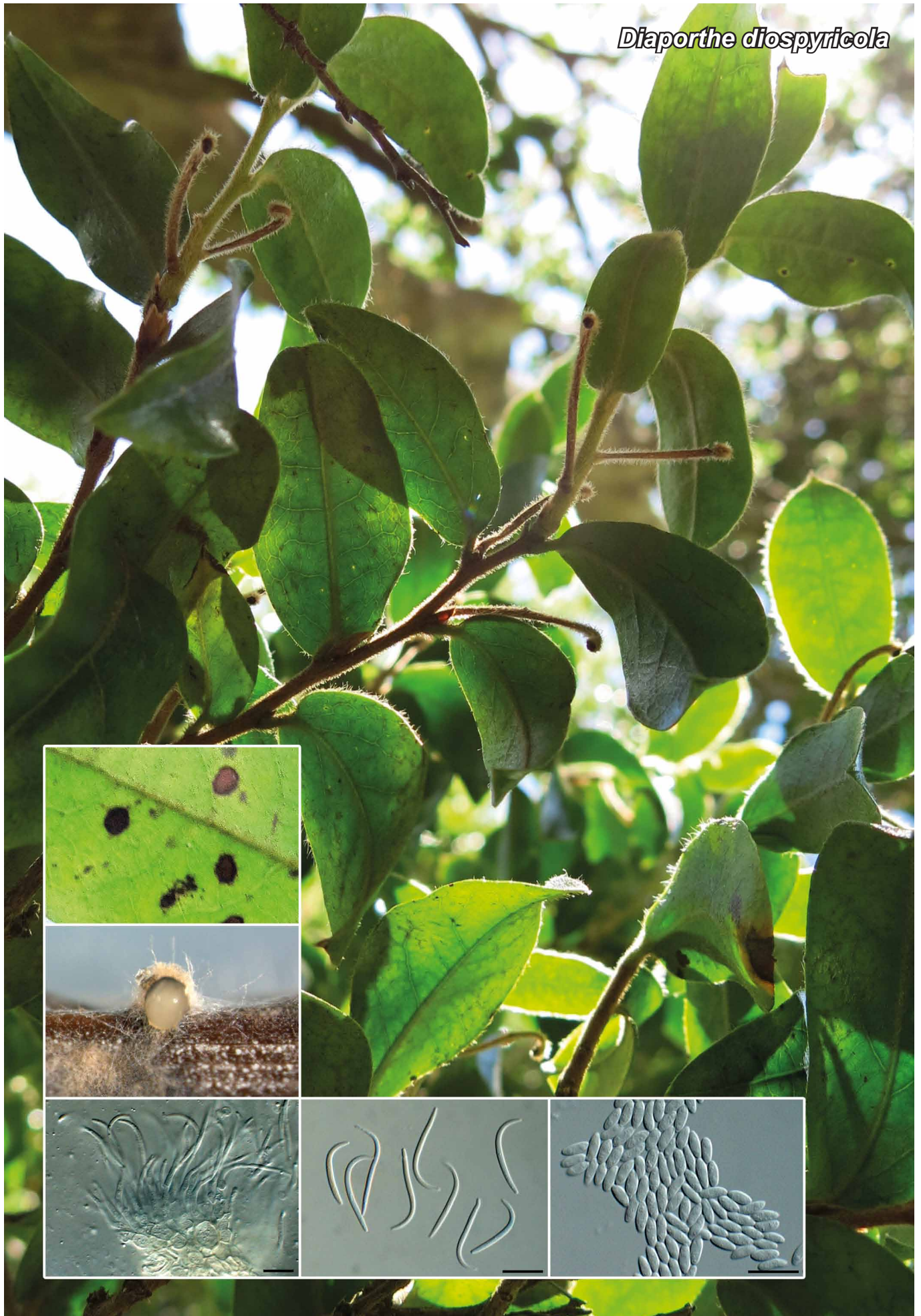


Diaporthe diospyricola



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Diaporthe diospyricola Crous, sp. nov.

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

On PNA. *Conidiomata* pycnidial, globose, up to 400 µm diam, black, erumpent, exuding creamy conidial droplets from central ostioles; walls of 3–6 layers of medium brown *textura angularis*. *Conidiophores* hyaline, smooth, 2–4-septate, branched, densely aggregated, cylindrical, straight to sinuous, 20–50 × 2.5–4 µm. *Conidiogenous cells* 7–15 × 1.5–2.5 µm, phialidic, cylindrical, terminal and lateral, with slight taper towards apex, 1–1.5 µm diam, with visible periclinal thickening; collarette not observed. *Paraphyses* not observed. *Alpha conidia* aseptate, hyaline, smooth, guttulate, fusoid-ellipsoid, tapering towards both ends, straight, apex subobtusate, base subtruncate, (5.5–) 6–7(–7.5) × (2–)2.5(–3) µm. *Gamma conidia* not observed. *Beta conidia* spindle-shaped, aseptate, smooth, hyaline, apex acutely rounded, base truncate, tapering from lower third towards apex, curved, (18–)25–27(–30) × 1.5(–2) µm.

Culture characteristics — Colonies covering dish in 2 wk with sparse aerial mycelium. On OA surface dirty white; on MEA centre iron-grey, outer region dirty white, reverse iron-grey in centre, outer region apricot; on PDA surface ochreous, reverse saffron.

Typus. SOUTH AFRICA, Western Cape Province, Kirstenbosch Botanical Garden, on leaves of *Diospyros whyteana* (*Ebenaceae*), 30 July 2012, P.W. Crous (holotype CBS H-21450, culture ex-type CPC 21170, 21169 = CBS 136552, ITS sequence GenBank KF777156, LSU sequence GenBank KF777209, MycoBank MB805856).

Notes — Morphologically *D. diospyricola* has shorter and wider conidia than *P. diospyri* (Sacc.) Traverso & Spessa (conidia 7–8 × 2 µm), and its homonyms, *P. diospyri* Zerova (conidia 7.2–9 × 2.1–2.9 µm), *P. diospyri* Grove (conidia 8–10 × 2 µm) and *P. diospyri* Bongini (conidia 6–7 × 3.5 µm) (Uecker 1988). *Diaporthe diospyricola* is also phylogenetically distinct from *D. foeniculaceae* (= *D. diospyri*, CBS 287.56; Gomes et al. 2013).

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the LSU sequence are *Diaporthe oncostoma* (GenBank AF408353; Identities = 852/853 (99 %), no gaps), *D. eres* (GenBank AF362565; Identities = 851/853 (99 %), no gaps) and *D. canthii* (GenBank JX069848; Identities = 844/845 (99 %), no gaps). Closest hits using the ITS sequence had highest similarity to *Phomopsis sophorae* (GenBank JQ694110; Identities = 589/608 (97 %), Gaps = 6/608 (0 %)), *D. chamaeropis* (GenBank KC343049; Identities = 557/576 (97 %), Gaps = 5/576 (0 %)) and *D. neotheicola* (GenBank KC145902; Identities = 583/607 (96 %), Gaps = 9/607 (1 %)).

Colour illustrations. Leaves of *Diospyros whyteana* in Kirstenbosch Botanical Garden, South Africa; conidioma on PNA; beta and alpha conidia. Scale bars = 10 µm.