





Fungal Planet 779 – 13 July 2018

***Discosia macrozambiae* Crous, sp. nov.**

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

*Classification* — *Sporocadaceae*, *Amphisphaeriales*, *Sordariomycetes*.

*Conidiomata* pycnidial, erumpent, subglobose to lenticular, unilocular, dark brown, to 250 µm diam; wall of polyclonal brown cells. *Conidiophores* lining the inner cavity, hyaline, smooth, subcylindrical to ampulliform, 0–2-septate, rarely branched at base, 7–15 × 2.5–3 µm. *Conidiogenous cells* terminal, integrated, hyaline, smooth, subcylindrical, 5–7 × 2–2.5 µm; proliferating inconspicuously percurrently at apex. *Conidia* cylindrical, 3-septate, pale brown, smooth with appendage at both ends, (25–)30–32(–35) × (2.5–)3 µm; basal cell 6–7 µm long, obconic with truncate hilum; second cell from base (9–)10–11(–12) µm long; third cell 4–5 µm long, with obtusely rounded apex. *Appendages* cellular, unbranched, filiform, excentric; apical appendage 7–11 µm long; basal appendage 10–16 µm long.

*Culture characteristics* — Colonies flat, spreading, with moderate aerial mycelium, covering dish after 2 wk at 25 °C. On MEA, PDA and OA surface olivaceous grey, and reverse iron-grey.

*Typus.* AUSTRALIA, New South Wales, Australian Botanical Garden Mount Annan, on leaves of *Macrozamia miquelii* (*Zamiaceae*), 25 Nov. 2016, P.W. Crous (holotype CBS H-23593, culture ex-type CPC 32113 = CBS 144436, ITS, LSU, *tef1* and *tub2* sequences GenBank MH327819.1, MH327855.1, MH327883.1 and MH327894.1, MycoBank MB825435).

*Additional material examined.* AUSTRALIA, New South Wales, Australian Botanical Garden Mount Annan, on leaves of *Macrozamia miquelii*, CPC 32109 = CBS 144437, ITS, LSU, *tef1* and *tub2* sequences GenBank MH327820.1, MH327856.1, MH327884.1 and MH327895.1.

*Colour illustrations.* *Macrozamia miquelii* at Australian Botanical Garden Mount Annan; conidiomata sporulating on PNA (scale bar = 250 µm), conidiogenous cells and conidia (scale bars = 10 µm).

*Notes* — In a phylogenetic treatment of *Discosia*, Tanaka et al. (2011) established genera for former 'sections' of the genus, recognizing *Adisciso* (*Discosia* spp. with a sexual morph), and *Immersidiscosia* (species occurring on *Eucalyptus*). Following the 'one fungus one name' approach, it is preferable to treat *Adisciso* under the older name, *Discosia*. The present collection is allied to, but distinct from, species presently recognized in this subclade, and a new species is introduced to accommodate this taxon.

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the ITS sequence of CPC 32109 had highest similarity to *Discosia* cf. *pleurochaeta* (GenBank AB594777.1; Identities = 546/546 (100 %), no gaps), *Discosia italica* (GenBank KM678041.1; Identities = 552/556 (99 %), 1 gap (0 %)) and *Discosia pseudoartocreas* (GenBank NR\_132068.1; Identities = 550/556 (99 %), 1 gap (0 %)). The ITS sequences of CPC 32109 and 32113 are identical (556/556). Closest hits using the LSU sequence of CPC 32109 are *Adisciso yakushimense* (GenBank AB593721.1; Identities = 802/803 (99 %), no gaps), *Discosia fagi* (GenBank KM678048.1; Identities = 871/873 (99 %), no gaps) and *Adisciso tricellulare* (GenBank NG\_042334.1; Identities = 800/803 (99 %), no gaps). The LSU sequences of CPC 32109 and 32113 are identical (873/873). Closest hits using the *tef1* sequence of CPC 32109 had highest similarity to *Discosia brasiliensis* (GenBank KF827465.1; Identities = 363/399 (91 %), 12 gaps (3 %)), *Pestalotiopsis diversiseta* (GenBank JX399073.1; Identities = 224/249 (90 %), 12 gaps (4 %)) and *Pestalotiopsis yanglingensis* (GenBank KX895197.1; Identities = 221/246 (90 %), 6 gaps (2 %)). The *tef1* sequences of CPC 32109 and 32113 are identical (529/529). Closest hits using the *tub2* sequence of CPC 32109 had highest similarity to *Discosia brasiliensis* (GenBank KF827469.1; Identities = 805/832 (97 %), no gaps), *Pestalotiopsis microspora* (GenBank AF115396.1; Identities = 782/826 (95 %), no gaps) and *Pestalotiopsis paeoniicola* (GenBank KY930635.1; Identities = 781/826 (95 %), no gaps). The *tub2* sequences of CPC 32109 and 32113 are identical (874/874).

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