

Lectera philenopterae



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Lectera philenopterae Crous, *sp. nov.*

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

Classification — *Plectosphaerellaceae*, *Glomerellales*, *Sordariomycetes*.

Conidiomata sporodochial, cushion-shaped, 100–200 µm diam, pale olivaceous with intermixed setae, brown, verruculose to warty, thick-walled, flexuous, 3–6-septate, tapering to acutely rounded apices, 60–150 × 5–8 µm. *Conidiogenous cells* cylindrical, proliferating percurrently at apex, 7–10 × 2.5–3.5 µm. *Conidia* (on SNA) straight, hyaline (olivaceous in mass), smooth, aseptate, cylindrical with obtuse ends, base with truncate scar, 0.5–1 µm diam, (10–)11(–12) × 2(–2.5) µm.

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 surface olivaceous black, reverse olivaceous grey. On PDA surface and reverse grey olivaceous in centre, cream in outer region. On OA surface cream.

Typus. SOUTH AFRICA, Mpumalanga Province, Kruger National Park, Letaba lodge, on *Philenoptera violacea* (*Fabaceae*), 6 Aug. 2014, P.W. Crous, HPC 2578 (holotype CBS H-24242, culture ex-type CPC 36266 = CBS 146045, ITS, LSU, *rpb2*, *tef1* and *tub2* sequences GenBank MN562117.1, MN567625.1, MN556801.1, MN556821.1 and MN556839.1, MycoBank MB832872).

Notes — *Lectera* was recently revised (Giraldo & Crous 2019, Giraldo et al. 2019). *Lectera philenopterae* is phylogenetically related to *L. nordwiniana* (from soil, the Netherlands, conidia 6–8 × 2–3 µm; Crous et al. 2018a), but distinct based on its conidial dimensions.

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Lectera nordwiniana* (strain CBS 144922, GenBank MK047463.1; Identities = 538/561 (96 %), 5 gaps (0 %)), *Lectera colletotrichoides* (strain CBS 109728, GenBank KM231851.1; Identities = 539/563 (96 %), 6 gaps (1 %)), and *Lectera capsici* (strain CBS:142534, GenBank NR_155338.1; Identities = 533/559 (95 %), 6 gaps (1 %)). Closest hits using the **LSU** sequence are *Lectera capsici* (strain CBS 142534, GenBank NG_058474.1; Identities = 816/829 (98 %), no gaps), *Lectera longa* (strain IMI 366179, GenBank LR025898.1; Identities = 778/791 (98 %), no gaps), and *Lectera colletotrichoides* (strain IMI 265740, GenBank LR025896.1; Identities = 778/791 (98 %), no gaps). Closest hits using the **rpb2** sequence had highest similarity to *Lectera colletotrichoides* (strain CBS 109728, GenBank KM232427.1; Identities = 312/353 (88 %), 1 gap (0 %)), *Lectera longa* (strain IMI 181698, GenBank LR026170.1; Identities = 638/743 (86 %), no gaps), and *Lectera colletotrichoides* (strain IMI 332702, GenBank LR026168.1; Identities = 638/743 (86 %), no gaps). No significant hits were obtained when the **tef1** and **tub2** sequences were used in blastn and megablast searches.

Colour illustrations. *Philenoptera violacea* tree at Letaba lodge. Colony on synthetic nutrient poor agar; conidiophores with conidiogenous cells; setae; conidia. Scale bars = 10 µm.