

*Neoplatysporoides aloes*



Fungal Planet 961 – 18 December 2019

## *Neoplatysporoides aloes* Crous, sp. nov.

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

*Classification* — *Libertasomycetaceae*, *Pleosporales*, *Dothi-  
deomycetes*.

*Conidiomata* unilocular, separate, globose, immersed to erumpent, brown, 200–250 µm diam, opening via central ostiole, exuding a brown conidial mass; wall of 3–6 layers of brown *textura angularis*. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* lining inner cavity, hyaline, smooth, ampulliform to doliiform, 5–9 × 4–5 µm, with percurrent proliferation at apex. *Conidia* solitary, golden brown, subcylindrical to ellipsoid, straight to curved, 0–1-septate, apex obtuse, base truncate with longitudinal striations along the length of the conidium, (7–)8–9(–10) × (4–)4.5(–5) µm.

*Culture characteristics* — Colonies flat, spreading, with moderate aerial mycelium and feathery margin, reaching 50 mm diam after 2 wk at 25 °C. On MEA surface buff, reverse cinnamon. On PDA surface and reverse cinnamon. On OA surface honey.

*Typus.* SOUTH AFRICA, Limpopo Province, Tzaneen, on leaves of *Aloe* sp. (*Asphodelaceae*), 2010, P.W. Crous, HPC 2476 (holotype CBS H-24249, culture ex-type CPC 36068 = CBS 146054, ITS and LSU sequences GenBank MN562111.1 and MN567619.1, MycoBank MB832867).

*Additional material examined.* SOUTH AFRICA, Gauteng Province, Pretoria, University of Pretoria campus, on leaf of *Aloe* sp., 2010, P.W. Crous, HPC 2457, cultures CPC 35988 = CBS 146090, CPC 36060 = CBS 146053, ITS and LSU sequences GenBank MN562112.1–MN562113.1 and MN567620.1–MN567621.1.

*Notes* — *Neoplatysporoides aloes* is similar to *N. aloecicola* (on leaves of *Aloe* sp., Tanzania; conidia (8–)9–10(–12) × (4–)5(–6) µm; Crous et al. 2015b), but distinguished based on its slightly smaller conidia. *Neoplatysporoides* is presently only known from leaves of *Aloe* spp. occurring in Africa.

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the ITS sequence of CPC 36068 had highest similarity to *Neoplatysporoides aloecicola* (strain CBS 139901, GenBank NR\_154230.1; Identities = 544/564 (96 %), 2 gaps (0 %)), *Libertasomyces myopori* (strain CBS 141302, GenBank NR\_145200.1; Identities = 522/568 (92 %), 14 gaps (2 %)), and *Libertasomyces quercus* (strain CBS 134.97, GenBank NR\_155337.1; Identities = 513/559 (92 %), 11 gaps (1 %)). The ITS sequence of CPC 36068 is 99 % (558/564 bases, including 1 gap) similar to those of CPC 36060 and CPC 35988. Closest hits using the LSU sequence of CPC 36068 are *Neoplatysporoides aloecicola* (strain CBS 139901, GenBank MH878657.1; Identities = 853/858 (99 %), 3 gaps (0 %)), *Foliophoma fallens* (strain CBS 284.70, GenBank GU238078.1; Identities = 860/871 (99 %), 1 gap (0 %)), and *Camarosporium quaternatum* (strain CBS 483.95, GenBank DQ377884.1; Identities = 851/863 (99 %), no gaps). The LSU sequence of CPC 36068 differs with a single nucleotide from CPC 35988 and CPC 36060 (884/885 bases similar).

*Colour illustrations.* *Aloe* sp. *Neoplatysporoides aloes* was isolated from. Conidioma on pine needle agar; conidiogenous cells; conidia. Scale bars = 250 µm (conidioma), 10 µm (all others).

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