
Cercospora dianellicola

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Cercospora dianellicola Crous, *sp. nov.*

Etymology. Named after the host genus from which it was collected, *Dianella*.

Classification — *Mycosphaerellaceae*, *Capnodiales*, *Dothideomycetes.*

On potato dextrose agar. *Conidiophores* solitary to fasciculate, arising from superficial hyphae but most frequently from a well-developed erumpent stroma up to 200 µm diam (ascomatal initials), erect, flexuous-geniculate, subcylindrical, 1–5-septate, branched below or unbranched, 70–150 × 4–6 µm, medium brown, thick-walled, basal region roughened. *Conidiogenous cells* terminal and intercalary, proliferating sympodially, medium brown, smooth, subcylindrical with slight apical taper, scars thickened, darkened, 1–2 µm diam, 25–60 × 4–5 µm. *Conidia* solitary, undergoing microcyclic conidiation in culture, hyaline, smooth, granular, obclavate but subcylindrical when small, 3–6-septate, curved, apex subobtuse, base obconically truncate, hilum slightly thickened and darkened, 2 µm diam, (13–)26–33(–40) × (3–)4 µm.

Culture characteristics — Colonies erumpent, spreading, with moderate aerial mycelium and feathery, lobate margins, reaching 40 mm diam after 1 mo at 25 °C. On MEA, PDA and OA surface grey olivaceous, reverse iron-grey.

Typus. Australia, Victoria, Mount Best Tin Mine Road, on *Dianella* sp. (*Iridaceae*), 28 Nov. 2016, *P.W. Crous* (holotype CBS H-23321, culture ex-type CPC 32597 = CBS 143453, ITS, LSU, *actA* and *cmdA* sequences GenBank MG386075, MG386128, MG674152 and MG674153, MycoBank MB823424).

Notes — Several species of *Mycosphaerellaceae* have been described from *Dianella*, namely *Mycosphaerella queenslandica*, *M. dianellae* and *Cercospora dianellae*, the latter which has since been shown to be a member of *Zasmidium* (Bensch et al. 2012). Because its not possible to determine to which asexual genus the two *Mycosphaerella* spp. belong (Videira et al. 2017), *C. dianellicola* is accepted as the only confirmed *Cercospora* sp. occurring on this host.

Based on a megablast search using the ITS sequence, the closest matches in NCBIs GenBank nucleotide database were *C. asparagi* (GenBank KY549098; Identities 533/536 (99 %), 2 gaps (0 %)), *C. malayensis* (GenBank MF435168; Identities 533/536 (99 %), 2 gaps (0 %)) and *C. glycinicola* (GenBank NR_147293; Identities 533/536 (99 %), 2 gaps (0 %)). The highest similarities using the LSU sequence were *C. ischaemi* (GenBank KM055432; Identities 828/830 (99 %), no gaps), *C. senecionis-walkeri* (GenBank KC677921; Identities 832/836 (99 %), no gaps) and *C. sojina* (GenBank KX286969; Identities 831/836 (99 %), no gaps). The highest similarities using the *actA* sequence were *C. beticola* (GenBank AF443281; Identities 552/618 (89 %), 25 gaps (4 %)), *C. sojina* (GenBank JQ325008; Identities 540/610 (89 %), 15 gaps (2 %)) and *C. malayensis* (GenBank KY082664; Identities 540/612 (88 %), 19 gaps (3 %)). The highest similarities using the *cmdA* sequence were *C. coniogrammes* (GenBank KT037466; Identities 374/445 (84 %), 13 gaps (2 %)), *C.* cf. *malloti* (GenBank KT193753; Identities 375/446 (84 %), 13 gaps (2 %)) and *C. cypericola* (GenBank KT193727; Identities 376/447 (84 %), 15 gaps (3 %)).

Colour illustrations. *Dianella* sp. at Mount Best Tin Mine Road; conidiophores sporulating on PNA and conidia. Scale bars = 10 µm.

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