Helminthosporium syzygii
helminthosporium syzygii Crous & M.J. Wingf., sp. nov.

Etymology. Name refers to Syzygium, the host genus from which this fungus was isolated.

Classification — Massarinaceae, Pleosporales, Dothideomycetes.

Colony on natural substrate black, hairy, effuse, 1–2 mm long. Mycelium immersed, forming a brown stroma on the surface, 40–150 mm diam, giving rise to erect conidiophores. Conidiophores 150–400 x 10–15 mm, multiseptate, arising in fascicles, unbranched, dark brown, somewhat clavate at apex, rejuvenating percurrently. Conidiogenous cells terminal with well-defined pore, 3–4 mm diam, thickened and darkened, 20–40 x 13–15 mm. Conidia (70–)80–100(–150) x (19–)22–23(–25) mm, obclavate, curved, apex subobtuse, warty, inner surface striate, medium brown, (7–)9–12-distoseptate, with angular lumina; wall 5–7 mm thick; hila thickened and darkened, 4–5 mm diam.

Culture characteristics — Colonies flat, spreading, with moderate aerial mycelium and smooth, lobate margin, reaching 60 mm diam after 2 wk at 25 °C. On MEA surface mouse grey, reverse greyish sepia. On PDA surface mouse grey, reverse olivaceous grey. On OA surface pale luteous in centre, mouse grey in outer region.

Typus. SOUTH AFRICA, Eastern Cape Province, Haga Haga, Amathole, on bark canker of Syzygium sp. (Myrtaceae), 20 Dec. 2016, M.J. Wingfield, HPC 2295 (holotype CBS H-23962, culture ex-type CPC 35312 = CBS 145570, ITS, LSU and rpb2 sequences GenBank MK876392.1, MK876433.1 and MK876487.1, MycoBank MB830853).

Notes — Helminthosporium syzygii is phylogenetically related to but morphologically distinct from H. hispanicum (Vogl-mayr & Jaklitsch 2017), and characterised by an association with bark cankers on Syzygium sp. in the Eastern Cape Province of South Africa.

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the ITS sequence had highest similarity to Helminthosporium hispanicum (GenBank NR_155196.1; Identities = 551/588 (94 %), 7 gaps (1 %)), Helminthosporium quercinum (GenBank KY984337.1; Identities = 433/495 (87 %), 18 gaps (3 %)) and Helminthosporium microsorum (GenBank KY984329.1; Identities = 496/589 (84 %), 25 gaps (4 %)). Closest hits using the LSU sequence are Helminthosporium magnisporum (GenBank AB807522.1; Identities = 845/857 (99 %), 2 gaps (0 %)), Helminthosporium quercinum (GenBank KY984338.1; Identities = 844/857 (98 %), 2 gaps (0 %)) and Helminthosporium microsorum (GenBank KY984326.1; Identities = 844/857 (98 %), 2 gaps (0 %)). Closest hits using the rpb2 sequence had highest similarity to Helminthosporium hispanicum (GenBank KY984381.1; Identities = 912/949 (96 %), no gaps), Helminthosporium quercinum (GenBank KY984401.1; Identities = 892/949 (94 %), no gaps) and Helminthosporium microsorum (GenBank KY984386.1; Identities = 885/949 (93 %), no gaps).

Colour illustrations. Beach at Haga Haga. Conidiophores on host tissue; conidiogenous cells and conidia. Scale bars = 10 µm.