

Outlineoffungi.org - Note 1195 *Neochrosporium*

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Neochrosporium R.P. Liu, Meng Zhang & Y.H. Geng

The monotypic genus *Neochrosporium* was established to accommodate *Neochrosporium camelliae-sinensis* R.P. Liu, Meng Zhang & Y.H. Geng based on morphology and phylogeny using ITS and LSU sequence data, which was isolated from the leaves of *Camellia sinensis* in China (Liang et al. 2023). The taxonomic placement of *Neochrosporium* is in an uncertain position in *Pleosporales*. In the phylogenetic tree with combined sequences of ITS and LSU datasets, *Neochrosporium* formed a sister clade to *Ochrocladosporium*. Morphologically, *Neochrosporium* and *Ochrocladosporium* differ from each other by the morphology of colony and conidial forms. Furthermore, *Neochrosporium camelliae-sinensis* is distinguished from all similar *Cladosporium*-like hyphomycetes by its white colonies on PDA, and the absence of ramoconidia. In *Neochrosporium camelliae-sinensis*, conidiophores are micronematous with monophialidic integrated, subcylindrical to doliiform and smooth conidiogenous cells. Conidia are aseptate, oval, and thin-walled. The sexual morph has not been observed (Liang et al. 2023).

Reference

Liang LY, Liu RP, Ma QZ, Cao JY et al. 2023– *Neochrosporium camelliae-sinensis* gen. & sp. nov. from tea in China. *Mycotaxon* 137(4), 813–819.

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