

*Verrucoconiothyrium acaciae*



Fungal Planet 685 – 20 December 2017

## *Verrucoconiothyrium acaciae* Crous, *sp. nov.*

*Etymology.* Name refers to *Acacia*, the host genus from which this fungus was collected.

*Classification* — *Didymellaceae*, *Pleosporales*, *Dothideomycetes*.

*Conidiomata* solitary, globose, 100–250 µm diam, brown with central ostiole, 10–15 µm diam; wall of 3–4 layers of brown *textura angularis*. *Conidiophores* reduced to conidiogenous cells, ampulliform, hyaline, smooth, 5–8 × 5–6 µm, phialidic with minute percurrent proliferations at apex. *Conidia* solitary, aseptate, fusoid-ellipsoid, medium brown, verruculose, apex obtuse to subobtuse, base truncate, 1.5 µm diam, (6.5–)8–9(–10) × (3–)3.5(–4) µm.

*Culture characteristics* — Colonies flat, spreading, with moderate aerial mycelium and feathery, lobate margins, reaching 50 mm diam after 2 wk at 25 °C. On MEA surface and reverse saffron with black conidiomata. On PDA surface grey olivaceous, reverse mouse grey. On OA surface pale luteous with black conidiomata.

*Typus.* AUSTRALIA, New South Wales, Nullica State Forest, on leaves of *Acacia falciformis* (*Fabaceae*), 29 Nov. 2016, P.W. Crous (holotype CBS H-23292, culture ex-type CPC 32330 = CBS 143448, ITS, LSU, *rpb2* and *tub2* sequences GenBank MG386054, MG386107, MG386143 and MG386165, MycoBank MB823403).

*Notes* — *Verrucoconiothyrium* (Crous et al. 2015a) accommodates coniothyrium-like species with verruculose conidia.

Based on a megablast search using the ITS sequence, the closest matches in NCBI's GenBank nucleotide database were *V. nitidae* (GenBank JN712452; Identities 521/530 (98 %), 4 gaps (0 %)), *V. eucalyptigenum* (GenBank KY979771; Identities 515/531 (97 %), 5 gaps (0 %)) and *V. prosopidis* (GenBank NR\_137604; Identities 514/531 (97 %), 5 gaps (0 %)). The highest similarities using the LSU sequence were 99 % to species from numerous genera in *Didymellaceae*, e.g., *Phoma eupyrena* (GenBank GU238072; Identities 851/854 (99 %), no gaps), *Didymella glomerata* (GenBank KX896095; Identities 850/854 (99 %), no gaps) and *Peyronellaea calorpreferens* (GenBank LN907448; Identities 850/854 (99 %), no gaps). The highest similarities using the *rpb2* sequence were *V. eucalyptigenum* (GenBank KY979852; Identities 790/841 (94 %), no gaps), *Nothophoma gossypicola* (GenBank KT389658; Identities 552/595 (93 %), no gaps) and *N. infossa* (GenBank KT389659; Identities 532/580 (92 %), no gaps). The highest similarities using the *tub2* sequence were *V. eucalyptigenum* (GenBank KY979935; Identities 311/326 (95 %), no gaps), *V. nitidae* (as *Coniothyrium nitidae*; GenBank JN712647; Identities 305/321 (95 %), 3 gaps (0 %)) and *Nothophoma quercina* (GenBank KU973704; Identities 307/328 (94 %), no gaps).

*Colour illustrations.* *Acacia* sp.; conidiomata sporulating on PDA, conidiogenous cells 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  
Brett A. Summerell, Royal Botanic Gardens and Domain Trust, Mrs. Macquaries Road, Sydney, NSW 2000, Australia; e-mail: brett.summerell@rbgsyd.nsw.gov.au  
Angus J. Carnegie, Forest Health & Biosecurity, NSW Department of Primary Industries, Level 12, 10 Valentine Ave, Parramatta, NSW 2150, Locked Bag 5123, Parramatta, NSW 2124, Australia; e-mail: angus.carnegie@dpi.nsw.gov.au