

## Outlineoffungi.org - Note 1474 *Lipomyces*

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***Lipomyces*** M. Groenew., Hittinger, Ofulente & A. Rokas1

*Lipomyces* was introduced to accommodate *Lipomycesales* M. Groenew., Hittinger, Ofulente & A. Rokas as the type order 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). *Lipomyces* only included *Lipomycesales*. The identification of *Lipomyces* is based on class-specific protein families OG0010973, OG0011052, OG0008472, OG0009553. Phylogenetic analyses incorporate various DNA sequences, including LSU rDNA, SSU rDNA, mtSSU rDNA, and EF-1 $\alpha$ . (Kurtzman et al., 2007). *Lipomyces* strains are characterized by the production of intracellular lipids and extracellular starch-like compounds. They do not engage in fermentation, and nitrate assimilation is not observed. It is known that the higher levels of genomic diversity in *Saccharomycotina* stem from an acceleration of the evolutionary rate that occurred within the subphylum, after the divergence of *Lipomycesales* from the rest of the *Saccharomycotina*. This acceleration can also be observed in the genetic divergence that exists between the *Lipomyces* and the rest of the *Saccharomycotina* classes as presented by Groenewald et al. (2023). *Lipomyces* is classified under *Saccharomycotina*, *Ascomycota* (Groenewald et al. 2023).

### References

- 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.
- Kurtzman CP, Albertyn J, Basehoar-Powers E. 2007 – Multigene phylogenetic analysis of the *Lipomycesales* and the proposed transfer of *Zygozoma* species to *Lipomyces* and *Babjevia anomala* to *Dipodascopsis* *FEMS Yeast Research* 7, 1027–1034.

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