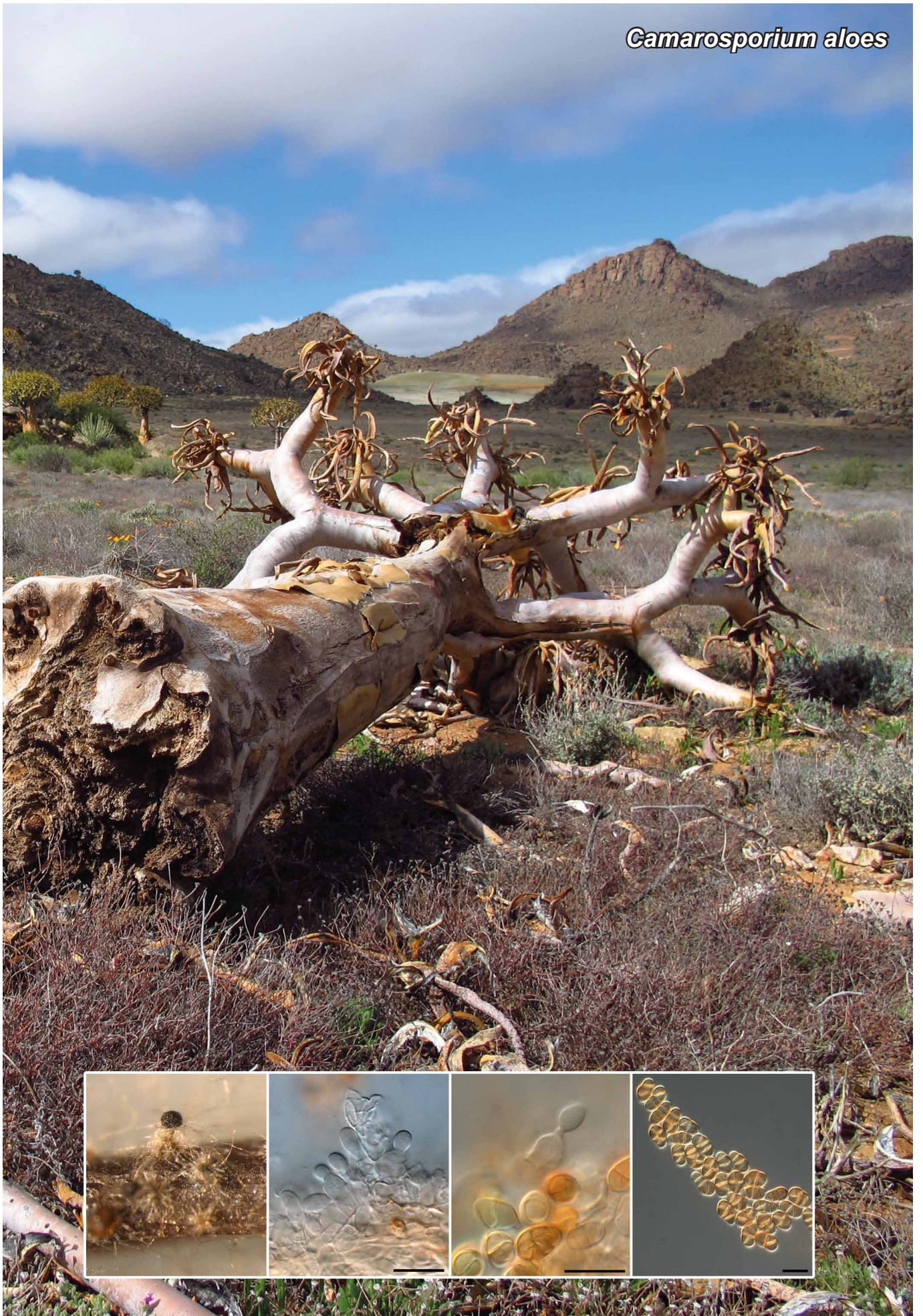


Camarosporium aloes



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Camarosporium aloes Crous & M.J. Wingf., *sp. nov.*

Etymology. Named after the host genus from which it was isolated, *Aloe*.

Conidiomata erumpent, brown, globose, pycnidial with central ostiole, up to 250 µm diam; wall of 3–6 layers of brown *textura angularis*. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* lining the inner cavity, hyaline, smooth, ampulliform to doliiform, 5–10 × 4–5 µm; apex with several inconspicuous percurrent proliferations. *Conidia* solitary, initially hyaline, smooth, aseptate, ellipsoid, becoming subcylindrical to clavate or obovoid with 3 transverse eusepta, developing vertical and oblique septa, constricted at median septum or not, apex obtuse, base bluntly rounded to truncate, (9–)11–13(–14) × (4–)6–7(–8) µm.

Culture characteristics — Colonies flat, spreading, with sparse aerial mycelium and smooth, even margins, reaching 50 mm diam after 2 wk. On MEA surface olivaceous-grey with patches of iron-grey, reverse iron-grey; on OA surface isabelline with patches of cinnamon.

Typus. SOUTH AFRICA, Western Cape Province, Clanwilliam, on dark lesions on dead bark of *Aloe dichotoma* (*Xanthorrhoeaceae*), Sept. 2012, M.J. Wingfield (holotype CBS H-21446, culture ex-type CPC 21572 = CBS 136437, ITS sequence GenBank KF777142, LSU sequence GenBank KF777198, MycoBank MB805852).

Notes — As far as we could determine, no species of *Camarosporium* have been named on *Aloe*. Ramaley & Barr (1995) described several species from 'Agavaceae' (= *Asparagaceae*). None of these taxa, however, have conidia small enough to compare with those of *C. aloes*.

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the LSU sequence are *Camarosporium quaternatum* (GenBank DQ377884; Identities = 859/863 (99 %), Gaps = 1/863 (0 %)), *Herpotrichia parasitica* (GenBank GQ387617; Identities = 846/853 (99 %), no gaps) and *Coniothyrium telephii* (GenBank GQ387599; Identities = 846/853 (99 %), no gaps). Closest hits using the ITS sequence had highest similarity to *Trametes ochracea* (GenBank KC292372; Identities = 470/494 (95 %), Gaps = 4/494 (0 %)), *Ochrocladosporium frigidarii* (GenBank EU040234; Identities = 469/494 (95 %), Gaps = 4/494 (0 %)) and *Coniothyrium carteri* (GenBank KF251209; Identities = 534/563 (95 %), Gaps = 4/563 (0 %)).

Colour illustrations. Dead *Aloe dichotoma*, Clanwilliam, South Africa. Conidioma on PNA; conidiogenous cells; conidia. Scale bars = 10 µm.

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