

Devriesia shakazului



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Devriesia shakazului Crous, sp. nov.

Etymology. Named after Shaka kaSenzangakhona (also known as Shaka Zulu), a former king of the Zulu Nation, who used to send his handmaidens to collect dried salt off the rocks (Salt Rock) at low tide.

Colonies on synthetic nutrient-poor agar. *Mycelium* consisting of smooth, pale brown, septate, branched, 1.5–2 µm diam hyphae. *Conidiophores* erect, subcylindrical, pale brown, smooth, straight or flexuous, branched or not, reduced to conidiogenous cells or up to 2-septate, 5–25 × 3–4 µm. *Conidiogenous cells* terminal, integrated, subcylindrical, smooth, pale brown, proliferating sympodially, 5–15 × 2.5–4 µm; scars flattened, thickened, somewhat darkened, 0.5–1.5 µm diam. *Ramoconidia* 0(–)1-septate, guttulate, subcylindrical, smooth, pale brown, 10–15 × 2–3 µm; hila somewhat thickened and darkened, 1–1.5 µm diam, giving rise to conidia in long branched or unbranched chains (–15). *Intercalary conidia* subcylindrical to somewhat fusoid-ellipsoidal, pale brown, smooth, guttulate, 1-septate, 10–15 × 2–2.5 µm. *Terminal conidia* subcylindrical to fusoid-ellipsoidal, apex obtuse, pale brown, smooth, guttulate, (6–)8–9(–11) × 2(–2.5) µm, (0–)1-septate; hila flattened, truncate, somewhat thickened and darkened, 0.5–1 µm diam. *Chlamydospores* not observed.

Culture characteristics — (in the dark, 25 °C after 2 wk): Colonies on potato-dextrose agar (PDA), malt extract agar (MEA) and oatmeal agar (OA) erumpent, spreading, with smooth, even margin and moderate aerial mycelium. Surface grey-olivaceous (OA and PDA) to hazel (MEA), reverse iron-grey, reaching 16 mm diam.

Typus. SOUTH AFRICA, KwaZulu-Natal, Durban, Salt Rock, on leaves of *Aloe* sp. (*Xanthorrhoeaceae*), 24 July 2011, P.W. Crous, holotype CBS H-21081, cultures ex-type CPC 19784, CPC 19782 = CBS 133579, ITS sequence GenBank KC005775–KC005776, LSU sequence GenBank KC005797, MycoBank MB801775.

Notes — Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the LSU sequence are *Devriesia queenslandica* (GenBank JF951168; Identities = 880/887 (99 %), Gaps = 0/887 (0 %)), *Devriesia hilliana* (GenBank GU214414; Identities = 875/885 (99 %), Gaps = 0/885 (0 %)) and *Devriesia xanthorrhoeae* (GenBank HQ599606; Identities = 867/879 (99 %), Gaps = 0/879 (0 %)). Closest hits using the ITS sequence had highest similarity to *Devriesia queenslandica* (GenBank JF951148; Identities = 554/575 (96 %), Gaps = 8/575 (1 %)), *Devriesia lagerstroemiae* (GenBank GU214634; Identities = 526/577 (91 %), Gaps = 24/577 (4 %)) and *Devriesia hilliana* (GenBank GU214633; Identities = 530/587 (90 %), Gaps = 27/587 (5 %)). Although phylogenetically closely related to *D. queenslandica* (conidiophores 5–45 × 3–4 µm, ramoconidia 10–20 × 2–3 µm, terminal conidia (5–)7–9(–11) × 2–2.5 µm; Crous et al. 2011), structures of *D. shakazului* are slightly shorter.

Colour illustrations. Salt Rock, KwaZulu-Natal; colony sporulating on oatmeal agar; conidiophores, conidiogenous cells and conidia. Scale bars = 10 µm.