

Neoanungitea eucalyptorum



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Neoanungitea eucalyptorum Crous, *sp. nov.*

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

Classification — *Microthyriaceae*, *Microthyriales*, *Dothideo-mycetes*.

Mycelium consisting of brown, smooth to warty, 2.5–3 µm diam hyphae. *Conidiophores* dimorphic. *Microconidiophores* reduced to conidiogenous loci on hyphae, subcylindrical to doliiform with truncate apex, 5–10 × 5–6 µm. *Macroconidiophores* erect, subcylindrical, flexuous, dark brown, thick-walled, multiseptate, up to 200 µm tall, 4–7 µm wide, arising from superficial to immersed hyphae. *Conidiogenous cells* terminal, subcylindrical, dark brown, 15–25 × 5–7 µm; proliferating sympodially with subdenticulate scars, 2 µm diam, not thickened nor darkened. *Conidia* occurring in unbranched chains, fusoid-ellipsoid, apex subobtuse, base truncate, 1.5–2 µm diam, brown, smooth, guttulate, 3-septate, (17–)20–23(–25) × (3–)4–5(–6) µm.

Culture characteristics — Colonies flat, spreading, with sparse aerial mycelium and feathery, lobate margin, reaching 10 mm diam after 2 wk at 25 °C. On MEA, PDA and OA surface sepia, reverse brown vinaceous.

Typus. AUSTRALIA, New South Wales, Yabbra State Forest, Boomi Creek plantation, on leaves of *Eucalyptus grandis* (*Myrtaceae*), 19 Apr. 2018, A.J. Carnegie, HPC 2432 (holotype CBS H-24156, culture ex-type CPC 35763 = CBS 146028, ITS and LSU sequences GenBank MN562099.1 and MN567607.1, MycoBank MB832858).

Notes — *Neoanungitea eucalyptorum* is closely related to *N. eucalypti* (conidia (0–)3-septate, (13–)15–17(–22) × (3.5–)4–5 µm) described from leaves of *Eucalyptus obliqua* collected in Australia (Crous et al. 2017a). The two species can be distinguished in that *N. eucalyptorum* has longer conidia.

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Neoanungitea eucalypti* (strain CBS 143173, GenBank NR_156383.1; Identities = 477/526 (91 %), 18 gaps (3 %)), *Anungitopsis speciosa* (strain CBS 181.95, GenBank EU035401.1; Identities = 387/467 (83 %), 26 gaps (5 %)), and *Anungitopsis lauri* (strain CBS 145067, GenBank NR_161129.1; Identities = 414/507 (82 %), 30 gaps (5 %)). Closest hits using the **LSU** sequence are *Anungitopsis speciosa* (strain CBS 181.95, GenBank EU035401.1; Identities = 763/790 (97 %), no gaps), *Spirosphaera beverwijkiana* (strain CBS 470.66, GenBank MH870500.1; Identities = 727/796 (91 %), 8 gaps (1 %)), and *Microthyrium quercus* (strain HKAS 92487, GenBank KY911453.1; Identities = 726/795 (91 %), 6 gaps (0 %)).

Colour illustrations. *Eucalyptus grandis* trees where *N. eucalyptorum* was collected. Colony on synthetic nutrient poor agar; conidiophores with conidiogenous cells. Scale bars = 10 µm.

Pedro W. Crous & Johannes Z. Groenewald, Westerdijk Fungal Biodiversity Institute, P.O. Box 85167, 3508 AD Utrecht, The Netherlands; e-mail: p.crous@wi.knaw.nl & e.groenewald@wi.knaw.nl
Angus J. Carnegie, Forest Health & Biosecurity, Forest Science, NSW Department of Primary Industries, Level 12, 10 Valentine Ave, Parramatta NSW 2150, Australia; e-mail: angus.carnegie@dpi.nsw.gov.au