Hypsotheca eucalyptorum
Hypsotheca eucalyptorum Crous & Carnegie, sp. nov.

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

Classification — Coryneliaceae, Coryneliales, Eurotiomycetes.

Conidiomata sparsely formed in culture, pycnidial, brown, globose, 180–200 µm diam, developing in aerial mycelium. Dominant morph hypomycetous. Mycelium initially hyaline, smooth, becoming brown, verruculose to warty, septate, branched, 2–3 µm diam. Conidiophores erect on superficial hyphae, 0–1-septate, unbranched, subcylindrical, straight to flexuous, brown, verruculose, 5–20 × 1.5–2.5 µm. Conidiogenous cells terminal, pale brown, verruculose, subcylindrical, phialidic with flared collarette, 2–3 µm diam, 5–15 × 1.5–2.5 µm. Conidia aseptate, solitary, hyaline, smooth, guttulate, subcylindrical with obtuse ends, (3–)3.5–4(–4.5) × 1.5(–2) µm.

Culture characteristics — Colonies erumpent, spreading, with moderate aerial mycelium and smooth, lobate margin, reaching 60 mm diam after 2 wk at 25 °C. On MEA, PDA and OA surface brown vinaceous, reverse leaden black.

Type. AUSTRALIA, New South Wales, Booambie State Forest, McCorquodale plantation, on leaves of Eucalyptus grandis × camaldulensis clone (Myrtaceae), 20 Apr. 2016, A.J. Carnegie, HPC 2431 (holotype CBS H-23966, culture ex-type CPC 35734 = CBS 145576, ITS and LSU sequences GenBank MK876393.1 and MK876434.1, MycoBank MB830858).

Additional material examined. AUSTRALIA, New South Wales, Orara State Forest, on leaves of Eucalyptus grandis, 7 Mar. 2016, D. Sargeant, HPC 2304, CPC 35391 = CBS 145577, ITS and LSU sequences GenBank MK876394.1 and MK876435.1.

Notes — The genus Hypsotheca was recently resurrected as sister genus to Caliciopsis. Species of Hypsotheca are distinguished from Caliciopsis in having a phaeoacremonium-like synasexual morph in culture (Pascoe et al. 2018, Crous et al. 2019). Hypsotheca eucalyptorum is related to H. pleomorpha (conidia (3–)4–5(–6) x 1.5(–2) µm), but distinct in that the hyphomycetous morph is dominant in culture.

Based on a megablast search of NCBI’s GenBank nucleotide database, the closest hits using the ITS sequence of CPC 35734 had highest similarity to Hypsotheca pleomorpha (as Caliciopsis pleomorpha, GenBank MG641785.1; Identities = 500/552 (91 %), 23 gaps (4 %)), Caliciopsis eucalypti (GenBank NR_154836.1; Identities = 396/429 (92 %), 10 gaps (0 %)) and Corynelia uberata (GenBank KJ204606.1; Identities = 497/551 (90 %), 26 gaps (4 %)). The ITS sequences of CPC 35734 and CPC 35391 are 541/549 (99 %, including two gaps) similar. Closest hits using the LSU sequence are Hypsotheca pleomorpha (GenBank MK442528.1; Identities = 800/829 (97 %), 3 gaps (0 %)), Caliciopsis valentina (GenBank NG_060419.1; Identities = 776/824 (94 %), no gaps) and Caliciopsis pinea (GenBank DQ678097.1; Identities = 776/824 (94 %), no gaps). The LSU sequences of CPC 35734 and CPC 35391 are 831/835 (99 %, including one gap) similar.