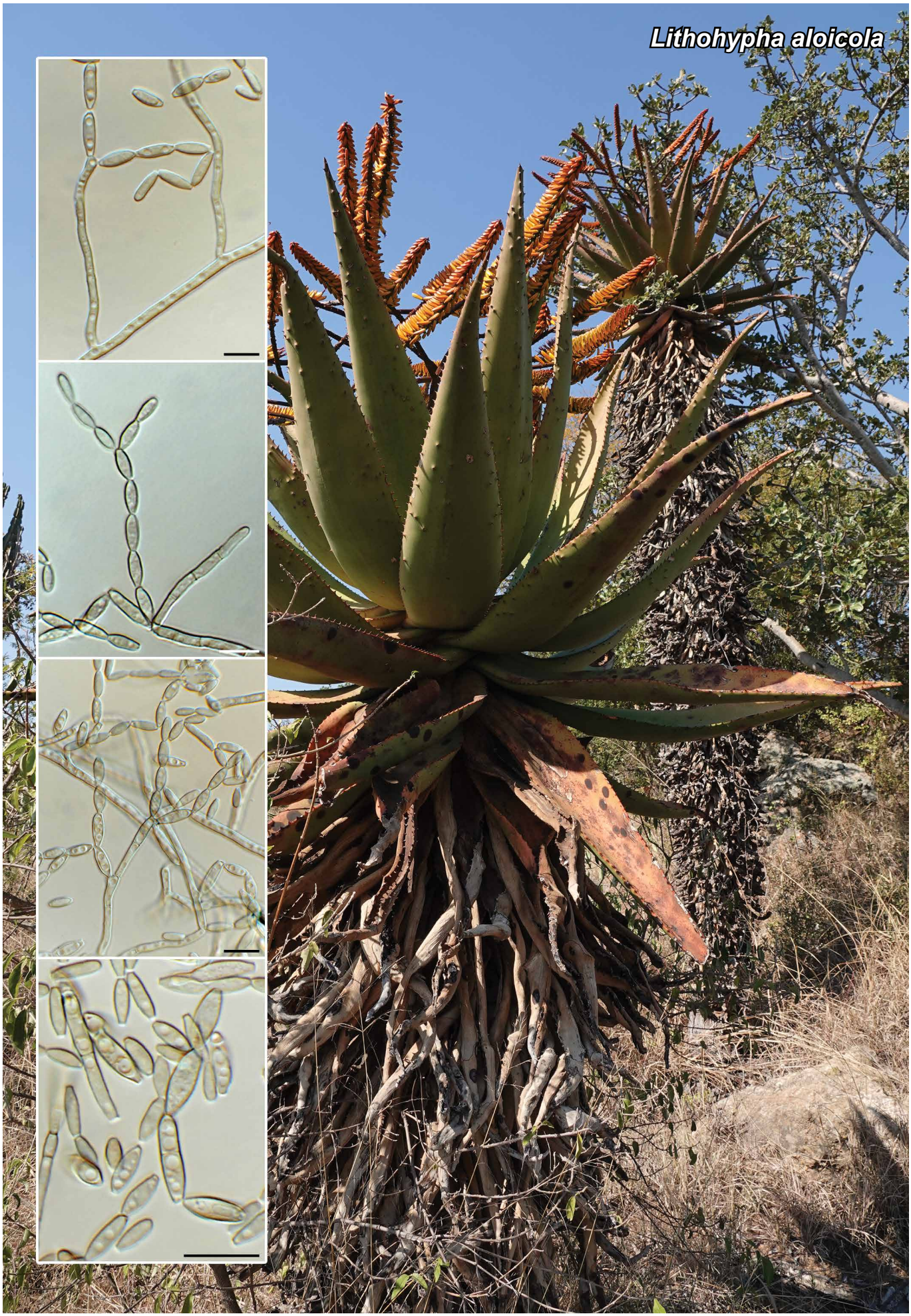
Lithohypha aloicola

Fungal Planet 957 – 18 December 2019

Lithohypha aloicola Crous, *sp. nov.*

Etymology. Name refers to the host genus *Aloe* from which it was isolated.

Classification — *Trichomeriaceae*, *Chaetothyriales*, *Eurotiomycetes.*

Mycelium consisting of smooth, pale brown, branched, septate, 2–2.5 µm diam hyphae. *Conidiophores* reduced to conidiogenous loci on hyphae. *Conidiogenous cells* pale brown, smooth, 6–10 µm long, with truncate locus, 1 µm diam, not thickened nor darkened. *Conidia* ramoconidia 10–13 × 2.5–3 µm; terminal conidia occurring in branched chains, (6–)7–9(–10) × 2.5–3 µm; hila not thickened nor darkened.

