

Arxiella dolichandrae



Fungal Planet 287 – 24 November 2014

Arxiella dolichandrae Crous, *sp. nov.*

Etymology. Name reflects the host genus *Dolichandra*, from which the species was isolated.

Conidiomata sporodochial, forming loose, brown, superficial sporodochia on agar surface, up to 300 µm diam, consisting of brown *textura angularis* to *textura globulosa*, that become fertile at the edges. *Conidiogenous cells* smooth, brown, globose to somewhat elongated, 4–6 µm diam, phialidic, with minute periclinal thickening. *Conidia* solitary, hyaline, smooth, guttulate, reniform, medianly 1-septate, inner plane with apical and basal horn-like appendages following curvature of inner plane, 2–3 µm long; conidia (incl. appendages) 10–11 × 2.5–3 µm, with a slightly raised hilum (0.5 µm diam) at the base where the basal appendage joins the conidium body.

Culture characteristics — Colonies flat, appressed, spreading with sparse aerial mycelium, surface folded with smooth, lobate margin, reaching 3 cm diam after 2 wk at 25 °C in the dark. On MEA surface dirty white, reverse ochreous. On PDA surface dirty white, reverse pale luteous. On OA surface pale luteous.

Typus. SOUTH AFRICA, KwaZulu-Natal, Pietermaritzburg, S29°37'50.95" E30°25'51.67", on leaves of *Dolichandra unguiscati* (*Bignoniaceae*), 24 May 2013, A. King (holotype CBS H-21983, culture ex-type CPC 22951 = CBS 138853; ITS sequence GenBank KP004449, LSU sequence GenBank KP004477, MycoBank MB810595).

Notes — The genus *Arxiella* was established for a fungus collected from leaf litter and soil under *Acacia karroo* in South Africa (Papendorf 1967) and presently includes two species. *Arxiella dolichandrae* is distinct from these species by its conidial dimensions (*A. terrestris*, 6–16 × 3–4.5 µm; *A. lunata*, 10–17 × 3–4 µm) (Papendorf 1967, Ruscoe 1970).

ITS. Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the ITS sequence are *Mycoleptodiscus terrestris* (GenBank JN711860; Identities = 363/420 (86 %), Gaps = 17/420 (4 %)), *Polychaeton citri* (GenBank GU214649; Identities = 445/538 (83 %), Gaps = 22/538 (4 %)) and *Leptoxyphium madagascariense* (GenBank GQ303277; Identities = 409/501 (82 %), Gaps = 28/501 (5 %)).

LSU. Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the LSU sequence are *Chlamydotubeufia huaikangplaensis* (GenBank JN865198; Identities = 722/809 (89 %), Gaps = 5/809 (0 %)), *Hysterium vermiforme* (GenBank GQ221897; Identities = 719/810 (89 %), Gaps = 6/810 (0 %)) and *Chlamydotubeufia khunkornensis* (GenBank JN865190; Identities = 720/813 (89 %), Gaps = 11/813 (1 %)).

Colour illustrations. Symptomatic leaves of *Dolichandra unguiscati*; colonies on OA, conidiogenous cells and conidia. Scale bars = 10 µm.

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