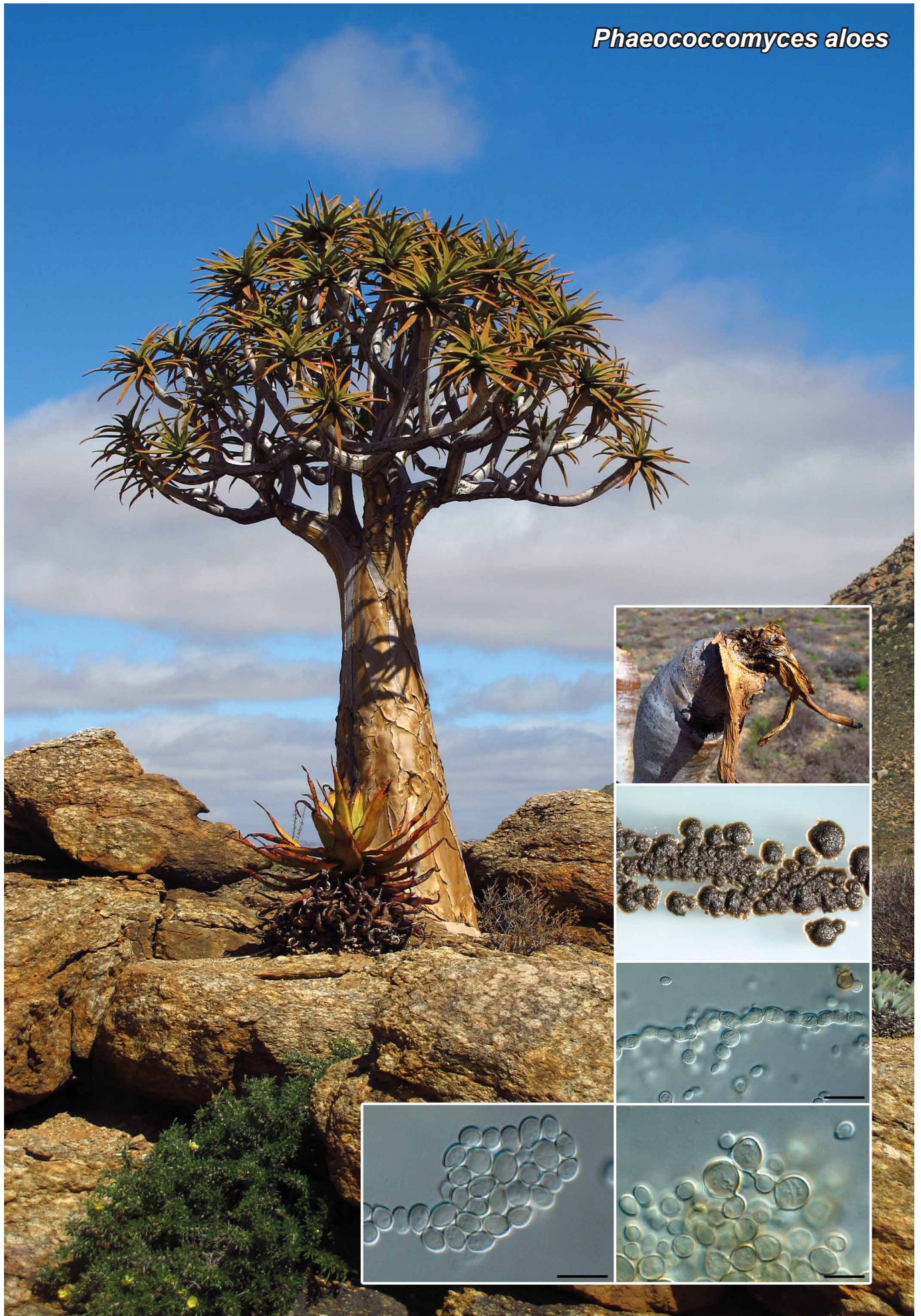


Phaeococcomyces aloes



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

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

Colonies lacking mycelium but consisting of a globular mass of chlamydospore-like cells; cells aseptate, brown (hyaline when young), 3–7 µm diam, covered in mucus, globose, thin-walled, remaining attached to one another through younger end cells at colony margin, which detach during slide preparation; ellipsoid to globose, hyaline, thin-walled, covered in mucus, smooth, 4–7 × 3.5–6.5 µm.

Culture characteristics — Colonies reaching 7 mm diam after 2 wk, lacking aerial mycelium, erumpent with smooth, lobate margins; surface and reverse on OA, MEA and PDA iron-grey.

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-21441, culture ex-type CPC 21873 = CBS 136431, ITS sequence GenBank KF777182, LSU sequence GenBank KF777234, MycoBank MB805846).

Notes — Although traditionally regarded as a genus associated with phaeohyphomycosis of humans, species of *Phaeococcomyces* are commonly isolated from a range of substrates including leaves, twigs and even rocks. The genus *Phaeococcomyces* presently contains six species. When compared to these taxa, conidia of *Phaeococcomyces aloes* are larger than those of *P. eucalypti* (conidia 3–5 × 2.5–5 µm; Crous et al. 2012a), but more similar to that of *P. nigricans* (conidia globose to broadly ellipsoidal, 4–6.5 × 4–5 µm; de Hoog 1979).

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the LSU sequence are *Phaeococcomyces catenatus* (GenBank AF050277; Identities = 884/886 (99 %), no gaps), *Exophiala placitae* (GenBank EU040215; Identities = 880/882 (99 %), no gaps) and *Sarcinomyces petricola* (GenBank FJ358249; Identities = 871/873 (99 %), no gaps). Closest hits using the ITS sequence had highest similarity to *E. placitae* (GenBank EU040215; Identities = 631/653 (97 %), Gaps = 7/653 (1 %)), *P. catenatus* (GenBank AF050277; Identities = 569/584 (97 %), Gaps = 5/584 (0 %)) and *Cladophialophora proteae* (GenBank FJ372388; Identities = 487/591 (82 %), Gaps = 40/591 (6 %)).

Colour illustrations. *Aloe dichotoma* in Clanwilliam, South Africa; colonies on SNA; ellipsoid to globose conidia remaining attached to one another. Scale bars = 10 µm.

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