

*Diaporthe isoberliniae*



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

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

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, 2–3-septate, branched, densely aggregated, cylindrical, straight to sinuous, 15–40 × 3–4 µm. *Conidiogenous cells* 10–14 × 2.5–3 µm, phialidic, cylindrical, terminal and lateral, with slight taper towards apex, 1 µm diam, with visible periclinal thickening; collarette flared, up to 4 µm long. *Paraphyses* not observed. *Alpha conidia* aseptate, hyaline, smooth, guttulate, fusoid-ellipsoid, tapering towards both ends, straight, apex subobtuse, base subtruncate, (6.5–)8–9(–10) × (2.5–)3(–3.5) µm. *Gamma conidia* not observed. *Beta conidia* not observed.

*Culture characteristics* — Colonies covering the dish within 2 wk at 22 °C, spreading, with moderate aerial mycelium. On PDA surface smoke-grey, with patches of dirty white, reverse olivaceous-grey. On OA surface dirty white. On MEA surface dirty white, reverse olivaceous-grey.

*Typus.* ZAMBIA, B&B13467, on *Isoberlinia angolensis* (*Fabaceae*), 23 Feb. 2013, M. van der Bank (holotype CBS H-21693, culture ex-type CPC 22549 = CBS 137981; ITS sequence GenBank KJ869133, LSU sequence GenBank KJ869190, TUB sequence GenBank KJ869245, MycoBank MB808909).

*Notes* — Presently there are no known species of *Diaporthe* (incl. *Phomopsis*) that have been described from *Isoberlinia*. Furthermore, *D. isoberliniae* also appears to be phylogenetically distinct from the species presently accommodated in GenBank, being most similar to sequences of *D. foeniculacea*, *P. theicola* and *D. neotheicola*.

*ITS.* Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the ITS sequence are *Diaporthe foeniculacea* (GenBank KC343103; Identities = 541/558 (97 %), Gaps = 6/558 (1 %)), *Phomopsis theicola* (GenBank HE774477; Identities = 534/551 (97 %), Gaps = 6/551 (1 %)) and *Diaporthe neotheicola* (GenBank KC145914; Identities = 561/579 (97 %), Gaps = 6/579 (1 %)).

*LSU.* Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the LSU sequence are *Phomopsis columnaris* (GenBank AF439627; Identities = 826/836 (99 %), no gaps), *Diaporthe eres* (GenBank AF362565; Identities = 826/836 (99 %), no gaps) and *Phomopsis vaccinii* (GenBank AF439630; Identities = 825/836 (99 %), no gaps).

*TUB.* Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the TUB sequence are *Diaporthe maytenicola* (GenBank KF777250; Identities = 693/739 (94 %), Gaps = 9/739 (1 %)), *Diaporthe hickoriae* (GenBank KC344086; Identities = 649/693 (94 %), Gaps = 1/693 (0 %)) and *Diaporthe stictica* (GenBank KC344180; Identities = 650/695 (94 %), Gaps = 6/695 (0 %)).

*Colour illustrations.* *Isoberlinia angolensis* in Zambia (photo: Mike Bingham); conidiomata, conidiophores and conidia in culture. Scale bars = 10 µm.

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