

*Davidhawksworthia quintiniae*



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***Davidhawksworthia quintinae* Crous, sp. nov.**

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

*Classification* — *Dermateaceae*, *Helotiales*, *Leotiomyces*.

*Mycelium* consisting of hyaline, smooth, septate, 2–3 µm diam hyphae. *Conidiophores* reduced to phialidic conidiogenous cells, ampulliform to doliiform, hyaline, smooth, erect, becoming aggregated in clusters, forming sporodochia on agar surface, 4–15 × 3–5 µm. *Conidia* solitary, hyaline, smooth, guttulate, aseptate, subcylindrical, ends obtuse, (10–)11–12(–15) × 2(–2.5) µm.

*Culture characteristics* — Colonies erumpent, spreading, with sparse aerial mycelium and lobate, smooth margin, reaching 12 mm diam after 2 wk at 25 °C. On MEA surface dirty white, reverse buff; on PDA surface and reverse dirty white; on OA surface buff.

*Typus.* AUSTRALIA, New South Wales, Limpinwood Nature Reserve, Corina lookout, on leaves of *Quintinia sieberi* (*Paracryphiaceae*), 26 May 2015, B.A. Summerell, HPC 2945 (holotype CBS H-24399, culture ex-type CPC 38153 = CBS 146963, ITS, LSU, *rpb2* and *tub2* sequences GenBank MW175338.1, MW175378.1, MW173113.1 and MW173132.1, MycoBank MB837828).

*Notes* — The erect, ampulliform to doliiform phialides, and hyaline, aseptate conidia are reminiscent of the monotypic genus *Davidhawksworthia* (Crous & Groenewald 2016). *Davidhawksworthia quintinae* is easily distinguished from *D. illicicola* (on *Ilex aquifolium*, Netherlands; conidia 17–22 × 3–3.5 µm) by its smaller conidia.

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Dermea libocedri* (strain CBS 138.46, GenBank MH856142.1; Identities = 526/560 (94 %), five gaps (0 %)), *Dermea acerina* (strain CBS 161.38, GenBank MH855942.1; Identities = 524/560 (94 %), eight gaps (1 %)), *Pseudotryblidium neesii* (strain HE300, GenBank MK894293.1; Identities = 524/563 (93 %), six gaps (1 %)) and *Davidhawksworthia illicicola* (strain CBS 261.95, GenBank KU728516.1; Identities = 517/556 (93 %), 15 gaps (2 %)). Closest hits using the **LSU** sequence are *Davidhawksworthia illicicola* (strain CBS 734.94, GenBank NG\_067307.1; Identities = 892/898 (99 %), no gaps), *Coleophoma cylindrospora* (strain BP-6252, GenBank MH762908.1; Identities = 892/900 (99 %), no gaps), and *Coleophoma camelliae* (strain CBS 101376, GenBank KU728521.1; Identities = 886/894 (99 %), no gaps). Closest hits using the **rpb2** sequence had highest similarity to *Rhizodermea veluwensis* (strain CBS 110615, GenBank KR859354.1; Identities = 747/882 (85 %), no gaps), *Pezicula cornina* (strain CBS 285.39, GenBank KR859333.1; Identities = 731/871 (84 %), four gaps (0 %)), and *Pezicula neoheterochroma* (strain CBS 127388, GenBank KR859338.1; Identities = 744/889 (84 %), no gaps). Closest hits using the **tub2** sequence had highest similarity to *Davidhawksworthia illicicola* (strain CBS 261.95, GenBank KU728630.1; Identities = 300/371 (81 %), 14 gaps (3 %)), *Monilia yunnanensis* (strain GND3, GenBank KT736016.1; Identities = 304/378 (80 %), 17 gaps (4 %)), and *Monilinia fructigena* (strain CBS 101499, GenBank KT736015.1; Identities = 303/378 (80 %), 17 gaps (4 %)).

*Colour illustrations.* Rainforest at Limpinwood Nature Reserve (photo B. Summerell). Conidiogenous cells giving rise to conidia; conidia. Scale bars = 10 µm.