

Phoma aloes



Fungal Planet 183 – 26 November 2013

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

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

Conidiomata pycnidial, erumpent, globose, up to 180 µm diam, brown, with central ostiole; wall of 3–6 layers of brown *textura angularis*. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* hyaline, smooth, ampulliform to doliiform, 5–7 × 3–4 µm; apex with minute periclinal thickening. *Conidia* dimorphic. *Macroconidia* ellipsoid, medium brown, smooth, medianly (0–)1-septate, widest at septum, apex subobtuse, tapering towards truncate base, (7–)8(–9) × (3–)4 µm. *Microconidia* subcylindrical, straight to slightly curved, ends obtuse, aseptate, hyaline, becoming pale brown, 4–7 × 2–2.5 µm.

Culture characteristics — Colonies reaching 50–60 mm diam after 2 wk on MEA and OA, with moderate aerial mycelium and even, smooth margins; on PDA only reaching 20 mm diam after 2 wk, and margins feathery. On MEA surface pale olivaceous-grey, reverse iron-grey; on PDA surface umber, reverse chestnut; on OA surface olivaceous-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-21442, cultures ex-type CPC 21549 = CBS 136432, ITS sequence GenBank KF777183, LSU sequence GenBank KF777235, MycoBank MB805847).

Notes — *Phoma aloes* can be distinguished from two other similar taxa that have been described from this host based on the size of its conidia. Conidia of *Macrophoma aloes* are larger, 14.8 × 6.4 µm, while those of *Phoma aloicola* are again somewhat smaller, 4.5–7 × 2–4.5 µm.

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the LSU sequence are *Phoma cladoniicola* (GenBank JQ238625; Identities = 910/914 (99 %), no gaps), *Phaeosphaeria avenaria* f. sp. *avenaria* (GenBank EU223257; Identities = 908/914 (99 %), Gaps = 1/914 (0 %)) and *Phaeosphaeriopsis musae* (GenBank DQ885894; Identities = 907/914 (99 %), no gaps). Closest hits using the ITS sequence are *Phoma foliaceiphila* (GenBank JQ318008; Identities = 559/587 (95 %), Gaps = 3/587 (0 %)), *Sclerococcum parmeliae* (GenBank JQ342180; Identities = 556/584 (95 %), Gaps = 3/584 (0 %)) and *Phoma cladoniicola* (GenBank JQ238629; Identities = 561/591 (95 %), Gaps = 4/591 (0 %)).

Colour illustrations. *Aloe dichotoma* in Clanwilliam, South Africa; conidiomata on PDA; conidiogenous cells, young and mature conidia. Scale bars = 10 µm.

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