

Diaporthe acaciarum



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***Diaporthe acaciarium* Crous & M.J. Wingf., sp. nov.**

Etymology. Name reflects the host genus *Acacia*, from which this species was isolated.

Sporulating on PNA. *Conidiomata* pycnidial, globose, up to 300 µm diam, black, erumpent, exuding creamy conidial droplets from central ostioles; walls consisting of 3–6 layers of medium brown *textura angularis*. *Conidiophores* hyaline, smooth, 2–3-septate, branched, densely aggregated, cylindrical, straight to sinuous, 20–30 × 2.5–4 µm. *Conidiogenous cells* 15–25 × 2–3 µm, phialidic, cylindrical, terminal and intercalary, with slight apical taper, 1–1.5 µm diam, with visible periclinal thickening; collarette not flared, up to 2 µm long. *Paraphyses* not observed. *Alpha conidia* (6–)6.5–7(–7.5) × (2–)2.5(–3) µm, aseptate, hyaline, smooth, bi-guttulate, fusoid-ellipsoid, tapering towards both ends, straight apex subobtuse, base subtruncate, 1 µm diam. *Beta conidia* spindle-shaped, aseptate, smooth, hyaline, apex acutely rounded, base truncate, tapering from the lower third towards the base, (20–)25–35(–40) × 1.5(–2) µm.

Culture characteristics — Colonies covering the dish after 2 wk at 25 °C in the dark, with sparse to moderate aerial mycelium. On MEA, PDA and OA surface dirty white with patches of grey-olivaceous, reverse dirty white with patches of sienna.

Typus. TANZANIA, Serengeti, on thorns of *Acacia tortilis* (*Fabaceae*), Feb. 2014, M.J. Wingfield (holotype CBS H-21994, culture ex-type CPC 24324 = CBS 138862; ITS sequence GenBank KP004460, LSU sequence GenBank KP004488, HIS sequence GenBank KP004504, TUB sequence GenBank KP004509, MycoBank MB810606).

Notes — No *Diaporthe* (incl. *Phomopsis*) species have been described from *Acacia tortilis* (Uecker 1988, Gomes et al. 2013). Phylogenetically, *D. acaciarium* is closely related to several species based on ITS (see below), but it can be distinguished from them based on TUB sequence data.

ITS. Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the ITS sequence are *Phomopsis chimonanthi* (GenBank KF746059; Identities = 505/513 (98 %), Gaps = 5/513 (0 %)), *Diaporthe helianthi* (GenBank JQ936257; Identities = 546/556 (98 %), Gaps = 1/556 (0 %)) and *Diaporthe infecunda* (GenBank KF939614; Identities = 525/536 (98 %), Gaps = 4/536 (0 %)).

LSU. Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the LSU sequence are *Diaporthe leucospermi* (GenBank JN712524; Identities = 836/839 (99 %), no gaps), *Taeniolella alta* (GenBank DQ377938; Identities = 834/839 (99 %), no gaps) and *Diaporthe arctii* (GenBank AF362562; Identities = 831/836 (99 %), no gaps).

HIS. Closest hits using the HIS sequence had highest similarity to *Diaporthe infecunda* (GenBank KC343613; Identities = 359/369 (97 %), Gaps = 1/369 (0 %)), *Diaporthe terebinthifolii* (GenBank KC343702; Identities = 353/371 (95 %), Gaps = 6/371 (1 %)) and *Diaporthe melonis* (GenBank KC343626; Identities = 351/373 (94 %), Gaps = 5/373 (1 %)).

TUB. Closest hits using the TUB sequence had highest similarity to *Diaporthe infecunda* (GenBank KF939619; Identities = 753/783 (96 %), Gaps = 4/783 (0 %)), *Diaporthe beilharziae* (GenBank KF170921; Identities = 743/777 (96 %), Gaps = 1/777 (0 %)) and *Diaporthe terebinthifolii* (GenBank KC344186; Identities = 662/708 (94 %), Gaps = 1/708 (0 %)).

Colour illustrations. Leopard in *Acacia tortilis* tree in the Serengeti, Tanzania; conidiomata on PNA, conidiogenous cells, alpha and beta conidia. Scale bars = 10 µm.

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