

Devriesia stirlingiae



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***Devriesia stirlingiae* Crous, sp. nov.**

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

Colonies on synthetic nutrient-poor agar. *Mycelium* consisting of smooth, pale brown, septate, branched, 2–3 µm diam hyphae. *Conidiophores* erect, subcylindrical, pale brown, smooth, straight or flexuous, branched or not, reduced to conidiogenous cells or 1–8-septate, 10–50 × 4–5 µm. *Conidiogenous cells* terminal, integrated, subcylindrical, smooth, pale brown, proliferating sympodially, 8–15 × 3–4 µm; scars flattened, thickened, somewhat darkened, 1–2 µm diam. *Ramiconidia* 1–3-septate, granular to guttulate, subcylindrical, smooth, pale brown, 15–30 × 4–5 µm, frequently with lateral branch at apex, up to 10 µm long, hila somewhat thickened and darkened, 1.5–2(–3) µm diam. *Conidia* subcylindrical to fusoid-ellipsoidal, apex obtuse, pale brown, smooth, guttulate, (7–)12–16(–20) × (3–)4(–5) µm, 0–3-septate; hila flattened, truncate, somewhat thickened and darkened, 1–2 µm diam. *Chlamydospores* thick-walled, brown, globose, in intercalary chains, up to 10 µm diam.

Culture characteristics — (in the dark, 25 °C after 2 wk): Colonies erumpent with even, smooth margins and sparse aerial mycelium. On potato-dextrose agar, malt extract agar and oatmeal agar surface olivaceous-grey, reverse iron-grey, reaching 7 mm diam.

Typus. WESTERN AUSTRALIA, Perth, Wandoo National Park, on leaves of *Stirlingia latifolia* (*Proteaceae*), 13 July 2011, *W. Gams*, holotype CBS H-21083, cultures ex-type CPC 19948 = CBS 133581, ITS sequence GenBank KC005778, LSU sequence GenBank KC005799, MycoBank MB801777.

Notes — Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the LSU sequence are *Devriesia hilliana* (GenBank GU214414; Identities = 843/856 (98 %), Gaps = 2/856 (0 %)), *Devriesia xanthorrhoeae* (GenBank HQ599606; Identities = 841/856 (98 %), Gaps = 2/856 (0 %)), and *Teratosphaeria knoxdavesii* (GenBank EU707865; Identities = 839/853 (98 %), Gaps = 0/853 (0 %)). Closest hits using the ITS sequence had highest similarity to *Devriesia fraseriae* (GenBank HQ599602; Identities = 491/501 (98 %), Gaps = 2/501 (0 %)), *Devriesia lagerstroemiae* (GenBank GU214634; Identities = 478/508 (94 %), Gaps = 13/508 (3 %)), and *Teratosphaeria knoxdavesii* (GenBank EU707866; Identities = 473/507 (93 %), Gaps = 11/507 (2 %)). Although phylogenetically closely related to *D. fraseriae* (intercalary and terminal conidia (6–)8–10(–11) × 3(–4) µm; Crous et al. 2010a), *D. stirlingiae* is easily distinguishable by having larger conidia.

Colour illustrations. Flowers of *Stirlingia latifolia*; colony sporulating on potato-dextrose agar; conidiophores, conidiogenous cells and conidia. Scale bar = 10 µm.

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