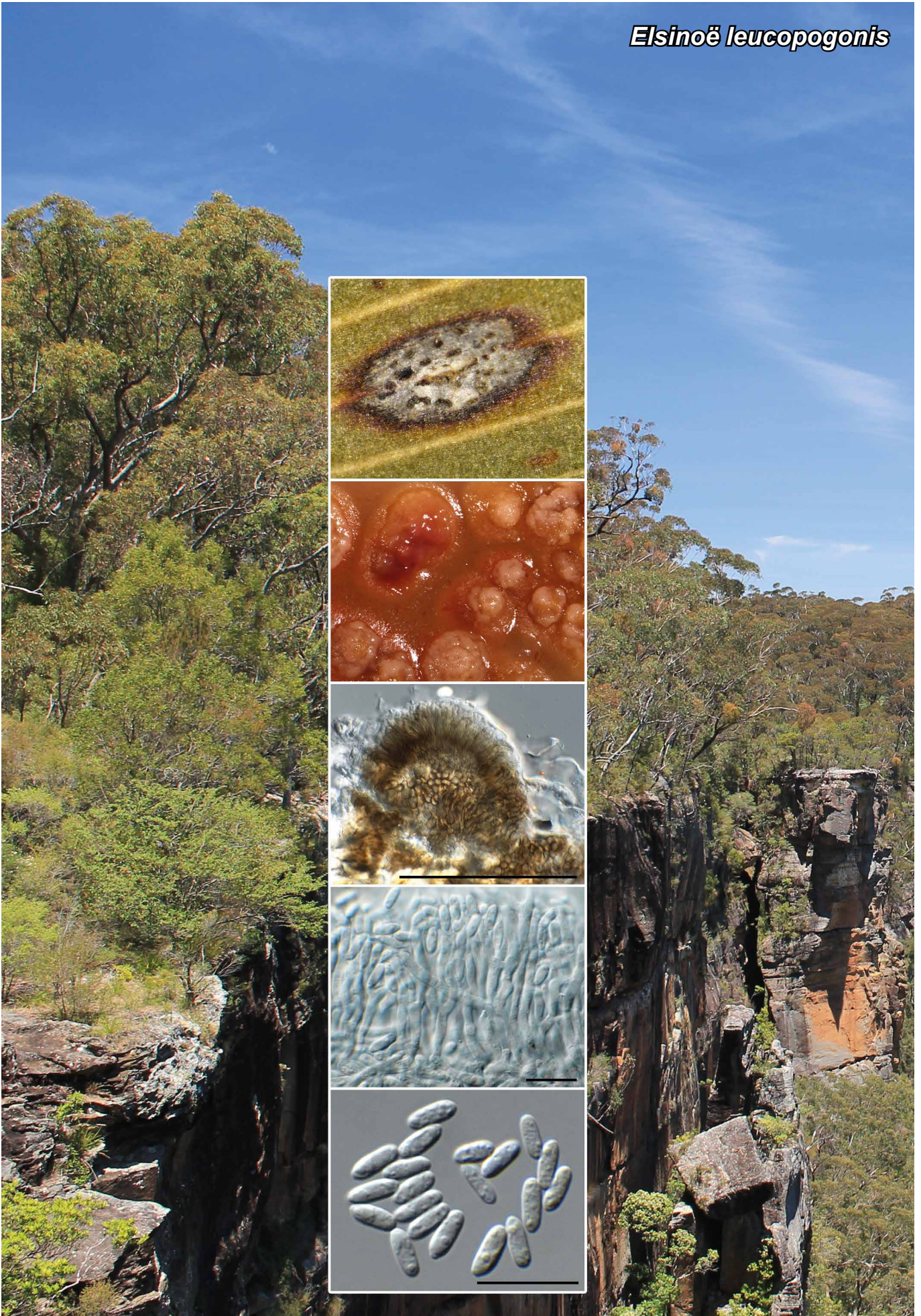


Elsinoë leucopogonis

Fungal Planet 781 – 13 July 2018

***Elsinoë leucopogonis* Crous, sp. nov.**

Etymology. Name refers to *Leucopogon*, the host genus from which this fungus was collected.

