

Corynespora pseudocassiicola



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***Corynespora pseudocassiicola* Crous & M.J. Wingf., sp. nov.**

Etymology. Name refers to the morphological similarity to *Corynespora cassiicola*.

Classification — *Corynesporascaceae*, *Pleosporales*, *Dothi-deomycetes*.

Leaf spots amphigenous, but more prominent on upper leaf surface, medium brown with broad, dark brown border, circular to subcircular, 5–20 mm diam. *Mycelium* immersed, stromata absent. *Conidiophores* 200–400 × 5–7 µm, septate, dark brown, smooth, cylindrical, flexuous, thick-walled, solitary, at times arising in clusters of 3–6 from a reduced stroma consisting of a few brown, globose cells, 10–13 µm diam. *Conidiogenous cells* terminal, integrated, dark brown, smooth, cylindrical, with obtuse apex with tretic central pore, 12–50 × 5–7 µm. *Conidia* medium brown, finely roughened, subcylindrical to obclavate, apex obtuse, base obconically truncate, with slightly darkened hilum, (3–)4–5(–7) µm diam, (4–)8–12(–17)-distoseptate, straight to flexuous, frequently in short, unbranched chains, (70–)95–160(–230) × (7–)9–10 µm.

Culture characteristics — Colonies flat, spreading, with moderate aerial mycelium and smooth, lobate margin, reaching 40 mm diam after 2 wk at 25 °C. On MEA surface pale olivaceous grey, reverse olivaceous grey. On PDA surface olivaceous grey, reverse iron-grey. On OA surface pale olivaceous grey.

Typus. COLOMBIA, Llanos, on leaves of *Byrsonima* sp. (*Malpighiaceae*), July 2010, *M.J. Wingfield* (holotype CBS H-23590, culture ex-type CPC 31708 = CBS 144412, ITS, LSU, *actA*, *tef1* and *tub2* sequences GenBank MH327794.1, MH327830.1, MH327864.1, MH327877.1 and MH327888.1, MycoBank MB825399).

Notes — *Corynespora cassiicola* (from leaves of *Cassia* sp. in Cuba) is a common pathogen of a range of crops in the tropics, which is morphologically and phylogenetically highly diverse (Dixon et al. 2009), including several different species. *Corynespora pseudocassiicola* is morphologically similar to several species that are presently treated as *C. 'cassiicola'*, but is associated with leaf spots of *Byrsonima* in Colombia, and is herewith distinguished based on its phylogenetic placement, and described as new.

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the ITS sequence had highest similarity to *Corynespora cassiicola* (GenBank FJ852587.1; Identities = 520/553 (94 %), 11 gaps (1 %)), *Corynespora torulosa* (GenBank NR_145181.1; Identities = 517/551 (94 %), 10 gaps (1 %)) and *Corynespora smithii* (GenBank KY984300.1; Identities = 513/551 (93 %), 9 gaps (1 %)). Closest hits using the LSU sequence are *Corynespora cassiicola* (GenBank LC177365.1; Identities = 805/809 (99 %), no gaps), *Corynespora torulosa* (GenBank KF777207.1; Identities = 847/855 (99 %), no gaps) and *Corynespora smithii* (GenBank KY984299.1; Identities = 845/855 (99 %), no gaps). Closest hits using the *actA* sequence had highest similarity to *Parastagonospora nodorum* (GenBank CP022803.1; Identities = 474/523 (91 %), 10 gaps (1 %)), *Phaeosphaeria podocarp* (GenBank KP004502.1; Identities = 458/503 (91 %), 5 gaps (0 %)) and *Alternaria intercepta* (GenBank JQ671651.1; Identities = 469/521 (90 %), 8 gaps (1 %)). Closest hits using the *tef1* sequence had highest similarity to *Corynespora smithii* (GenBank KY984436.1; Identities = 372/431 (86 %), 14 gaps (3 %)), *Neocucurbitaria juglandicola* (GenBank MF795861.1; Identities = 351/440 (80 %), 23 gaps (5 %)) and *Protopenestella ulmi* (GenBank MF795879.1; Identities = 351/440 (80 %), 30 gaps (6 %)). The best hit using the *tub2* sequence was with *Corynespora cassiicola* (GenBank KU605248.1; Identities = 360/404 (89 %), 6 gaps (1 %)).

Colour illustrations. *Byrsonima* sp. growing in Colombia; symptomatic leaf, conidiogenous cells and conidia. Scale bars = 10 µm.