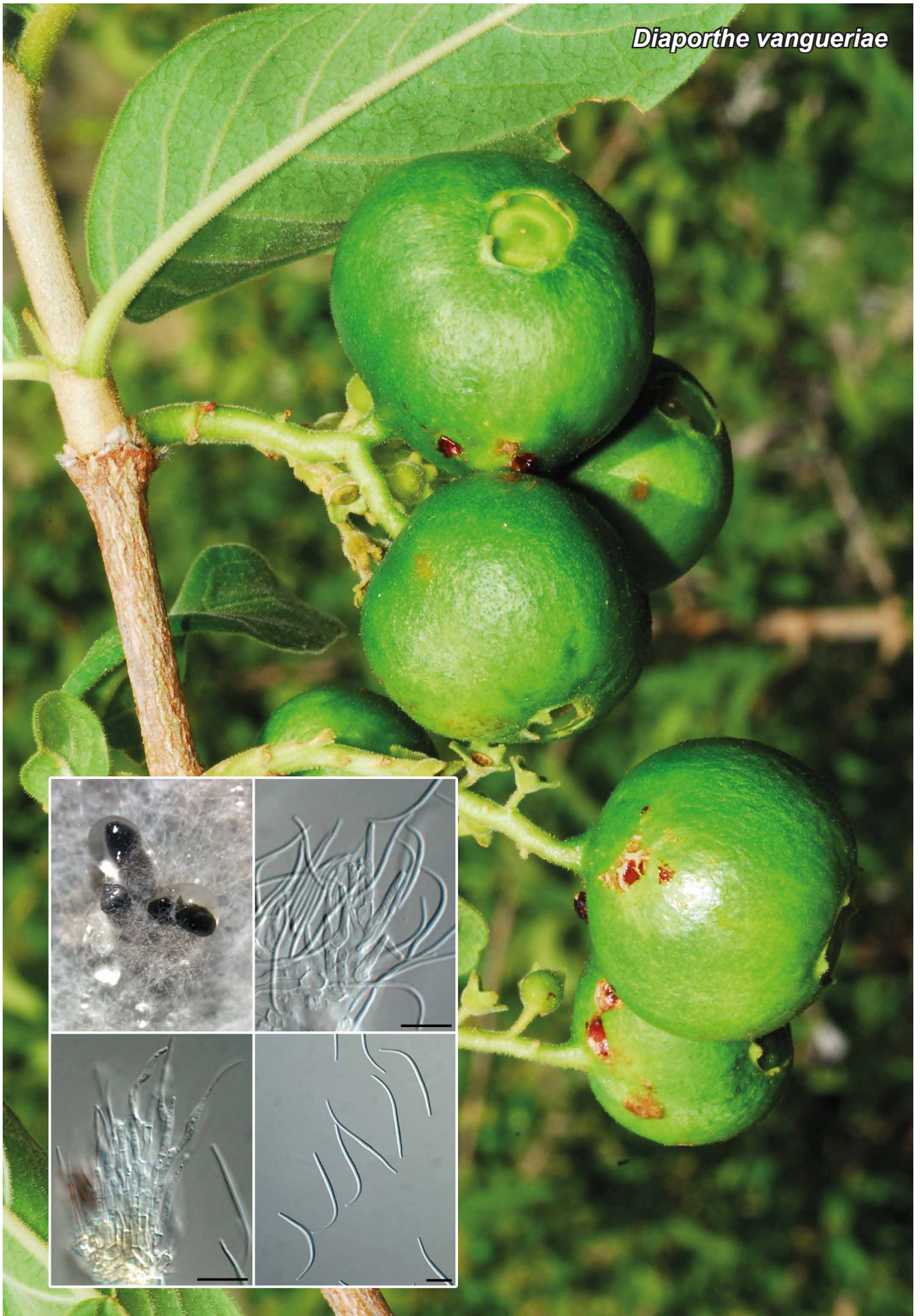


Diaporthe vangeriae



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Diaporthe vangueriae Crous, sp. nov.

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

On OA, sporulating poorly. *Conidiomata* pycnidial, globose, up to 350 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, 20–30 × 2.5–4 µm. *Conidiogenous cells* 15–20 × 2–3 µm, phialidic, cylindrical, terminal and lateral, with slight taper towards apex, 1–1.5 µm diam, with visible periclinal thickening; collarette not flared, up to 2 µm long. *Paraphyses* subcylindrical, septate, dispersed among conidiophores, up to 50 µm long, 2–3 µm diam. *Alpha conidia* not observed. *Gamma conidia* not observed. *Beta conidia* spindle-shaped, aseptate, smooth, hyaline, apex acutely rounded, base truncate, tapering from the lower third towards the apex, (20–)28–35(–40) × 1.5(–2) µm.

Culture characteristics — Colonies covering the dish in 2 wk at 22 °C, with moderate aerial mycelium. On PDA surface honey, reverse honey with border of isabelline. On OA surface buff, with olivaceous-grey conidiomata. On MEA surface buff, reverse brick, with patches of isabelline.

Typus. ZAMBIA, S16°27.627' E27°31.775', on twigs of *Vangueria infausta* (*Rubiaceae*), 20 Feb. 2012, M. van der Bank (holotype CBS H-21697, culture ex-type CPC 22703 = CBS 137985; ITS sequence GenBank KJ869137, LSU sequence GenBank KJ869194, TUB sequence GenBank KJ869247, MycoBank MB808916).

Notes — As far as we could establish, no species of *Diaporthe* (incl. *Phomopsis*) are presently known from *Vangueria*. Furthermore, *D. vangueriae* appears to be phylogenetically distinct from the taxa presently accommodated in GenBank, and is therefore introduced as a novel species, being closely related to *D. inconspicua*, *D. anacardii* and *D. neotheicola*.

ITS. Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the ITS sequence are *Diaporthe inconspicua* (GenBank KC343125; Identities = 558/569 (98 %), Gaps = 3/569 (0 %)), *Diaporthe anacardii* (GenBank KC343024; Identities = 557/569 (98 %), Gaps = 3/569 (0 %)) and *Diaporthe neotheicola* (GenBank KC145897; Identities = 571/585 (98 %), Gaps = 4/585 (0 %)).

LSU. Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the LSU sequence are *Diaporthe maytenicola* (GenBank KF777210; Identities = 821/822 (99 %), no gaps), *Diaporthe canthii* (GenBank JX069848; Identities = 821/822 (99 %), no gaps) and *Diaporthe diospyricola* (GenBank KF777209; Identities = 820/822 (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 = 716/731 (98 %), no gaps), *Diaporthe oncostoma* (GenBank KC344129; Identities = 659/691 (95 %), Gaps = 7/691 (1 %)) and *Diaporthe foeniculacea* (GenBank KC344070; Identities = 655/688 (95 %), Gaps = 3/688 (0 %)).

Colour illustrations. *Vangueria infausta* in Zambia (photo: Olivier Maurin); conidiomata, conidiophores and beta conidia in culture. Scale bars = 10 µm.

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