Harknessia banksiiigena
**Harknessia banksiigena** Crous & Barber, *sp. nov.*

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

**Classification —** Harknessiaceae, Diaporthales, Sordariomycetes.

Foliicolous. *Conidiomata* pycnidial, separate to gregarious, subepidermal, becoming erumpent, stromatic, globose, up to 250 μm diam, with irregular opening and border of yellowish furfuraceous cells; wall of *textura angularis*. *Conidiophores* reduced to conidiogenous cells lining the inner cavity. *Conidiogenous cells* 6–10 × 4–6 μm, ampulliform to subcylindrical, hyaline, smooth, invested in mucilage, proliferating percurrently at apex. *Conidia* (19–)21–24(–26) × (13–)14(–15) μm (av. 23 x 14 μm) in vitro, fusoid-ellipsoid, apex acutely rounded, aseptate, apiculate, pale yellow-brown, thick-walled, smooth, lacking striations, multi-guttulate. Basal appendage (1.5–)3–4(–7) × 2–2.5 μm in vitro, hyaline, tubular, smooth, thin-walled, devoid of cytoplasm. *Spermatia* not seen.

**Culture characteristics —** Colonies spreading, fluffy, with moderate to abundant aerial mycelium, covering dish in 2 wk at 25 °C. On MEA surface dirty white, reverse pale luteous. On PDA surface dirty white, reverse pale luteous. On OA surface dirty white.

**Typus.** *Australia*, Western Australia, Perth, St. Claire Park, on leaves of *Banksia sessilis var. cygnorum* (*Proteaceae*), 24 June 2015, P.A. Barber (holotype CBS H-23103, culture ex-type CPC 28232 = CBS 142540, ITS, LSU, and cmdA sequences GenBank KY979784, KY979839, and KY979874, MycoBank MB820966).

**Notes —** *Harknessia banksiigena* is phylogenetically related to (see phylogenetic tree in Fungal Planet 591) *H. renispora* (conidia reniform, (13–)14–17 × 9–12.5 μm, av. 15.5 × 11 μm; Nag Raj 1993) and *H. ellipsoidea* (conidia broadly ellipsoid to subglobose, (9–)11–12(–13) × 7(–8) μm, av. 11.5 × 7 μm; Crous et al. 2012b), but can be distinguished morphologically by having larger, fusoid-ellipsoid conidia. Based on a megablast search using the ITS sequence, the best matches were to *H. ravenstreetina* (GenBank JQ706113; Identities = 430/431 (99 %), no gaps) and to *H. ellipsoidea* (GenBank JQ706087; Identities = 618/624 (99 %), 2 gaps (0 %)). However, based on a megablast search using the cmdA sequence, the best matches were to *H. eucalyptorum* (GenBank JQ706178; Identities = 469/482 (97 %), 1 gap (0 %)) and to *H. ravenstreetina* (GenBank JQ706198; Identities = 465/483 (96 %), 3 gaps (0 %)).

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*Colour illustrations.* St. Claire Park, Perth; conidiomata sporulating on OA; conidiogenous cells and conidia. Scale bars = 10 μm.