

Phlogicylindrium tereticornis



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Phlogicylindrium tereticornis Crous, *sp. nov.*

Etymology. Name refers to *Eucalyptus tereticornis*, the host species from which this fungus was collected.

Classification — *Phlogicylindriaceae*, *Xylariales*, *Sordariomycetes*.

Associated with amphigenous, circular to angular, brown leaf spots (3–7 mm diam), with red-purple margins. On SNA. *Conidiomata* sporodochial, with *conidiophores* subcylindrical, hyaline, smooth, giving rise to terminal *conidiogenous cells*, 3–8 × 2–3 µm, proliferating sympodially. *Conidia* solitary, hyaline, smooth, medianly septate, straight to curved subcylindrical, guttulate, tapering to subobtuse apex and truncate hilum, (20–) 25–35(–40) × (2–)3 µm.

Culture characteristics — Colonies erumpent, spreading, with sparse aerial mycelium and feathery margins, reaching 30 mm diam after 2 wk at 25 °C. On MEA surface saffron, reverse amber. On PDA surface chestnut, reverse amber. On OA surface hazel.

Typus. AUSTRALIA, New South Wales, Australian Botanic Garden, Mount Annan, on leaves of *Eucalyptus tereticornis* (*Myrtaceae*), 25 Nov. 2016, *P.W. Crous* (holotype CBS H-23279, culture ex-type CPC 32197 = CBS 143168, ITS, LSU, *rpb2* and *tef1* sequences GenBank MG386042, MG386095, MG386142 and MG386151, MycoBank MB823389).

Notes — *Phlogicylindrium* is characterised by forming sporodochia, and having sympodially proliferating conidiogenous cells that give rise to hyaline, subcylindrical, septate conidia (Summerell et al. 2006). The present collection appears to be phylogenetically closely allied to *Phlogicylindrium*, and as it is also morphologically similar, we describe it here as *P. tereticornis*. The foliar symptoms associated with the fungus were quite dramatic, but the occurrence of *Phlogicylindrium* on these lesions may be secondary.

Based on a megablast search using the ITS sequence, the closest matches in NCBI's GenBank nucleotide database were *Phlogicylindrium eucalyptorum* (GenBank EU040223; Identities 417/436 (96 %), 1 gap (0 %)), *P. eucalypti* (GenBank NR_132813; Identities 425/449 (95 %), 1 gap (0 %)) and *P. uniforme* (GenBank JQ044426; Identities 425/449 (95 %), 2 gaps (0 %)). The highest similarities using the LSU sequence were *P. mokarei* (GenBank KY173521; Identities 810/818 (99 %), no gaps), *P. uniforme* (GenBank JQ044445; Identities 830/840 (99 %), no gaps) and *P. eucalyptorum* (GenBank EU040223; Identities 830/840 (99 %), no gaps). The highest similarities using the *rpb2* sequence were distant hits with *Creosphaeria sassafras* (GenBank KU684308; Identities 647/820 (79 %), 12 gaps (1 %)), *Lopadostoma linospermum* (GenBank KC774544; Identities 658/848 (78 %), 15 gaps (1 %)) and *Daldinia concentrica* (GenBank DQ368651; Identities 638/828 (77 %), 15 gaps (1 %)). No significant hits were found when the *tef1* sequence was used in a blast search.

Colour illustrations. Symptomatic *Eucalyptus* leaves; conidiogenous cells on PNA, and 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@westerdijkinstituut.nl & e.groenewald@westerdijkinstituut.nl
Michael J. Wingfield, Forestry and Agricultural Biotechnology Institute (FABI), University of Pretoria, Pretoria 0002, South Africa; e-mail: mike.wingfield@fabi.up.ac.za
Treena I. Burgess & Giles E.St.J. Hardy, Centre for Phytophthora Science and Management, Murdoch University, 90 South Street, Murdoch, WA 6150, Australia; e-mail: tburgess@murdoch.edu.au & g-hardy@murdoch.edu.au