

Davidiellomyces juncicola



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Davidiellomyces juncicola Crous, *sp. nov.*

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

Classification — *Cladosporiaceae*, *Capnodiales*, *Dothideomycetes*.

Ascomata pseudothecial, dark brown, erumpent, globose, 80–120 µm diam, with central ostiole 10 µm diam; ascomata aggregated in clusters and linked via a brown stroma (in agar, not observed on host); wall of 2–3 layers of brown *textura angularis*. *Asci* paraphysate, fasciculate, bitunicate, subsessile, obovoid, straight to slightly curved, 8-spored, with apical chamber, 30–35 × 9–10 µm. *Ascospores* multiseriate, hyaline guttulate, constricted at median septum, thick-walled, surrounded by mucoid sheath, tapering towards both ends, but more prominently towards lower end, (9–)11–12(–13.5) × (3.5–)4 µm. *Ascospores* germinating initially via both ends, 5–6 µm diam, becoming brown, verruculose, with mucoid sheath, distorting, the two original ascospore cells dividing into two; outer two cells germinating via two germ tubes parallel to the long axis, inner two cells germinating later, with germ tubes perpendicular to the long axis of the ascospore.

Culture characteristics — Colonies flat, spreading, with sparse aerial mycelium and smooth, lobate margin, reaching 30 mm diam after 2 wk at 25 °C. On MEA, PDA and OA surface and reverse olivaceous grey.

Typus. USA, California, Davis, UC Davis, on culms of *Juncus effusus* (*Juncaceae*), 2 Apr. 2019, P.W. Crous, HPC 2894 (holotype CBS H-24255, culture ex-type CPC 38038 = CBS 146130, ITS, LSU and *actA* sequences GenBank MN562152.1, MN567659.1 and MN556792.1, MycoBank MB832912).

Notes — *Davidiellomyces* (on leaves of *Cyperaceae*, Western Australia) is characterised by a mycosphaerella-like sexual morph in which ascospores are encased in a prominent mucoid sheath, and become brown and verruculose upon germination (Crous et al. 2017b). *Davidiellomyces juncicola* represents a new species in this hitherto monotypic genus.

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Davidiellomyces australiensis* (strain CBS 142165, GenBank NR_154036.1; Identities = 655/683 (96 %), 4 gaps (0 %)), *Verrucocladosporium dirinae* (strain CR16, GenBank KY111909.1; Identities = 418/443 (94 %), 11 gaps (2 %)), and *Neocladosporium leucadendri* (strain CBS 131317, GenBank NR_152324.1; Identities = 489/528 (93 %), 15 gaps (2 %)). Closest hits using the **LSU** sequence are *Davidiellomyces australiensis* (strain CBS 142165, GenBank NG_059164.1; Identities = 810/812 (99 %), no gaps), *Neocladosporium leucadendri* (strain CBS 131317, GenBank NG_057949.1; Identities = 809/819 (99 %), no gaps), and *Verrucocladosporium dirinae* (strain CBS 112794, GenBank MH874471.1; Identities = 806/819 (98 %), no gaps). Closest hits using the **actA** sequence had highest similarity to *Davidiellomyces australiensis* (strain CBS 142165, GenBank KY979853.1; Identities = 495/528 (94 %), 2 gaps (0 %)), *Cladosporium sinuosum* (strain CPC 18365, GenBank KT600643.1; Identities = 451/499 (90 %), 4 gaps (0 %)), and *Cladosporium rugulovarians* (strain CPC 18444, GenBank KT600656.1; Identities = 467/523 (89 %), 18 gaps (3 %)).

Colour illustrations. *Juncus effusus* plants *Davidiellomyces juncicola* was isolated from. Colony on oatmeal agar; asci with ascospores; germinating ascospores. Scale bars = 120 µm (ascomata), 10 µm (all others).