Fungal Planet 56 – 23 December 2010

Strelitziana albiziae Crous & H.D. Shin, *sp. nov.*

Strelitzianae australiensis similis, sed conidiis minoribus et obclavatis, (17–)38–65(–80) × (2.5–)3 µm, (1–)3–8(–10)-septatis, distinguitur.

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

Mycelium consisting of smooth, septate, branched hyphae, pale brown, 2.5–3 µm diam. *Conidiophores* erect, solitary, subcylindrical, straight to geniculous-sinuous, pale brown, 1–9-septate, 20–100 × 3–4 µm. *Conidiogenous cells* terminal, integrated, pale brown, with several short, conspicuous apical denticles, 2–4 µm long, 1–1.5 µm wide; conidiogenesis rhexolytic with remnants of separating cell clearly visible on conidiogenesis cell, and at times visible on conidium hilum as a minute marginal frill, 15–50 × 3–4 µm. *Conidia* pale brown, smooth, long obclavate, widest at basal septum, tapering to a subobtusely rounded apex and long obconically subtruncate base, 1 µm wide, at times with inconspicuous marginal frill, (17–)38–65(–80) × (2.5–)3 µm, (1–)3–8(–10)-septate; microcyclic conidiation present in culture.

Culture characteristics — (in the dark, 25 °C, after 1 mo): Colonies on oatmeal agar (OA) spreading with moderate aerial mycelium, with even, smooth margins; surface greenish black, with patches of olivaceous-grey; greenish black on malt extract agar (MEA) (surface and reverse), olivaceous-grey on potato-dextrose agar (PDA) (surface), iron-grey (reverse); colonies reaching 40 mm diam on OA, 25 mm on MEA, and PDA.

Typus. Korea, Jecheon, on leaves of *Albizia julibrissin* infected with *Camptomeris albiziae*, 19 Oct. 2007, *H.-D. Shin*, CBS-H 20489 holotype, cultures ex-type CPC 14750, 14749 = CBS 126497, ITS sequence GenBank HQ599584 and LSU sequence GenBank HQ599585, MycoBank MB517535.

Notes — A megablast search in GenBank using the LSU sequence retrieved as closest sisters *Strelitziana australiensis* (GenBank GQ303326; Identities = 856/891 (97 %), Gaps = 10/891 (1 %)) and *S. africana* (GenBank DQ885895; Identities = 890/928 (96 %), Gaps = 12/928 (1 %)). These same two species were also obtained when a megablast was performed with the ITS sequence, albeit with a slightly lower sequence identity (*S. australiensis* GenBank GQ303295, Identities = 659/716 (93 %), Gaps = 27/716 (3 %) and *S. africana* GenBank DQ885895, Identities = 668/724 (93 %), Gaps = 25/724 (3 %)). Therefore on DNA sequence data, *S. albiziae* is related to *S. africana* (conidia (18–)50–70(–95) × 3(–3.5) µm, 3–5(–10)-septate), and *S. australiensis* (30–)50–60(–73) × 2.8–3.2 µm, 4–8-septate)[1, 2]. Conidia of *S. australiensis* are similar in size to those of *S. albiziae*, and also have a small, globose, hyaline, apical mucilaginous appendage. On average though, conidia of *S. albiziae* are smaller, have more septa, and are obclavate rather than subcylindrical.

Colour illustrations. Leaves of *Albizia julibrissin* infected with *Camptomeris albiziae*; conidiophore with conidiogenous cell giving rise to conidium (note separating cell); conidiogenous cell with remnants of separating cells; conidia. Scale bars = 10 µm.

References. [1]Arzanlou M, Crous PW. 2006. Strelitziana africana. Fungal Planet No. 8. [2]Cheewangkoon R, Groenewald JZ, Summerell BA, Hyde KD, To-anun C, Crous PW. 2009. Myrtaceae, a cache of fungal biodiversity. Persoonia 23: 55–85.

