

Castanediella eucalyptigena



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Castanediella eucalyptigena Crous, sp. nov.

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

Classification — *Castanediellaceae*, *Xylariales*, *Sordariomycetes*.

Mycelium consisting of hyaline, smooth, branched, septate, 2–4 µm diam hyphae. *Conidiophores* erect on hyphae, subcylindrical, smooth, hyaline, 0–2-septate, frequently reduced to conidiogenous loci on hyphae, up to 15 µm tall, 3–5 µm diam. *Conidiogenous cells* hyaline, smooth, solitary, terminal and intercalary, ampulliform or subcylindrical, polyblastic, with inconspicuous scars at apex, 2–10 × 2–5 µm. In older cultures (4 wk) conidiophores and conidiogenous cells become pale brown. *Conidia* solitary but aggregated in mucoid clusters, hyaline, smooth, aseptate, falcate, tapering to acute ends that are subobtusely rounded, biguttulate, (13–)18–24(–30) × 2(–2.5) µm.

Culture characteristics — Colonies flat, spreading, with sparse aerial mycelium and smooth, lobate margins, reaching 30 mm diam after 2 wk at 25 °C. On MEA surface iron-grey, reverse olivaceous grey. On PDA surface and reverse isabelline. On OA surface iron-grey.

Typus. AUSTRALIA, New South Wales, Barren Grounds Nature Reserve, on leaves of *Eucalyptus* sp. (*Myrtaceae*), 26 Nov. 2016, P.W. Crous (holotype CBS H-23272, culture ex-type CPC 32055 = CBS 143178, ITS and LSU sequences GenBank MG386036 and MG386089, MycoBank MB823378).

Notes — The genus *Castanediella* is morphologically similar to *Microdochium*, but differs in having brown, branched conidiophores (Crous et al. 2015b, Hernández-Restrepo et al. 2016, 2017). Several species of *Castanediella* are known from *Eucalyptus* (Crous et al. 2016a), but *C. eucalyptigena* is phylogenetically distinct from all taxa presently known.

Based on a megablast search using the ITS sequence, the closest matches in NCBI's GenBank nucleotide database were *Xyladictyochaeta lusitanica* (GenBank KY853479; Identities 531/576 (92 %), 12 gaps (2 %)), *C. cagnizarii* (GenBank KP859054; Identities 517/575 (90 %), 30 gaps (5 %)) and *C. malaysiana* (GenBank KX306752; Identities 520/580 (90 %), 24 gaps (4 %)). The highest similarities using the LSU sequence were *C. cagnizarii* (GenBank KP858991; Identities 793/814 (97 %), 3 gaps (0 %)), *Pidoplitchkoviella terricola* (GenBank AF096197; Identities 799/822 (97 %), 5 gaps (0 %)) and *C. eucalypti* (GenBank KR476758; Identities 794/819 (97 %), 1 gap (0 %)).

Colour illustrations. Barren Grounds Nature Reserve; conidiophores and conidia. Scale bars = 10 µm.

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