

*Corynespora endiandrae*



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## *Corynespora endiandrae* Crous & Summerell, *sp. nov.*

*Etymology.* Name reflects the host genus *Endiandra*, from which the species was isolated.

*Mycelium* consisting of hyaline, smooth, branched, septate, 3–4 µm diam hyphae. *Conidiophores* solitary, erect, straight to flexuous, subcylindrical, unbranched, brown, thick-walled, finely roughened, base bulbous, lacking rhizoids, 10–12 µm diam, stipe 200–300 × 5–7 µm, 8–16-septate. *Conidiogenous cells* integrated, terminal and lateral, monotretic, subcylindrical, brown, finely roughened, slightly darkened, 2 µm diam. *Conidia* obclavate, solitary or in short chains (2–3), thick-walled, brown, finely roughened, 3(–4) distoseptate, (35–)37–45(–57) × (7–)8(–9) µm; hila darkened, thickened, 2.5–3.5 µm diam.

*Culture characteristics* — Colonies reaching 20 mm diam after 2 wk at 25 °C in the dark, with moderate aerial mycelium and smooth, even margins. On MEA, PDA and OA surface and reverse dirty white.

*Typus.* AUSTRALIA, New South Wales, Nightcap National Park, S28.33.918 E153.20.228, on leaves of *Endiandra introrsa* (*Lauraceae*), 9 Mar. 2013, B.A. Summerell (holotype CBS H-21984, culture ex-type CPC 22194 = CBS 138902; ITS sequence GenBank KP004450, LSU sequence GenBank KP004478, MycoBank MB810596).

*Notes* — Species of *Corynespora* are commonly associated with leaf spots as necrotrophic pathogens. Species have mainly been described based on host association, and the genus is in need of revision. No species have thus far been recorded on *Endiandra*, and based on the key provided by Siboe et al. (1999), *C. endiandrae* appears to represent a novel taxon.

*ITS.* Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the ITS sequence are *Helminthosporium velutinum* (GenBank JN198435; Identities = 453/505 (90 %), Gaps = 9/505 (1 %)), *Helminthosporium solani* (GenBank KC106739; Identities = 501/560 (89 %), Gaps = 13/560 (2 %)) and *Helminthosporium chlorophorae* (GenBank AF120259; Identities = 422/475 (89 %), Gaps = 16/475 (3 %)).

*LSU.* Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the LSU sequence are *Corynespora leucadendri* (GenBank KF251654; Identities = 806/819 (98 %), no gaps), *Corynespora olivacea* (GenBank JQ044448; Identities = 806/820 (98 %), Gaps = 1/820 (0 %)) and *Byssothecium circinans* (GenBank GU205217; Identities = 802/819 (98 %), no gaps).

*Colour illustrations.* Nightcap National Park, Australia; conidiophores and conidia. Scale bars = 10 µm.

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