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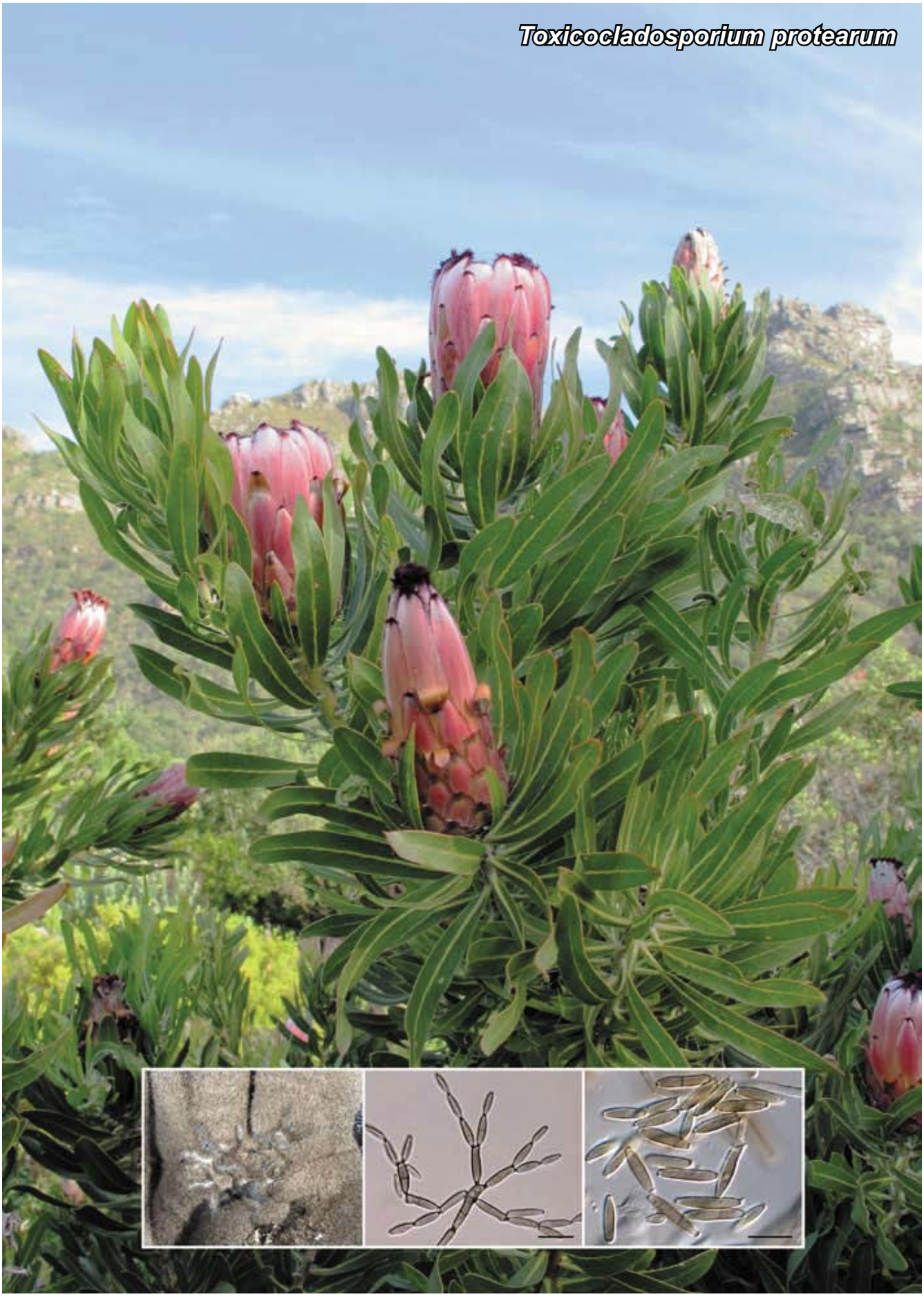
Toxicocladosporium protearum