Harknessia banksiae
Harknessia banksiae Crous, sp. nov.

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

Classification — Harknessiaceae, Diaporthales, Sordariomycetes.

Folicolous. 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 × 3–4 μm, ampulliform to subcylindrical, hyaline, smooth, invested in mucilage, proliferating percurrently at apex. Conidia (20–)22–26(–28) × (11–)12–13(–14) μm (av. 23 ± 12.5 μm) in vitro, broadly fusoid-ellipsoid, apex acutely rounded, aseptate, apiculate, pale yellow-brown, thick-walled, smooth, lacking striations, multi-guttulate. Basal appendage (3–)4–6(–10) × 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 luteous. On PDA surface dirty white, reverse luteous. On OA surface salmon.


Additional specimen examined. AUSTRALIA, Western Australia, Murray Road (at Ranger Station), on leaves of Banksia plumosa (Proteaceae), 21 Sept. 2015, P.W. Crous, HPC 613, CPC 29443, ITS, LSU, cmdA, and tub2 sequences GenBank KY979783, KY979838, KY979873, and KY979939.

Notes — Harknessia banksiae is phylogenetically related to (see phylogenetic tree in Fungal Planet 591) H. ravenstreetina (conidia broadly venticose, (14–)16–18(–20) × (7–)8(–9) μm, av. 17 × 9 μm; Crous et al. 2012b), and H. karwarrae (conidia ellipsoid to ventricose, (12–)13–16(–19) × (10–)11(–12) μm, av. 15 × 11 μm; Lee et al. 2004), although it is distinct in having larger, broadly fusoid-ellipsoid conidia. Based on a megablast search using the ITS sequence of the ex-type strain, the best matches were to H. ravenstreetina (GenBank JQ706113; Identities = 429/431 (99 %), no gaps) and to H. ellipsoidea (GenBank JQ706087; Identities = 620/626 (99 %), 4 gaps (0 %)). However, based on a megablast search using the cmdA sequence of the ex-type strain, the best matches were to H. eucalyptorum (GenBank JQ706178; Identities = 467/483 (97 %), 2 gaps (0 %)) and to H. ravenstreetina (GenBank JQ706198; Identities = 463/484 (96 %), 4 gaps (0 %)). Based on a megablast search using the tub2 sequence of the ex-type strain, the best match was to H. eucalyptorum (GenBank JQ706136; Identities = 823/860 (96 %), 17 gaps (1 %)).

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