Classification — *Elsinoaceae*, *Myriangiales*, *Dothideomycetes*.

Leaf spots amphigenous, but chiefly epiphyllous, ellipsoid, solitary, grey-brown, 1–3 µm diam, surrounded by a red-brown border. *Conidiomata* acervular, brown, 70–150 µm diam, coalescing with maturity, composed of *textura angularis*. *Conidiophores* subcylindrical, brown, smooth, 1–2-septate, 15–25 × 3–4 µm. *Conidiogenous cells* polyphialidic, with 1–2 integrated loci, pale brown, smooth, subcylindrical, 5–15 × 3–4 µm. *Conidia* hyaline, smooth, aseptate, guttulate, ellipsoid to subcylindrical, with obtuse apex and truncate hilum, 1 µm diam, (5–)6(–6.5) × (2–)2.5 µm *in vitro*.

Culture characteristics — Colonies erumpent, with sparse aerial mycelium, surface folded, with even, lobed margin, reaching 7 mm diam after 2 wk at 25 °C. On MEA and PDA surface saffron, reverse ochreous. On OA surface peach with diffuse scarlet pigment.

Typus. AUSTRALIA, New South Wales, Barron Ground Nature Reserve, on leaves of *Leucopogon* sp. (*Epicridaceae*), 26 Nov. 2016, P.W. Crous (holotype CBS H-23564, culture ex-type CPC 32097 = CBS 144439, ITS, LSU, *rpb2*, *tef1* and *tub2* sequences GenBank MH327822.1, MH327858.1, MH327874.1, MH327885.1 and MH327897.1, MycoBank MB825437).

Notes — A phylogenetic analysis of the genus *Elsinoë* was recently published by Fan et al. (2017), showing that most species are highly host specific. None of the species of *Elsinoë* are presently known from *Leucopogon*, and *E. leucopogonis* is also phylogenetically distinct from the taxa presently known based on their DNA sequence data (see Fungal Planet 782).

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the ITS sequence had highest similarity to *Elsinoë hederæ* (GenBank NR_148146.1; Identities = 502/522 (96 %), 13 gaps (2 %)), *Elsinoë proteae* (GenBank NR_132796.1; Identities = 546/591 (92 %), 22 gaps (3 %)) and *Elsinoë theae* (GenBank NR_148174.1; Identities = 496/520 (95 %), 13 gaps (2 %)). Closest hits using the LSU sequence are *Elsinoë lepagei* (GenBank KX887004.1; Identities = 731/736 (99 %), no gaps), *Elsinoë hederæ* (GenBank KX886994.1; Identities = 730/736 (99 %), no gaps) and *Elsinoë tectificae* (GenBank KX887055.1; Identities = 729/736 (99 %), no gaps). Closest hits using the *rpb2* sequence had highest similarity to *Elsinoë hederæ* (GenBank KX887113.1; Identities = 640/744 (86 %), no gaps), *Elsinoë theae* (GenBank KX887175.1; Identities = 618/741 (83 %), 2 gaps (0 %)) and *Elsinoë eelemani* (GenBank KX398204.1; Identities = 648/812 (80 %), 10 gaps (1 %)). No significant hits were obtained when the *tef1* sequence was used in BLASTn and megablast searches, while the *tub2* sequence resulted in *Cyphellophora reptans* (GenBank KC455233.1; Identities = 261/332 (79 %), 22 gaps (6 %)) as best hit.

Colour illustrations. Forest trees close to collection site; leaf spot on *Leucopogon* sp., conidioma *in vivo* (scale bar = 150 µm), colony on MEA, conidiogenous cells and conidia (scale bars = 10 µm).

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