

Falcocladium eucalypti



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Falcocladium eucalypti Crous, sp. nov.

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

Classification — *Falcocladiaceae*, *Falcocladiales*, *Sordariomycetes*.

Conidiophores penicillate on host, but rarely penicillate in culture, mostly aggregated in sporodochia, arising from superficial mycelium or from chlamydospores that are intercalary, in chains, brown, globose, 10–12 µm diam. *Conidiophores* with hyaline stipe extensions, aseptate, thick-walled, 40–70 × 1.5–2 µm, terminating in ellipsoid to globose vesicles, 4–6(–7) µm diam. *Conidiophores* with compact conidiogenous apparatus, consisting of primary and secondary branches, smooth, hyaline, giving rise to phialidic conidiogenous cells, ampulliform, 5–10(–20) × 2.5(–3) µm. *Conidia* hyaline, smooth, aseptate, falcate with a short acute apical beak (1.5–2 µm long), and a basal appendage, 2–3 µm long, (22–)32–37(–41) × (2–)2.5(–3) µm.

Culture characteristics — Colonies erumpent, spreading, with sparse aerial mycelium and smooth, lobate margin, reaching 5 mm diam after 2 wk at 25 °C. On MEA, PDA and OA surface and reverse cinnamon to buff.

Typus. SOUTH AFRICA, Limpopo Province, Tzaneen, near turnoff coach road, on leaves of *Eucalyptus* sp. (*Myrtaceae*), 2010, P.W. Crous, HPC 2472 (holotype CBS H-24248, culture ex-type CPC 36050 = CBS 146052, ITS, LSU, *actA* and *rpb2* sequences GenBank MN562106.1, MN567614.1, MN556784.1 and MN556798.1, MycoBank MB832865).

Additional material examined. AUSTRALIA, New South Wales, Dundurabin, Neaves Plantation, on leaf of *Eucalyptus dunnii*, 21 Feb. 2017, A.J. Carnegie, HPC 2836, culture CPC 38019 = CBS 146061, ITS, LSU and *actA*, MN562107.1, MN567615.1 and MN556785.1. — SOUTH AFRICA, Limpopo Province, Tzaneen, on leaf litter of *Eucalyptus* sp., 2010, P.W. Crous, HPC 2465, culture CPC 36046 = CBS 146051, ITS, LSU, *actA* and *rpb2* sequences GenBank MN562108.1, MN567616.1, MN556786.1 and MN556799.1.

Notes — Species of *Falcocladium* are commonly isolated from leaf litter, and considered to be weak foliar pathogens of *Eucalyptus* (Crous et al. 1994, 1997, 2018a). Five species are presently known, having been collected on eucalypt leaves in Africa, Asia, Australia and South America. *Falcocladium eucalypti* represents the second species known from Africa, being closely related to *F. sphaeropedunculatum*, which is distinct in having sphaeropedunculate vesicles (Crous et al. 1997). Of interest is the fact that one collection originates from Australia, suggesting this fungus could have been introduced to South Africa along with its host.

Colour illustrations. *Eucalyptus* trees *Falcocladium eucalypti* was isolated from. Conidiophores with conidiogenous cells; stipe extensions with vesicles; chlamydospores; conidia. Scale bars = 10 µm.

Based on a blastn search of NCBI's GenBank nucleotide database, the closest hits using the ITS sequence of CPC 36050 had highest similarity to *Falcocladium sphaeropedunculatum* (strain CBS 111294, GenBank EU040220.1; Identities = 625/659 (95 %), 15 gaps (2 %)), *Falcocladium turbinatum* (strain BCC 22055, GenBank NR_138378.1; Identities = 620/688 (90 %), 41 gaps (5 %)), and *Falcocladium multivesiculatum* (strain CBS 120386, GenBank EU040217.2; Identities = 597/667 (90 %), 46 gaps (6 %)). The ITS sequences of CPC 36046, 36050 and 38019 are identical (650/650 bases). Closest hits using the LSU sequence of CPC 36050 are *Falcocladium sphaeropedunculatum* (strain CBS 111292, GenBank EU040218.1; Identities = 842/853 (99 %), no gaps), *Falcocladium africanum* (strain CPC 34007, GenBank MK047471.1; Identities = 851/863 (99 %), no gaps), and *Falcocladium thailandicum* (strain CPC 13489, GenBank EU040216.2; Identities = 848/861 (98 %), no gaps). The LSU sequences of CPC 36046, 36050 and 38019 are identical (824/824 bases). Closest hits using the *actA* sequence of CPC 36050 had highest similarity to *Falcocladium africanum* (strain CBS 145046, GenBank MK047519.1; Identities = 392/407 (96 %), no gaps), *Falcocladium thailandicum* (strain CBS 121717, GenBank KM231261.1; Identities = 391/407 (96 %), no gaps), and *Falcocladium sphaeropedunculatum* (strain CBS 111292, GenBank KM231260.1; Identities = 403/428 (94 %), no gaps). The *actA* sequences of CPC 36050 and 36046 are identical (651/651 bases), and CPC 36050 and 38019 are almost identical (649/652 bases, of which two bases are represented by an extra repetitive nucleotide). Closest hits using the *rpb2* sequence had highest similarity to *Falcocladium africanum* (strain CBS 145046, GenBank MK047533.1; Identities = 720/836 (86 %), no gaps), *Trichoderma austriacum* (strain CBS 122494, GenBank FJ860525.1; Identities = 688/904 (76 %), 24 gaps (2 %)), and *Trichoderma sulawesense* (strain G.J.S. 85-228, GenBank AY391954.1; Identities = 681/893 (76 %), 31 gaps (3 %)). The *rpb2* sequences of CPC 36050 and 36046 are identical (912/912 bases).

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