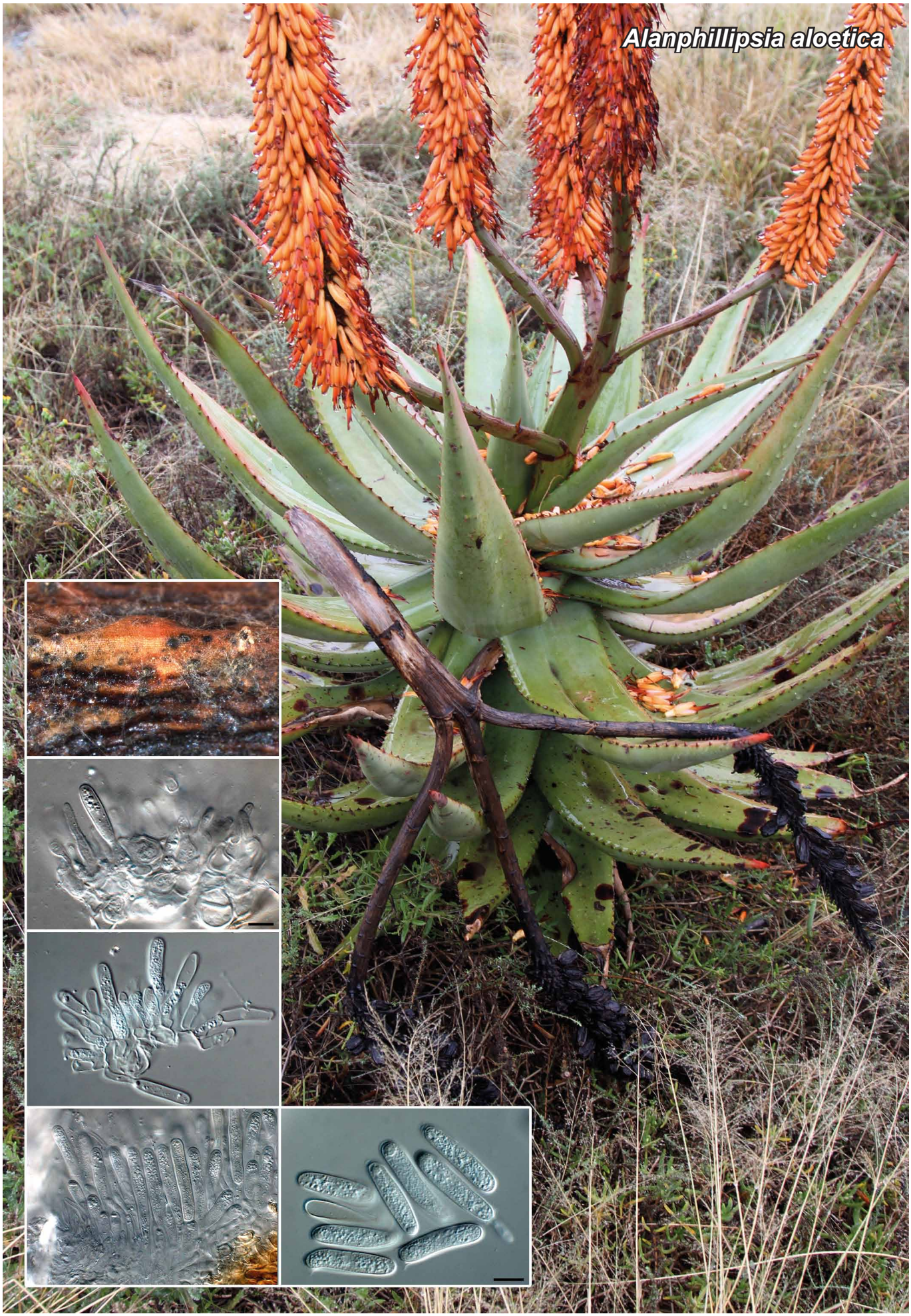
Alanphillipsia aloetica

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Alanphillipsia aloetica Crous, *sp. nov.*

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

Conidiomata erumpent in agar, globose, up to 400 µm diam, opening by means of a central ostiole, but appearing like a longitudinal rupture when mature, exuding a pale crystalline conidial mass; wall of 3–6 layers of *textura angularis*. *Conidiophores* reduced to conidiogenous cells, or a supporting cell. *Conidiogenous cells* lining the inner cavity, ampulliform to subcylindrical, hyaline, smooth, 10–20 × 4–5 µm, proliferating percurrently near apex. *Paraphyses* intermingled among conidiogenous cells, hyaline, smooth, subcylindrical, 30–60 × 3–5 µm, aseptate. *Conidia* hyaline, becoming pale brown at maturity, smooth, subcylindrical, granular, apex obtuse, base truncate, 3–4 µm diam, aseptate, (20–)30–33(–35) × (5–)6(–7) µm, encased in mucilaginous sheath, with long basal marginal flared appendage, 1–6 µm long.

Culture characteristics — Colonies after 2 wk on OA and PDA covering the dish, reaching 65 mm diam on MEA; aerial mycelium sparse, margins even, lobate. On MEA surface olivaceous-grey with iron-grey margins; reverse iron-grey. On PDA surface and reverse iron-grey. On OA surface iron-grey with pale olivaceous-grey aerial mycelium.

Typus. South Africa, Eastern Cape, Uitenhage, on *Aloe* sp. (*Xanthorrhoeaceae*), 14 July 2012, *P.W. Crous* (holotype CBS H-21420, culture ex-type CPC 21110, 21109 = CBS 136409, ITS sequence GenBank KF777139, LSU sequence GenBank KF777195, MycoBank MB805819).

Notes — *Alanphillipsia aloetica* is phylogenetically closely related to *A. aloeigena* (ITS: Identities = 689/693 (99 %), Gaps = 2/693 (0 %)), but morphologically distinct in that conidiomata frequently open by what appears to be a longitudinal slit, paraphyses can be present, and conidia are shorter and wider than those of *P. aloes*, (25–)28–38(–50) × (6–)7–8(–10) µm.

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the LSU sequence are *Diplodia corticola* (GenBank DQ377848; Identities = 852/ 859 (99 %), no gaps), *Botryosphaeria sumachi* (GenBank DQ377865; Identities = 870/878 (99 %), no gaps) and *Diplodia rosulata* (GenBank DQ377897; Identities = 869/878 (99 %), no gaps). Closest hits using the ITS sequence had highest similarity to *Phaeobotryosphaeria eucalypti* (GenBank JX646803; Identities = 512/533 (96 %), Gaps = 9/533 (1 %)), *P. citrigena* (GenBank EU673329; Identities = 534/556 (96 %), Gaps = 8/556 (1 %)) and *P. porosa* (GenBank AY343378; Identities = 474/495 (96 %), Gaps = 10/495 (2 %)).

Colour illustrations. Aloe sp. growing in Uitenhage, South Africa. Conidiomata on leaf; conidiogenous cells and conidia. Scale bars = 10 µm.

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