

Neodevriesia strelitziicola



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Neodevriesia strelitziicola Crous, *sp. nov.*

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

Classification — *Neodevriesiaceae*, *Capnodiales*, *Dothideomycetes*.

Mycelium consisting of pale brown, smooth, septate, branched, 1.5–2 µm diam hyphae. *Conidiophores* solitary, erect, straight to geniculous-sinuous, 1–4-septate, subcylindrical, brown, smooth, unbranched, 5–30 × 2.5–3 µm. *Conidiogenous cells* terminal, integrated, subcylindrical, pale brown, smooth, 5–12 × 2.5–3 µm; proliferating sympodially with loci thickened and darkened, 0.5 µm diam. *Conidia* and ramoconidia pale brown, smooth, 0(–1)-septate, occurring in branched chains, subcylindrical to fusoid-ellipsoid, (5–)7–9(–11) × 2 µm; loci thickened and darkened, 0.5 µm diam.

Culture characteristics — Colonies erumpent, spreading, with moderate aerial mycelium and smooth, lobate margin, reaching 15 mm diam after 2 wk at 25 °C. On MEA, PDA and OA surface and reverse olivaceous grey.

Typus. SOUTH AFRICA, Eastern Cape Province, Amathole, Haga Haga, on leaf litter of *Strelitzia nicolai* (*Strelitziaceae*), 2010, *M.J. Wingfield*, HPC 2748 (holotype CBS H-24192, cultures ex-type CPC 37387 = CBS 146019, CPC 37388 = CBS 146020, ITS, LSU, *rpb2* and *tub2* sequences GenBank MN562144.1–MN562145.1, MN567651.1–MN567652.1, MN556812.1–MN556813.1 and MN556844.1 (CPC 37387), MycoBank MB832905).

Notes — *Neodevriesia* is characterised by medium brown conidiophores and thick-walled, medium brown, sparsely septate conidia arranged in short, mostly unbranched chains (Quaedvlieg et al. 2014). *Neodevriesia strelitziicola* is related to *N. coccolobae* (on leaves of *Coccoloba uvifera*, Puerto Rico; conidia (6–)7–8(–10) × (2–)2.5(–3) µm; Crous et al. 2018a), and *N. tabebuiae* (on leaves of *Tabebuia chrysantha*, Puerto Rico, conidia (6–)7–8(–10) × (2–)2.5(–3) µm; Crous et al. 2018a), and is best distinguished based on its narrower conidia, and DNA phylogeny.

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence of CPC 37388 had highest similarity to *Neodevriesia coccolobae* (strain CBS 145064, GenBank NR_161126.1; Identities = 480/500 (96 %), 8 gaps (1 %)), *Neodevriesia tabebuiae* (strain CBS 145065, GenBank NR_161127.1; Identities = 498/533 (93 %), 15 gaps (2 %)), and *Neodevriesia lagerstroemiae* (strain CBS 125422, GenBank MH863701.1; Identities = 489/533 (92 %), 22 gaps (4 %)). The ITS sequence of CPC 37388 differs with 7 nucleotides from that of CPC 37387 (525/532 bases similar). Closest hits using the **LSU** sequence of CPC 37388 are *Neodevriesia coccolobae* (strain CBS 145064, GenBank MK047483.1; Identities = 816/817 (99 %), no gaps), *Neodevriesia cladophorae* (as *Devriesia* sp. MW-2016a, voucher OUCMBI11011, GenBank KU578114.1; Identities = 811/817 (99 %), no gaps), and *Neodevriesia knoxdaviesii* (strain CBS 122898, GenBank MH874778.1; Identities = 799/808 (99 %), 2 gaps (0 %)). The LSU sequences of CPC 37387 and CPC 37388 are identical (815/815 bases). No significant hits were obtained when the **rpb2** sequence was used in blastn and megablast searches. The **rpb2** sequences of CPC 37387 and CPC 37388 are identical (834/834 bases). No significant hits were obtained when the **tub2** sequence of CPC 37387 was used in blastn and megablast searches.

Colour illustrations. Forest area at Haga Haga. Conidiophores with conidiogenous cells; conidia. Scale bars = 10 µm.

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