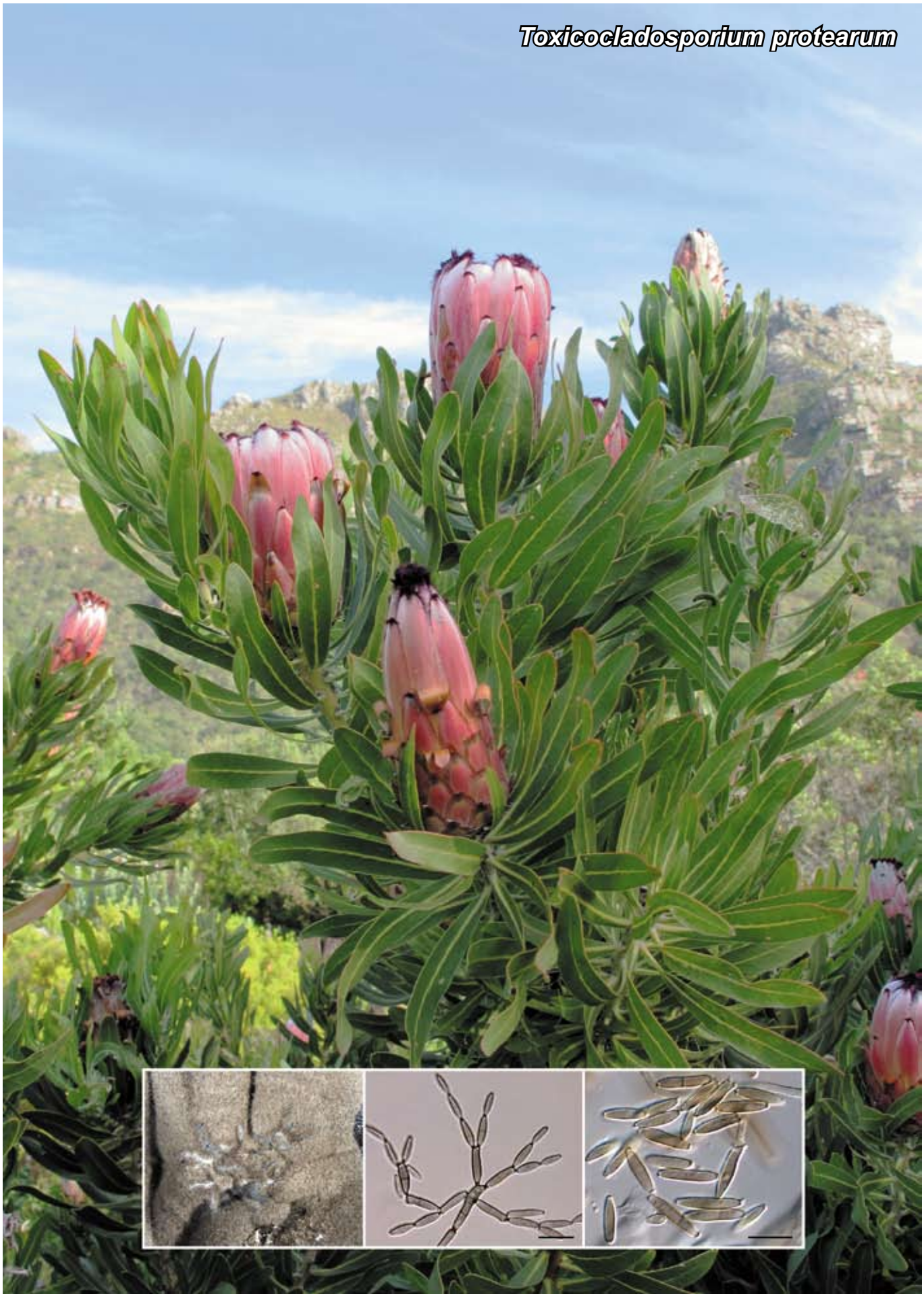
Toxicocladosporium protearum

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Toxicocladosporium protearum Crous & Roets, *sp. nov.*

Toxicocladosporio veloxo simile, sed conidiis majoribus, (9–)11–13(–16) × (2–)2.5(–3) µm, discernitur.

Etymology. Named after the host from which it was collected, *Protea*.

Mycelium consisting of smooth, septate, brown, branched, 2–3 µm diam hyphae. *Conidiophores* erect, medium brown, with an apical apparatus of penicillate branches; conidiophores cylindrical, smooth, 1–8-septate, 30–80 µm tall, 3–4 µm wide; base lacking rhizoids. *Conidiogenous cells* terminal, medium to dark brown, smooth, subcylindrical, 10–20 × 2.5–3 µm, with 1–2 apical loci, that are thickened, darkened, somewhat refractive, 1–1.5 µm wide. *Ramoconidia* subcylindrical, 0–1-septate, medium to dark brown, smooth, 15–20 × 2.5–3.5 µm. *Conidia* occurring in branched chains of up to 10, subcylindrical to narrowly fusoid-ellipsoidal, (9–)11–13(–16) × (2–)2.5(–3) µm, 0–1-septate; conidial hila somewhat thickened, darkened and refractive, 0.5–1 µm.

Culture characteristics — (in the dark, 25 °C, after 1 mo): Colonies on oatmeal agar flat, spreading, with sparse aerial mycelium, with even, smooth margins; surface greenish black, reaching 40 mm diam. On malt extract agar spreading, with moderate aerial mycelium, folded, green-black, with sectors of olivaceous-grey; greenish black in reverse. Similar on potato-dextrose agar.

Typus. South Africa, Stellenbosch, J.S. Marais Garden, on leaves of *Protea* sp., 22 Apr. 2008, *F. Roets*, CBS-H 20490 holotype, cultures ex-type CPC 15254 = CBS 126499, CPC 15255, 15256, ITS sequence of CPC 15254 GenBank HQ599586 and LSU sequence of CPC 15254 GenBank HQ599587, MycoBank MB517536.

Notes — A megablast search in GenBank using the LSU sequence retrieved as closest sisters *Toxicocladosporium chlamydosporum* (GenBank FJ790302; Identities = 881/883 (99 %), Gaps = 0/883 (0 %)), *Toxicocladosporium veloxum* (GenBank FJ790306; Identities = 880/883 (99 %), Gaps = 0/883 (0 %)) and *Toxicocladosporium irritans* (GenBank EU040243; Identities = 870/885 (99 %), Gaps = 4/885 (0 %)). These three species were also obtained when a megablast was performed with the ITS sequence, albeit with a slightly lower sequence identity (*T. veloxum* GenBank FJ790288, Identities = 609/613 (99 %), Gaps = 3/613 (0 %), *T. chlamydosporum* GenBank FJ790284, Identities = 604/614 (99 %), Gaps = 3/614 (0 %) and *T. irritans* GenBank EU040243, Identities = 517/542 (96 %), Gaps = 12/542 (2 %)). Therefore on DNA sequence data of the ITS region, *T. protearum* is 4 nucleotides different from *T. veloxum*[1]. Morphologically they differ in that *T. veloxum* has smaller intercalary (9–12 × 2.5–3 µm) and terminal (8–10 × 2–2.5 µm) conidia than *T. protearum*.

Colour illustrations. Protea burchellii in Kirstenbosch Botanical Garden; colony on malt extract agar; conidiophores with conidiogenous cells giving rise to conidia. Scale bars = 10 µm.

Reference. [1]Crous PW, Wingfield MJ, Groenewald JZ. 2009. Niche sharing reflects a poorly understood biodiversity phenomenon. Persoonia 22: 83–94.

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