

Chaetopsina eucalypti



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***Chaetopsina eucalypti* Crous, sp. nov.**

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

Classification — *Nectriaceae*, *Hypocreales*, *Sordariomycetes*.

Conidiomata sporodochial, hyaline, globose, 100–300 µm diam, with crystalline to creamy mucoid conidial mass. *Setae* dispersed throughout sporodochia, at times developing from a brown basal stroma of *textura angularis*, erect, flexuous, unbranched, brown, smooth, thick-walled, tapering to acute apex, multi-septate, 150–300 × 6–7 µm. *Conidiophores* densely aggregated, arising from a central stroma, hyaline, smooth, subcylindrical, 3–6-septate, 20–40 × 2.5–3 µm. *Conidiogenous cells* terminal and intercalary, subcylindrical to fusoid-ellipsoid, hyaline, smooth, phialidic, 7–12 × 2.5–3 µm. *Conidia* aseptate, hyaline, smooth, guttulate, cylindrical, straight, apex obtuse, base truncate, 1 µm diam, (13–)14–15(–18) × (1.5–)2 µm.

Culture characteristics — Colonies flat, spreading, with folded surface and sparse aerial mycelium and even, lobate margin, reaching 20 mm diam after 2 wk at 25 °C. On MEA surface saffron, reverse luteous. On PDA surface ochreous, reverse sienna. On OA surface pale luteous.

Typus. AUSTRALIA, New South Wales, Nullica State Forest, on *Eucalyptus* leaf litter (*Myrtaceae*), 29 Nov. 2016, P.W. Crous (holotype CBS H-23585, culture ex-type CPC 32857 = CBS 144417, ITS and LSU sequences GenBank MH327799.1 and MH327835.1, MycoBank MB825405).

Notes — *Chaetopsina eucalypti* is phylogenetically related to *C. pini*, known from needle litter of *Pinus caribaea* collected in Thailand (Crous et al. 2013). The genus *Chaetopsina* has nectria-like sexual morphs, and although the culture examined in this study formed ascomatal initials, these did not become fertile. Some species of *Chaetopsina* have been reported from *Eucalyptus*, namely *C. fulva* (Hawaii; conidia 7–11 × 1 µm) and *C. splendida* (Australia and Brazil; conidia 9.5–12 × 1.5 µm) (Sutton & Hodges 1976, Crous et al. 1989). *Chaetopsina eucalypti* is easily distinguished from these species based on its larger conidia.

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the ITS sequence had highest similarity to *Chaetopsina pini* (GenBank NR_137822.1; Identities = 528/588 (90 %), 24 gaps (4 %)) and *Chaetopsina pinicola* (GenBank NR_137823.1; Identities = 524/595 (88 %), 36 gaps (6 %)). Closest hits using the LSU sequence are *Chaetopsina pini* (GenBank KF777200.1; Identities = 872/881 (99 %), no gaps), *Chaetopsinectria chaetopsinae* (GenBank DQ119553.2; Identities = 877/889 (99 %), no gaps) and *Chaetopsina pinicola* (GenBank KF777201.1; Identities = 875/891 (98 %), no gaps).

Colour illustrations. *Eucalyptus* leaf litter next to a dead *Xanthorrhoea* at collection site; conidiomata sporulating on OA (scale bar = 300 µm), setae, conidiogenous cells and conidia (scale bars = 10 µm).

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