Fusicladium eucalyptigenum
**Fusicladium eucalyptigenum** Crous & M.J. Wingf., *sp. nov.*

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

**Classification.** Sympoventuriaceae, Venturiales, Dothideomycetes.

*Mycelium* consisting of medium brown, smooth, branched, septate, 2–2.5 mm diam hyphae. *Conidiophores* erect, 0–1-septate, mostly reduced to conidiogenous cells, straight to geniculose-sinuous, subcylindrical, 5–20 × 2.5–3 mm, medium brown, smooth, proliferating sympodially, scars thickened, darkened, not refractive, 1–1.5 mm diam. *Conidia* occurring in branched chains; ramoconidia medium brown, subcylindrical, 0–1-septate, 12–20 × 2–3 mm; conidia subcylindrical, straight, hyaline to pale brown, guttulate, medianly 1-septate; hila thickened and darkened, 1–1.5 mm diam, (13–)16–18(–20) × (1.5–)2–2.5 mm.

**Culture characteristics.** Colonies erumpent, spreading, with moderate aerial mycelium and smooth, lobate margin, reaching 20 mm diam after 2 wk at 25 °C. On MEA, PDA and OA surface and reverse umber.

**Typus.** MALAYSIA, on twigs of *Eucalyptus* sp. (Myrtaceae), 22 Mar. 2018, M.J. Wingfield, HPC 2394 (holotype CBS H-23942, culture ex-type CPC 35746 = CBS 145543, ITS and LSU sequences GenBank MK876390.1 and MK876431.1, MycoBank MB830831).

**Notes.** *Fusicladium eucalyptigenum* is closely related to *Fusicladium amoenum* (conidia (6–)10.5–12.8(–17.3) × (1.5–)2.4–3(–3.8) μm) and *F. paraamoenum* (conidia (13–)15–20 (–28) × (3–)3.5(–4) μm; Crous et al. 2016), but is distinct based on its conidial dimensions. The *Fusicladium* generic complex is presently being revised and will be published elsewhere. Based on a megablast search of NCBI’s GenBank nucleotide database, the closest hits using the ITS sequence had highest similarity to *Fusicladium amoenum* (GenBank MH862514.1; Identities = 529/554 (95 %), 1 gap (0 %)), *Fusicladium paraamoenum* (GenBank NR_155093.1; Identities = 527/557 (95 %), 4 gaps (0 %)) and *Fusicladium intermedium* (GenBank EU035432.1; Identities = 489/530 (92 %), 3 gaps (0 %)). Closest hits using the LSU sequence are *Fusicladium paraamoenum* (GenBank NG_058242.1; Identities = 721/728 (99 %), no gaps), *Fusicladium amoenum* (GenBank EU035425.1; Identities = 712/729 (98 %), 1 gap (0 %)).

![Colour illustrations. Eucalyptus forest. Colony on oatmeal agar; conidiophores, conidiogenous cells and conidia. Scale bars = 10 μm.](image-url)