

Xylaria eucalypti



Fungal Planet 974 – 18 December 2019

Xylaria eucalypti Crous, *sp. nov.*

Etymology. Name refers to the host genus *Eucalyptus* from which it was isolated.

Classification — *Xylariaceae*, *Xylariales*, *Sordariomycetes*.

Colonies established from ascospores shot out onto agar that were aseptate, hyaline, smooth, ellipsoid, resembling those of *Neophysalospora* and *Clypeophysalospora*. *Conidiomata* sporodochial, 180–200 µm diam, buff to pale brown, consisting of densely aggregated conidiophores in mucoid droplet. *Conidiophores* subcylindrical, smooth, pale brown at base, branched, septate, 20–40 × 2–3 µm. *Conidiogenous cells* hyaline to pale brown, smooth, terminal and intercalary, subcylindrical with apical taper, 7–15 × 1.5–2 µm, proliferating inconspicuously sympodially at apex. *Conidia* solitary, aseptate, hyaline, smooth, subcylindrical, apex subobtuse, base truncate, curved, (13–)15–17(–18) × 1.5 µm. In older cultures on oatmeal agar acervular conidiomata develop, 200–300 µm diam, brown, opening via irregular flaps, containing a similar asexual morph as observed on sporodochia in young colonies.

Culture characteristics — Colonies flat, spreading, with moderate aerial mycelium and smooth, lobate margin, reaching 40 mm diam after 2 wk at 25 °C. On MEA, PDA and OA surface and reverse rosy buff.

Typus. AUSTRALIA, New South Wales, Bombala, Coolanguba State Forest, on leaves of *Eucalyptus radiata* (*Myrtaceae*), 2016, A.J. Carnegie, HPC 2652 (holotype CBS H-24173, culture ex-type CPC 36723 = CBS 146092, ITS, LSU and *tub2* sequences GenBank MN562127.1, MN567634.1 and MN556841.1, MycoBank MB832884).

Notes — *Xylaria eucalypti* is tentatively placed in *Xylaria*, as it is phylogenetically closely related to the genus. However, the fact that it was cultured from neophysalospora-like ascospores, suggests that it probably represents an undescribed genus in *Xylariaceae*.

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Anthostomella brabeji* (strain CBS 110128, GenBank NR_153509.1; Identities = 526/605 (87 %), 26 gaps (4 %)), *Xylaria ianthinovelutina* (strain C24, GenBank JQ936302.1; Identities = 518/596 (87 %), 27 gaps (4 %)), and *Xylaria grammica* (strain KCTC 13121BP, GenBank KY490692.1; Identities = 514/592 (87 %), 22 gaps (3 %)). Closest hits using the **LSU** sequence are *Xylaria enteroleuca* (strain CBS 128357, GenBank MH876349.1; Identities = 809/829 (98 %), 1 gap (0 %)), *Xylaria vaporaria* (strain CBS 386.35, GenBank MH867226.1; Identities = 797/818 (97 %), 1 gap (0 %)), and *Xylaria longipes* (strain CBS 148.73, GenBank MH872351.1; Identities = 807/829 (97 %), 1 gap (0 %)). No significant hits were obtained when the **tub2** sequence was used in blastn and megablast searches.

Colour illustrations. *Eucalyptus radiata* trees at Coolanguba State Forest. Symptomatic leaves with purple leaf spots; conidiophores with conidiogenous cells; conidia. Scale bars = 10 µm.

Pedro W. Crous & Johannes Z. Groenewald, Westerdijk Fungal Biodiversity Institute, P.O. Box 85167, 3508 AD Utrecht, The Netherlands; e-mail: p.crous@wi.knaw.nl & e.groenewald@wi.knaw.nl
Angus J. Carnegie, Forest Health & Biosecurity, Forest Science, NSW Department of Primary Industries, Level 12, 10 Valentine Ave, Parramatta NSW 2150, Australia; e-mail: angus.carnegie@dpi.nsw.gov.au