

## Outlineoffungi.org - Note 764 *Neodactylariaceae*

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*Neodactylariaceae* H. Zheng & Z.F. Yu

*Neodactylariaceae* was introduced by Qiao et al. (2020) to accommodate *Neodactylaria*, which was previously placed in the genus *incertae sedis* in *Dothideomycetes* by Crous et al. (2017). This monotypic family constitutes only two species *Neodactylaria obpyriformis* Guevara-Suarez, Deanna A. Sutton, Wiederh. & Gené, the type species, and *N. simaoensis* H. Zheng & Z.F. Yu. The former was isolated from the human bronchoalveolar lavage while the latter is a freshwater fungus observed from submerged dicotyledonous leaves showing a broad distribution of this genus in different habitats (Crous et al. 2017; Qiao et al. 2020). *Neodactylaria* resembles species of *Dactylaria* (e.g., *D. kumamotoensis* and *D. madresensis*), *Pyricularia* (e.g., *P. valdalurensis*), and *Pseudopyricularia* (e.g., *P. higginsii*) but differs from conidial sizes and septation. Furthermore, the phylogenetic placements of these genera differ from *Neodactylaria* (*Dothideomycetes*) as *Dactylaria* belongs to *Helotiales* genera *incertae sedis* (*Leotiomycetes*) (Wijayawardene et al. 2022), while both *Pyricularia* and *Pseudopyricularia* belong to *Pyriculariaceae* (*Magnaporthales*, *Sordariomycetes*) (Klaubauf et al. 2014; Wijayawardene et al. 2022). *Neodactylaria obpyriformis* was introduced using LSU sequence data and *N. simaoensis* was introduced based on multi-locus (LSU, SSU, and *tef1*) phylogenetic analysis (Crous et al. 2017; Qiao et al. 2020). However, the placement of *Neodactylariaceae* is not strongly supported and further analysis is needed.

### References

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