**Harknessia corymbiicola** Crous, sp. nov.

*Etymology. Name refers to Corymbia, the host genus from which this fungus was isolated.*

*Classification — Harknessiaceae, Diaporthales, Sordariomycetes.*

*Foliculous. Conidiomata pycnidiod, separate to gregarious, subepidermal, becoming erumpent, stromatic, multilocular, up to 2 mm diam, individual locules 100–300 µm diam; with irregular opening and border of yellowish, furfuraceous cells; conidiomatal wall of textura angularis. Conidiophores reduced to conidiogenous cells lining the inner conidiomatal cavity. Conidiogenous cells 6–12 × 5–6 µm, ampulliform to subcylindrical, hyaline, smooth, invested in mucilage, percurrently proliferating once or twice near apex. Conidia (26–)28–32(–35) × (7–)8(–9) µm in vitro, fusoid with apiculus, aseptate, non-striate, medium brown, thick-walled, smooth-walled, granular to finely guttulate. Basal appendage (50–)65–80(–90) × 3(–4) µm in vitro, hyaline, tubular, smooth, thin-walled, devoid of cytoplasm. Microconidia not seen.*

*Culture characteristics — Colonies flat, spreading, with fluffy moderate aerial mycelium and smooth, lobate margin, covering dish after 2 wk at 25 °C. On MEA, PDA and OA surface dirty white to buff, reverse cinnamon.*


Notes — *Harknessia* (*Harknessiaceae; Crous et al. 2012a*) is a genus of appendaged coelomycetous fungi that is commonly isolated from Myrtaceae and Proteaceae. *Harknessia* was treated by Marin-Felix et al. (2019), who accepted 38 species, recognising the majority as either endophytes, saprobes or foliar pathogens of minor importance. *Harknessia corymbiicola* represents a phylogenetically distinct species in the *H. were-subiae* species complex, being characterised by fusoid, apiculate conidia that lack striations, and have (50–)65–80(–90) µm long basal appendages.

Based on a megablast search of NCBI GenBank nucleotide database, the closest hits using the ITS sequence had highest similarity to *Harknessia platyphyllae* (GenBank NR_155191.1; Identities = 625/640 (98 %), 11 gaps (1 %)), *Harknessia banksiae* (GenBank NR_155188.1; Identities = 625/641 (98 %), 5 gaps (0 %)) and *Harknessia banksiigena* (GenBank NR_155189.1; Identities = 614/630 (97 %), 7 gaps (1 %)). Closest hits using the LSU sequence are *Aurantiosacculus acutatus* (GenBank NG_042618.1; Identities = 840/843 (99 %), no gaps), *Harknessia ellipsoidea* (GenBank MH877405.1; Identities = 839/843 (99 %), no gaps) and *Harknessia pellitae* (GenBank KY979843.1; Identities = 839/843 (99 %), no gaps). Closest hits using the tub2 sequence had highest similarity to *Harknessia eucalyptorum* (GenBank JQ706136.1; Identities = 615/651 (94 %), 11 gaps (1 %)), *Harknessia fusiformis* (GenBank JQ706139.1; Identities = 614/655 (94 %), 12 gaps (1 %)) and *Harknessia renispora* (GenBank KY720769.1; Identities = 609/652 (93 %), 9 gaps (1 %)).

*Colour illustrations. Corymbia maculata, Bom Bom State Forest, Australia; Colony on oatmeal agar, conidiogenous cells and conidia with long basal appendages. Scale bars = 10 µm.*

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Pedro W. Crous & Johannes Z. Groenewald, Westerdijk Fungal Biodiversity Institute, P.O. Box 85167, 3508 AD Utrecht, The Netherlands; e-mail: p.crous@westerdijkinstitute.nl & e.groenewald@westerdijkinstitute.nl

Angus J. Carnegie, Forest Health & Biosecurity, NSW Department of Primary Industries - Forestry, Level 12, 10 Valentine Ave, Parramatta NSW 2150, NSW 2124, Australia; e-mail: angus.carnegie@dpi.nsw.gov.au

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