the CUG codon is translated into alanine, deviating from the common translation of leucine. This divergence has been identified through phylogenetic analyses that utilize DNA sequences encoding LSU rDNA, SSU rDNA, EF-1 α , and mtSSU rDNA. Additionally, budding occurs multilaterally, with a narrow base for support, and the ascospores exhibit a distinctive hemispherical or hat-shaped morphology (Groenewald et al. 2023). *Pachysolenaceae* is classified within *Alaninales*. Different genera were identified in *Alaninales*, namely *Nakazawaea*, *Pachysolen*, and *Peterozyma*. All genera categorized within this order were once part of the *Saccharomycetales incertae sedis*. The taxonomic placement of *Nakazawaea*, *Pachysolen*, and *Peterozyma* was previously uncertain for many years. Recent research has revealed that these genera collectively form a distinct group where the translation of the CUG codon into alanine, rather than leucine, is a shared characteristic. This unique trait has led to the recognition of the CUG-Ala clade as a monophyletic group. The biotechnological significance of *Nakazawaea peltata* lies in its production of a β -glucosidase enzyme, which when combined with purified cellulase, aids in the breakdown of cellulose. Additionally, this species is known for its efficient production of xylitol, a popular artificial sweetener. On the other hand, *Pachysolen tannophilus* is valuable for its ability to convert crude glycerol into ethanol. Furthermore, studies have demonstrated that strains of this species can transition from glucose to effectively fermenting xylose (Groenewald et al. 2023). The taxonomic placement of this new family is *Alaninales*, *Pichiomycetes*, *Saccharomycotina*, and *Ascomycota* (Groenewald et al. 2023).

Reference

Groenewald M, Hittinger CT, Bensch K, Ofulente DA, et al. 2023 – A genome-informed higher rank classification of the biotechnologically important fungal subphylum *Saccharomycotina*. *Studies in Mycology* 105(1), 1– 22.

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Published online 26 August 2024