

Diaporthe maytenicola



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Diaporthe maytenicola Crous, sp. nov.

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

On PNA. *Conidiomata* pycnidial, globose, up to 250 µm diam, black, erumpent, exuding creamy-white conidial droplets from central ostioles; walls of 3–6 layers of medium brown *textura angularis*. *Conidiophores* hyaline, smooth, 1–3-septate, branched, densely aggregated, cylindrical, straight to sinuous, 20–40 × 2–3 µm. *Conidiogenous cells* 10–20 × 1.5–2 µm, phialidic, cylindrical, terminal and lateral, with slight taper towards apex, 1–1.5 µm diam, with visible periclinal thickening; collarette flared, up to 2 µm long when present. *Paraphyses* not observed. *Alpha conidia* aseptate, hyaline, smooth, guttulate, fusoid-ellipsoid, tapering towards both ends, straight, apex subobtuse, base subtruncate, (7–)9–10(–12) × (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, 17–25 × 1.5(–2) µm.

Culture characteristics — Colonies covering dish within 2 wk, with sparse aerial mycelium. On PDA surface amber, reverse ochreous; on OA surface dirty white; on MEA surface ochreous, reverse ochreous with patches of umber due to sporulation.

Typus. SOUTH AFRICA, Western Cape Province, Kirstenbosch Botanical Garden, on leaves of *Maytenus acuminata* var. *acuminata* (Celastraceae), 29 Dec. 2012, P.W. Crous (holotype CBS H-21452, culture ex-type CPC 21896, 21897 = CBS 136441, ITS sequence GenBank KF777157, LSU sequence GenBank KF777210, TUB sequence GenBank KF777250, MycoBank MB805858).

Notes — Alpha conidia of *D. maytenicola* are larger than those of *D. mayteni* (5–7 × 2–3 µm), which was also recently described from *Maytenus ilicifolia* collected in Brazil (Gomes et al. 2013).

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the LSU sequence are *Diaporthe eres* (GenBank AF362565; Identities = 853/854 (99 %), no gaps), *Phomopsis vaccinii* (GenBank AF439630; Identities = 852/854 (99 %), no gaps) and *D. oncostoma* (GenBank AF408353; Identities = 852/854 (99 %), no gaps). Closest hits using the ITS sequence had highest similarity to *D. chamaeropsis* (GenBank KC343049; Identities = 562/572 (98 %), Gaps = 1/572 (0 %)), *D. neotheicola* (GenBank KC143192; Identities = 516/528 (98 %), Gaps = 2/528 (0 %)) and *D. elaeagni* (GenBank KC343064; Identities = 559/574 (97 %), Gaps = 3/574 (0 %)). Closest hits using the TUB sequence had highest similarity to *D. foeniculacea* (GenBank KC344069; Identities = 656/687 (95 %), Gaps = 3/687 (0 %)), *D. chamaeropsis* (GenBank KC344017; Identities = 656/687 (95 %), Gaps = 3/687 (0 %)) and *D. oncostoma* (GenBank KC344128; Identities = 654/690 (95 %), Gaps = 7/690 (1 %)).

Colour illustrations. *Maytenus acuminata* var. *acuminata* in Kirstenbosch Botanical Garden, South Africa; conidiomata on PNA; conidiogenous cells and alpha conidia. Scale bars = 10 µm.