

*Diaporthe cassines*



Fungal Planet 192 – 26 November 2013

## *Diaporthe cassines* Crous, sp. nov.

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

On PNA. *Conidiomata* pycnidial, globose, up to 300 µm diam, black, erumpent, exuding creamy conidial droplets from central ostioles; walls of 3–6 layers of medium brown *textura angularis*. *Conidiophores* hyaline, smooth, 0–1-septate, branched or not, densely aggregated, cylindrical, straight to sinuous, 10–20 × 2.5–4 µm. *Conidiogenous cells* 10–15 × 2–3 µm, phialidic, cylindrical, terminal and lateral, with slight taper towards apex, 1–1.5 µm diam, with visible periclinal thickening; collarette flared, up to 4 µm long. *Paraphyses* cylindrical, hyaline, smooth, branched, 1–3-septate, 20–50 × 2.5–3 µm diam. *Alpha conidia* aseptate, hyaline, smooth, guttulate, fusoid-ellipsoid, tapering towards both ends, straight, apex subobtusate, base subtruncate, (8–)9–11(–12) × (3–)3.5(–4) µm. *Gamma conidia* not observed. *Beta conidia* not observed.

Culture characteristics — Colonies reaching 60 mm diam after 2 wk, with sparse aerial mycelium and feathery, lobate margins. On PDA surface umber in centre, dirty white in outer region, similar in reverse; on OA surface dirty white; on MEA surface ochreous in centre, dirty white in outer region, umber in reverse.

*Typus.* SOUTH AFRICA, Western Cape Province, Kirstenbosch Botanical Garden, on leaves of *Cassine peragua* (*Celastraceae*), 29 Dec. 2012, P.W. Crous (holotype CBS H-21451, culture ex-type CPC 21916, 21917 = CBS 136440, ITS sequence GenBank KF777155, LSU sequence GenBank KF777208, TEF sequence GenBank KF777244, MycoBank MB805857).

Notes — Presently no species of *Diaporthe* have been reported on *Cassine*.

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the LSU sequence are *Diaporthe medusaea* (GenBank AF362560; Identities = 868/874 (99 %), no gaps), *D. cynaroidis* (GenBank EU552122; Identities = 861/867 (99 %), no gaps) and *D. pardalota* (GenBank AF408355; Identities = 855/861 (99 %), no gaps). Closest hits using the ITS sequence had highest similarity to '*Diaporthe* sp. 1' (GenBank JN225920; Identities = 568/586 (97 %), Gaps = 3/586 (0 %)), '*Diaporthe* sp. 2' (GenBank JN225919; Identities = 566/584 (97 %), Gaps = 3/584 (0 %)) and *D. beckhausii* (GenBank KC343041; Identities = 560/584 (96 %), Gaps = 3/584(0 %)). Closest hits using the TEF sequence had highest similarity to *Diaporthe* sp. (GenBank JX862536; Identities = 545/597 (91 %), Gaps = 5/597 (0 %)), *D. viticola* (GenBank KC343963; Identities = 544/604 (90 %), Gaps = 10/604 (1 %)) and *D. cynaroidis* (GenBank EU552093; Identities = 307/344 (89 %), Gaps = 4/344 (1 %)).

*Colour illustrations.* Leaf spots on *Cassine peragua* at Kirstenbosch Botanical Garden, South Africa; conidiomata on PNA; conidiogenous cells giving rise to alpha conidia. Scale bars = 10 µm.