

Neohelicomyces melaleucaae



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Neohelicomyces melaleucae Crous, sp. nov.

Etymology. Name refers to the host genus *Melaleuca* from which it was isolated.

Classification — *Tubeufiaceae*, *Tubeufiales*, *Dothideomycetes*.

Mycelium consisting of pale to medium brown, smooth, septate, branched, 3–4 µm diam hyphae. *Conidiophores* reduced to conidiogenous cells, integrated on hyphae, pale brown, smooth, 3–15(–35) × 3–4 µm, with one to several flat-tipped denticles, 2 µm diam; at times reduced to a single denticles directly on hyphae. *Conidia* single, pale brown, smooth, multiseptate, coiled in three rings (13–17 µm diam), base truncate, 2 µm diam.

Culture characteristics — Colonies flat, spreading, with sparse aerial mycelium and smooth, lobate margin, reaching 20 mm diam after 2 wk at 25 °C. On MEA, PDA and OA surface brown vinaceous, reverse honey.

Typus. USA, California, Davis, UC Davis, on leaves of *Melaleuca stypelioides* × *lanceolata* (*Myrtaceae*), 2 Apr. 2019, P.W. Crous, HPC 2897 (holotype CBS H-24209, culture ex-type CPC 38042 = CBS 146081, ITS, LSU and *tef1* sequences GenBank MN562154.1, MN567661.1 and MN556835.1, MycoBank MB832914).

Notes — *Neohelicomyces* differs from *Tubeufia* and *Helicomyces* in having elongate, erect, conspicuous conidiophores (Tsui et al. 2006, Crous et al. 2019b). *Neohelicomyces melaleucae* is closely related to '*Tubeufia*' *helicomyces* (CBS 272.52) and *N. pandanicola* but is distinct based on its DNA phylogeny.

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Tubeufia helicomyces* (strain MUCL 15702, GenBank AY916459.1; Identities = 557/601 (93 %), 25 gaps (4 %)), *Neohelicomyces deschampsiae* (strain CBS 145029, GenBank NR_163367.1; Identities = 546/598 (91 %), 24 gaps (4 %)), and *Helicosporium lumbricoides* (strain CBS 284.51, GenBank MH856861.1; Identities = 551/605 (91 %), 26 gaps (4 %)). Closest hits using the **LSU** sequence are *Tubeufia helicomyces* (strain CBS 272.52, GenBank MH868562.1; Identities = 825/828 (99 %), no gaps), *Neohelicomyces pandanicola* (strain KUMCC 16-0143, GenBank MH260307.1; Identities = 790/793 (99 %), no gaps), and *Neohelicomyces submersus* (as *Tubeufiaceae* sp. ZL-2017c, strain KUMCC 15-0251, GenBank KY320547.1; Identities = 824/828 (99 %), no gaps). Closest hits using the **tef1** sequence had highest similarity to *Neohelicomyces hyalosporus* (strain GZCC 16-0086, GenBank MH550936.1; Identities = 417/436 (96 %), no gaps), *Tubeufia helicomyces* (strain CBS 245.49, GenBank DQ767638.1; Identities = 403/423 (95 %), no gaps), and *Tubeufia guangxiensis* (strain MFLUCC 17-0046, GenBank MH550977.1; Identities = 414/437 (95 %), 2 gaps (0 %)).

Colour illustrations. Branch of *Melaleuca stypelioides* × *lanceolata* in California. Hyphae, conidiogenous cells and conidia. Scale bars = 10 µm.