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Neocelosporium corymbiae Crous, *sp. nov.*

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

Classification — *Neocelosporiaceae*, *Neocelosporiales*, *Dothideomycetes*.

Colonies erumpent, forming sporodochia with radiating hyphae. *Mycelium* consisting of brown, smooth, thick-walled, 5–7 µm diam hyphae encased in mucoid sheath; hyphae aggregate to form a brown stroma that gives rise to sporodochia. *Conidogenous cells* integrated on hyphae and on stroma, reduced to loci, phialidic with pore slightly darkened and flared, 2–4 µm diam, cells 5–10 µm long. *Conidia* solitary, aseptate, hyaline, smooth, ellipsoid, thick-walled, guttulate, apex obtuse, tapering to truncate hilum, 1.5–2 µm diam, with age becoming medianly 1-septate, brown, encased in mucoid sheath, (8–)10–11(–13) × (3.5–)4(–5) µm.

Culture characteristics — Colonies erumpent, spreading, with sparse aerial mycelium and smooth, even margin, reaching 4 mm diam after 2 wk at 25 °C. On MEA, PDA and OA surface and reverse brown vinaceous.

Typus. AUSTRALIA, New South Wales, Dyraba, private plantation, on stems of *Corymbia variegata* (*Myrtaceae*), Nov. 2015, A.J. Carnegie, HPC 3216 (holotype CBS H-24548, culture ex-type CPC 39297 = CBS 147080, ITS and LSU sequences GenBank MZ064452.1 and MZ064509.1, MycoBank MB 839538).

Notes — *Neocelosporium corymbiae* is closely related to *N. eucalypti* (on *Eucalyptus cyanophylla*, Mildura, Mungo National Park, primary conidia 5–12 × 3–5 µm, becoming brown, thick-walled and swollen with age; Crous et al. 2018a), but is morphologically and phylogenetically distinct from the latter species.

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Neocelosporium eucalypti* (strain CBS 145086, GenBank NR_164293.1; Identities = 559/578 (97 %), two gaps (0 %)), *Celosporium larixicola* (strain L3-1, GenBank FJ997287.1; Identities = 495/544 (91 %), 11 gaps (2 %)) and *Perusta inaequalis* (strain CBS 118271, GenBank NR_144958.1; Identities = 467/514 (91 %), 12 gaps (2 %)). Closest hits using the **LSU** sequence are *Neocelosporium eucalypti* (strain CBS 145086, GenBank NG_066297.1; Identities = 850/865 (98 %), one gap (0 %)), *Celosporium larixicola* (strain L3-1, GenBank FJ997288.1; Identities = 800/835 (96 %), five gaps (0 %)) and *Muellerites juniperi* (strain CBS 339.73, GenBank MH877745.1; Identities = 825/864 (95 %), six gaps (0 %)).

Colour illustrations. Eucalypt forest. Colonies on SNA; hyphae with conidogenous loci; conidia. Scale bars = 10 µm.

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