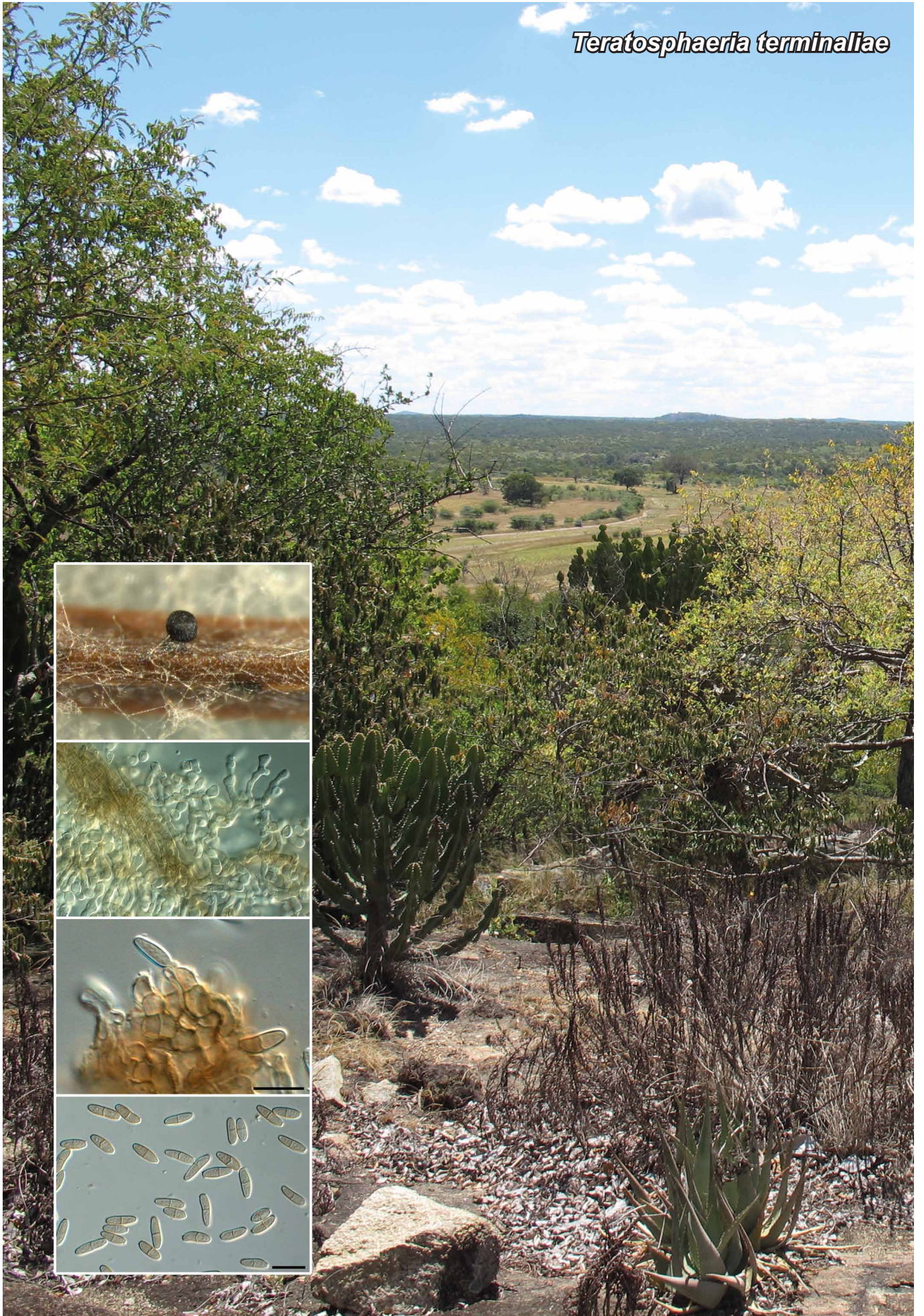


Teratosphaeria terminaliae



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Teratosphaeria terminaliae Crous & Jol. Roux, *sp. nov.*

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

On PNA. *Conidiomata* uniloculate, pycnidial, immersed, globose, dark brown to black, up to 200 µm diam with central ostiole; wall of 3–6 layers of brown *textura angularis*. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* lining the inner cavity, brown, verruculose, ampulliform to dolii-form, proliferating several times percurrently near apex, 4–8 × 3–5 µm. *Conidia* (8–)10–14(–22) × (2.5–)3(–4) µm, brown, smooth, guttulate, subcylindrical to obclavate, apex obtuse to subobtuse, widest in middle in small conidia, or in middle of basal cell in larger conidia, (0–)1–2(–4)-septate; base truncate, 1.5 µm diam with minute marginal frill when present.

Culture characteristics — Colonies reaching 60 mm diam after 2 wk with sparse to moderate aerial mycelium and even, lobed margins. On PDA surface and reverse iron-grey; on MEA surface olivaceous-grey, reverse iron-grey; on OA surface olivaceous-grey with patches of dirty white.

Typus. ZIMBABWE, 60 km from Zwivashane, Filabussi village, on leaves of *Terminalia cericea* (*Combretaceae*), 27 Mar. 2012, J. Roux & L. Jimu (holotype CBS H-21437, culture ex-type CPC 21175, 21176 = CBS 136428, ITS sequence GenBank KF777189, LSU sequence GenBank KF777240, MycoBank MB805842).

Notes — Presently no species of *Teratosphaeria* are known from *Terminalia*. Based on DNA sequence data it shares 98 % similarity (ITS) with *T. macowanii*. *Teratosphaeria macowanii* is a pathogen that attacks *Protea* spp. in South Africa and Malawi (Crous et al. 2013b), and is distinct in its superficial conidiomata, and sooty appearance on infected leaves.

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the LSU sequence are *Teratosphaeria macowanii* (GenBank EU019254; Identities = 873/878 (99 %), no gaps), *T. maxii* (GenBank DQ885898; Identities = 873/878 (99 %), no gaps) and *Colletogloeopsis dimorpha* (GenBank DQ923528; Identities = 869/878 (99 %), no gaps). Closest hits using the ITS sequence had highest similarity to *T. macowanii* (GenBank EU707894; Identities = 631/647 (98 %), Gaps = 3/647 (0 %)), *T. wingfieldii* (GenBank EU707896; Identities = 628/646 (97 %), Gaps = 2/646 (0 %)) and *T. maxii* (GenBank EU707869; Identities = 628/646 (97 %), Gaps = 2/646 (0 %)).

Colour illustrations. Filabussi village, Zimbabwe; conidioma on PNA; mycelium; conidiogenous cells and conidia. Scale bars = 10 µm.

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