Culture characteristics — Colonies flat, spreading, with moderate aerial mycelium and smooth, lobate margin, reaching 10 mm diam after 2 wk at 25 °C. On MEA, PDA and OA surface mouse grey, reverse dark mouse grey.

Typus. South Africa, Limpopo Province, Tzaneen, on leaves of *Aloe* sp. (*Asphodelaceae*), 2010, *P.W. Crous*, HPC 2481 (holotype CBS H-24159, culture ex-type CPC 35996 = CBS 146070, ITS, LSU, *rpb1*, *tef1* and *tub2* sequences GenBank MN562103.1, MN567611.1, MN556797.1, MN556829.1 and MN556837.1, MycoBank MB832862).

Notes — *Lithohypha* (as *Lithophila*) was introduced by Isola et al. (2016) for a fungus growing on marble stone in Italy. Other than the dark brown hyphae with enteroblastic conidiation, it lacked any visible morphology. *Lithohypha aloicola* is closely related to *L. guttulata*, but quite distinct morphologically, producing conidia arranged in chains, and occurring on leaves of *Aloe* in South Africa. Of interest is the fact that both substrates could be regarded as extreme environments.

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Lithophila guttulata* (as *Trichomeriaceae* sp. LS-2015c, strain CCFEE 5908, GenBank KP791770.1; Identities = 566/572 (99 %), 2 gaps (0 %)), *Bradymyces* sp. LS-2015b (strain CGMCC 3.16362, GenBank KP174849.1; Identities = 545/552 (99 %), 1 gap (0 %)), and *Knufia aspidiotus* (as *Knufia* sp. FH-2012, strain BJ01A17, GenBank JX843780.1; Identities = 406/461 (88 %), 18 gaps (3 %)). Closest hits using the **LSU** sequence are *Lithophila guttulata* (as *Trichomeriaceae* sp. LS-2015c, strain CCFEE 5884, GenBank KR781056.1; Identities = 855/855 (100 %), no gaps), *Bradymyces* sp. LS-2015b (strain CGMCC 3.17221, GenBank KP174952.1; Identities = 823/823 (100 %), no gaps), and *Neophaeococcomyces catenatus* (strain CBS 650.76, GenBank MH872793.1; Identities = 822/865 (95 %), 6 gaps (0 %)). Closest hits using the ***rpb1*** sequence had highest similarity to *Bradymyces* sp. LS-2015a (strain CGMCC 3.14008, GenBank KP226519.1; Identities = 447/632 (71 %), 14 gaps (2 %)), *Bradymyces graniticola* (strain CCF 5193, GenBank LT558716.1; Identities = 507/745 (68 %), 22 gaps (2 %)), and *Knufia peltigerae* (strain CGMCC 3.17283, GenBank KP226513.1; Identities = 312/436 (72 %), 7 gaps (1 %)). Closest hits using the ***tef1*** sequence had highest similarity to *Furfurella luteostiolata* (strain CE3, GenBank MK523302.1; Identities = 417/462 (90 %), 2 gaps (0 %)), *Gyrothrix inops* (strain BE108, GenBank KJ476974.1; Identities = 415/461 (90 %), no gaps), and *Gyrothrix ramosa* (strain MUCL 54061, GenBank KJ476975.1; Identities = 414/461 (90 %), no gaps). Closest hits using the ***tub2*** sequence had highest similarity to *Bradymyces* sp. LS-2015b (strain CGMCC 3.17221, GenBank KP226553.1; Identities = 216/222 (97 %), no gaps), *Arthrocladium caudatum* (strain CBS 457.67, GenBank LT558710.1; Identities = 347/451 (77 %), 32 gaps (7 %)), and *Aphanophora eugeniae* (strain CBS 124105, GenBank KC455221.1; Identities = 329/430 (77 %), 25 gaps (5 %)).

Colour illustrations. *Aloe* sp. *Lithophila aloicola* was isolated from. Conidiophores with conidiogenous cells; conidia. Scale bars = 10 µm.

Pedro W. Crous & Johannes Z. Groenewald, Westerdijk Fungal Biodiversity Institute, P.O. Box 85167, 3508 AD Utrecht, The Netherlands; e-mail: p.crous@wi.knaw.nl & e.groenewald@wi.knaw.nl
Michael J. Wingfield, Department of Biochemistry, Genetics and Microbiology, Forestry and Agricultural Biotechnology Institute (FABI), Faculty of Natural and Agricultural Sciences, University of Pretoria, Private Bag X20, Hatfield 0028, Pretoria, South Africa; e-mail: mike.wingfield@fabi.up.ac.za