



Fungal Planet 1208 – 13 July 2021

***Lapidomyces aloidendricola* Crous, sp. nov.**

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

Classification — *Teratosphaeriaceae*, *Mycosphaerellales*, *Dothideomycetes*.

Mycelium consisting of brown, finely verruculose, septate, branched, 3–6 µm diam hyphae, aggregating into a dense brown sporodochial stroma; upper layer developing brown cells, 4–7 × 4–6 µm with minute pores giving rise to solitary conidia. *Conidia* dry, ellipsoid to ovoid, brown, finely verruculose, aseptate (rarely 1-septate), (7–)8–10(–12) × 6(–7) µm.

Culture characteristics — Colonies erumpent, spreading, surface folded, with sparse aerial mycelium and lobate, even margin, reaching 7 mm diam after 2 wk at 25 °C. On MEA, PDA and OA surface and reverse iron-grey.

Typus. SOUTH AFRICA, Northern Cape Province, Nieuwoudtville, as epiphyte on brown stem of *Aloidendron dichotomum* (*Asphodelaceae*), Nov. 2018, P.W. Crous, HPC 3038 (holotype CBS H-24480, culture ex-type CPC 38703 = CBS 146968, ITS, LSU, *rpb2* and *tub2* sequences GenBank MZ064436.1, MZ064493.1, MZ078203.1 and MZ078268.1, MycoBank MB 839523).

Notes — *Lapidomyces aloidendricola* is closely related to *L. hispanicus* (isolated from rocks in Spain), a sterile hyphomycete with dark brown hyphae, constricted at their septa (Egidi et al. 2014). Morphologically and phylogenetically, *L. aloidendricola* represents a distinct species.

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to Fungal sp. (strain TRN453, GenBank AY843151.1; Identities = 464/467 (99 %), no gaps), *Lapidomyces hispanicus* (strain CBS 118355, GenBank NR_144960.1; Identities = 453/468 (97 %), three gaps (0 %)) and *Phaeotheoidea melaleuca* (strain CPC 17223, GenBank HQ599594.1; Identities = 508/536 (95 %), six gaps (1 %)). Closest hits using the **LSU** sequence are *Phaeotheoidea melaleuca* (strain CPC 17223, GenBank HQ599595.1; Identities = 831/844 (98 %), four gaps (0 %)), *Xenoconiothyrium catenata* (strain CMW 22113, GenBank JN712570.1; Identities = 833/849 (98 %), two gaps (0 %)) and *Neophaeotheoidea proteae* (strain CBS 114129, GenBank MH874518.1; Identities = 852/869 (98 %), no gaps). Distant hits obtained using the **rpb2** sequence had highest similarity to *Zasmidium eucalyptorum* (strain CBS 118500, GenBank MF951702.1; Identities = 377/492 (77 %), eight gaps (1 %)), *Zymoseptoria tritici* (strain ST99CH_3D1, GenBank LT854276.1; Identities = 349/455 (77 %), ten gaps (2 %)) and *Constantinomyces oldenburgensis* (strain T2.4, GenBank LT976528.1; Identities = 618/855 (72 %), 34 gaps (3 %)). Closest hits using the **tub2** sequence had highest similarity to *Lapidomyces hispanicus* (strain TRN500, GenBank KF546778.1; Identities = 338/407 (83 %), seven gaps (1 %)), *Cladosporium sphaerospermum* (strain UBOCC-A-101110, GenBank KJ596619.1; Identities = 344/415 (83 %), 20 gaps (4 %)) and *Cladosporium salinae* (strain EXF-322, GenBank EF101403.1; Identities = 396/496 (80 %), 32 gaps (6 %)).

Colour illustrations. *Aloidendron dichotomum*. Colony on SNA; conidigenous cells giving rise to conidia; conidia. Scale bars = 10 µm.

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