

Outlineoffungi.org - Note 1207 *Cyanoporus*

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Cyanoporus Y.C. Dai, W.L. Mao & Yuan Yuan

Based on morphological and phylogenetic analyses of ITS, LSU, *tef1*, *rpb1*, and *rpb2* sequence data, Mao et al. (2023) introduced *Cyanoporus* under *Polyporaceae* (*Polyporales*, *Agaricomycetes*, *Basidiomycota*) to accommodate *Cyanoporus fuligo*, and *C. camptogrammus*, previously classified as *Grammothele fuligo* and *Porogramme camptogrammus*, respectively (Patouillard 1913; Ryvarden 1979). The type species is *Cyanoporus fuligo* (Berk. & Broome) Y. C. Dai, W.L. Mao & Yuan Yuan. *Cyanoporus* is characterized by its annual, resupinate, adnate, and corky to coriaceous basidium; bluish gray to dark blue pore surface; dimitic hyphal system with clamped generative hyphae and skeletal hyphae IKI–, CB–; hyaline, thin-walled, smooth and ellipsoid basidiospores; typically found on Monocotyledons, causing white rot (Mao et al. 2023). The molecular analyses of a multi-locus dataset (ITS, LSU, *tef1*, *rpb1*, and *rpb2*) revealed that *Cyanoporus* formed a distinct clade closely related to genera *Epithele*, *Grammothele*, *Porogramme*, and *Theleporus*. Additionally, divergence time estimation indicated a well-supported lineage that diverged 62.1 million years ago (Mao et al. 2023). Subsequent research could focus on collecting more samples to thoroughly characterize the diversity and improve the systematic position of *Cyanoporus* (Mao et al. 2023).

References

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Entry by

Kezhocuyi Kezo, CAS in Botany, University of Madras, Guindy Campus, Chennai 600025, Tamil Nadu, India

(Edited by **Kevin D. Hyde**, **Maryam Tavakol Noorabadi** & **Subodini N. Wijesinghe**)

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