

Stemphylium carpobroti



Fungal Planet 1131 – 19 December 2020

***Stemphylium carpobroti* Crous, sp. nov.**

Etymology. Name refers to the host genus *Carpobrotus* from which it was isolated.

Classification — *Pleosporaceae*, *Pleosporales*, *Dothideo-mycetes*.

Mycelium consisting of brown, septate, branched, finely verruculose, 3–4 µm diam hyphae. *Conidiophores* solitary, erect, subcylindrical, mostly unbranched, brown, finely verruculose, 40–120 × 4–7 µm, 3–5-septate, becoming swollen towards conidiogenous cell. *Conidiogenous cells* terminal, clavate, brown, finely verruculose, thick-walled, 10–20 × 8–9 µm, with terminal locus, 3–4 µm diam. *Conidia* solitary, dark brown, verruculose, ellipsoid to obovoid, constricted at medium septum, tapering to subobtuse apex, (30–)35–45(–70) × (17–)20–25 µm, with (3–)4(–6) transverse septa, and 1–4 vertical or oblique septa per transverse section.

Culture characteristics — Colonies flat, spreading, with moderate aerial mycelium and smooth, even margin, reaching 50 mm diam after 2 wk at 25 °C. On MEA, PDA and OA surface and reverse iron-grey.

Typus. SOUTH AFRICA, Western Cape Province, Clanwilliam, on leaves of *Carpobrotus quadrifolius* (*Aizoaceae*), 2018, P.W. Crous, HPC 3027 (holotype CBS H-24428, culture ex-type CPC 38637 = CBS 146789, ITS, LSU and *gapdh* sequences GenBank MW175355.1, MW175395.1 and MW173103.1, MycoBank MB837846).

Notes — *Stemphylium carpobroti* is closely related to *S. novae-zelandiae* (conidia (31–)34–40.5(–45.5) × (9–)11–13(–14.5) µm, with 3–5(–7) transverse septa and 1–2 longitudinal or oblique septa per transverse sector; Woudenberg et al. 2017), but is distinct in having larger conidia. *Stemphylium vesicarium* is also closely related, but generally has shorter conidia (see Woudenberg et al. 2017).

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the ITS sequence had highest similarity to *Asteromyces cruciatus* (strain CBS 171.63, GenBank NR_159604.1; Identities = 548/564 (97 %), six gaps (1 %)), *Stemphylium vesicarium* (strain NIHHS404, GenBank KY555005.1; Identities = 553/571 (97 %), four gaps (0 %)), and *Stemphylium lucomagnoense* (strain CIRM-BRFM2667, GenBank MK691703.1; Identities = 560/579 (97 %), four gaps (0 %)). Closest hits using the LSU sequence are *Stemphylium botryosum* (strain CBS 714.68, GenBank NG_069738.1; Identities = 849/851 (99 %), no gaps), *Stemphylium vesicarium* (strain 18ALIM004, GenBank MT472605.1; Identities = 849/851 (99 %), no gaps), and *Stemphylium eturmiunum* (strain CBS 109845, GenBank NG_069866.1; Identities = 842/844 (99 %), no gaps). Closest hits using the *gapdh* sequence had highest similarity to *Stemphylium lycopersici* (strain G9RS, GenBank MN393479.1; Identities = 369/377 (98 %), no gaps), *Stemphylium vesicarium* (strain On16-499, GenBank MK675745.1; Identities = 369/377 (98 %), no gaps), and *Stemphylium globuliferum* (strain SWp202, GenBank KF479194.1; Identities = 369/377 (98 %), no gaps).

Colour illustrations. Leaves of *Carpobrotus quadrifolius*. Conidiophores and conidiogenous cells giving rise to conidia. Scale bars = 10 µm.