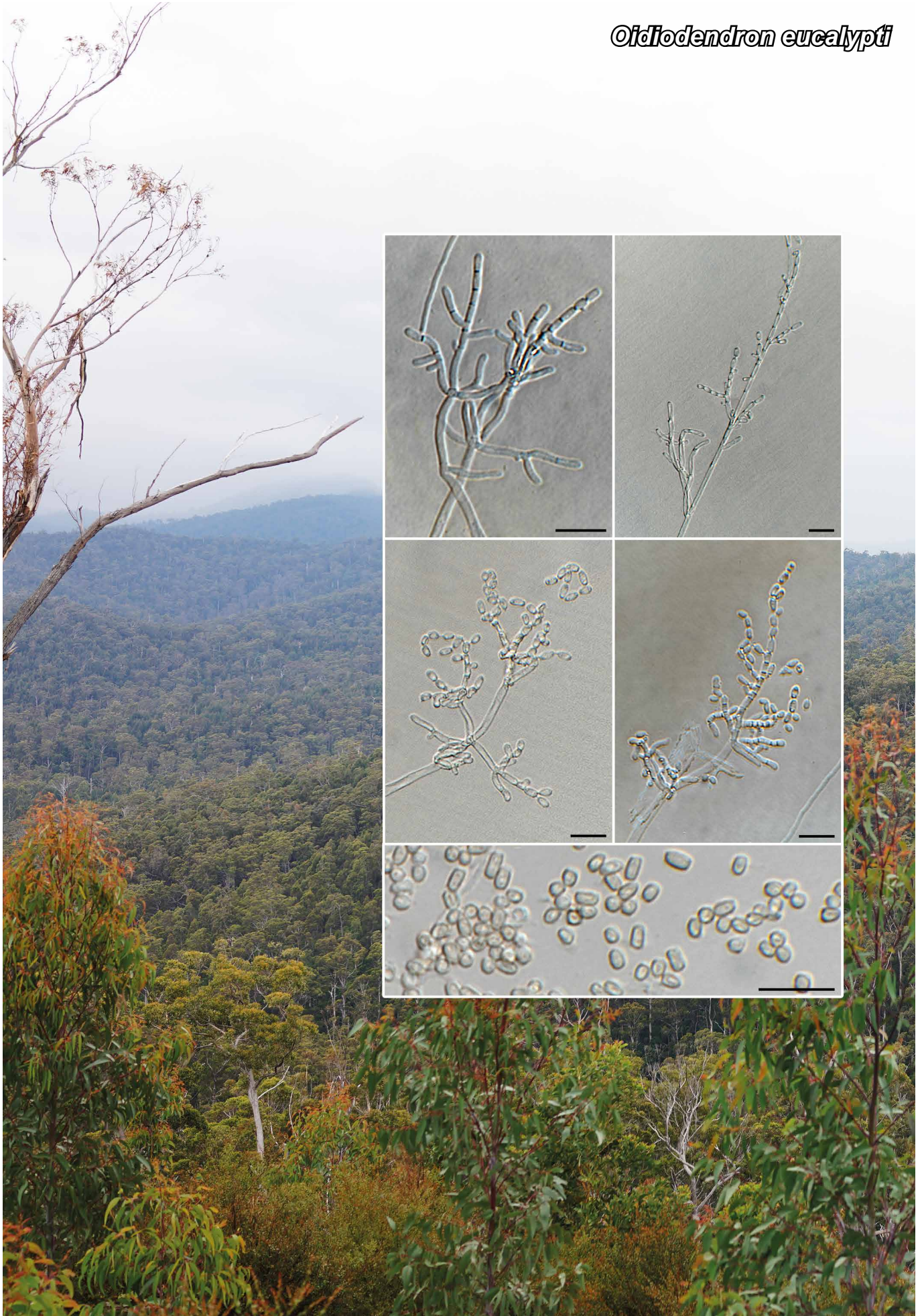


Oidiiodendron eucalypti

Fungal Planet 766 – 13 July 2018

***Oidiodendron eucalypti* Crous, sp. nov.**

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

Classification — *Myxotrichaceae*, *Onygenales*, *Eurotiomycetes*.

Conidiophores solitary, erect, flexuous, unbranched, with dry conidial masses, 80–160 × 2–2.5 μm, 4–6-septate. *Fertile hyphae* developing in upper third of conidiophore, 2–2.5 μm diam, dichotomously branched, fragmenting to form long chains of up to 10 conidia in a dry conidiogenous head. *Conidia* thin-walled, subhyaline, subglobose to cylindrical, (2–)3–4(–5) × (1.5–)2 μm, with asperulate perispore.

Culture characteristics — Colonies flat, spreading, with moderate aerial mycelium and even lobate margin, reaching 7 mm diam after 2 wk at 25 °C. On MEA, PDA and OA surface smoke-grey, reverse umber with diffuse umber pigment.

Typus. AUSTRALIA, New South Wales, Gnupa State Forest, on leaves of *Eucalyptus maidenii* (*Myrtaceae*), 29 Nov. 2016, P.W. Crous (holotype CBS H-23579, culture ex-type CPC 32659 = CBS 144423, ITS and LSU sequences GenBank MH327803.1 and MH327839.1, MycoBank MB825412).

Notes — The genus *Oidiodendron*, which commonly occurs in soil and on plant litter, was treated by Rice & Currah (2005), who provided keys to 23 species. Phylogenetically, *O. eucalypti* is related to *O. truncatum*, from which it can be distinguished based on its conidia. *Conidia* of *O. truncatum* are dark at maturity, barrel-shaped, truncate with distinct apical scars and reticulate ornamentation, (2–)3.5(–5) × (1–)2.5(–3.5) μm (Rice & Currah 2005).

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the ITS sequence had highest similarity to *Oidiodendron tenuissimum* (GenBank AF307773.1; Identities = 489/503 (97 %), 3 gaps (0 %)), *Oidiodendron griseum* (GenBank AF062797.1; Identities = 495/510 (97 %), 1 gap (0 %)) and *Oidiodendron fuscum* (GenBank NR_111035.1; Identities = 495/510 (97 %), 3 gaps (0 %)). Closest hits using the LSU sequence are *Oidiodendron truncatum* (GenBank KF835845.1; Identities = 860/877 (98 %), 1 gap (0 %)), *Myxotrichum deflexum* (GenBank AY541491.1; Identities = 857/885 (97 %), no gaps) and *Eremascus fertilis* (GenBank HQ540515.1; Identities = 807/838 (96 %), 2 gaps (0 %)).

Colour illustrations. *Eucalyptus* trees in Gnupa State Forest; conidiophores, conidiogenous cells with conidial chains, and conidia. Scale bars = 10 μm.

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