

Harknessia proteae



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Harknessia proteae Crous, sp. nov.

Etymology. Named after the host genus from which it was isolated, *Protea*.

Foliicolous. *Conidiomata* separate, immersed, globose to subglobose, unilocular, erumpent, punctiform, up to 400 µm diam; ostiole with pale brown furfuraceous margin; basal and lateral walls up to 7 layers thick, of *textura angularis*. *Conidiophores* reduced to conidiogenous cells. *Macroconidiogenous cells* discrete, hyaline, smooth, lageniform to subcylindrical, 15–25 × 3–5 µm; proliferating enteroblastically near apex. *Macroconidia* fusoid-ellipsoid, with longitudinal striations along its length, at times apiculate, granular to guttulate, brown, with central guttule, base truncate, (30–)33–36(–40) × (14–)15–16(–17) µm. Basal appendage 12–30 × 2–4 µm, collapsing once released from conidiogenous cell; conidiogenous cells and appendages at times enclosed in mucilage. *Microconidiogenous cells* in same conidioma, subcylindrical to lageniform, hyaline, smooth, with periclinal thickening at apex, 6–10 × 3–4 µm. *Microconidia* holoblastic, apical and lateral, hyaline, aseptate, smooth, ellipsoid to fusiform, 4–6 × 2.5–3 µm.

Culture characteristics — Colonies spreading with moderate to abundant aerial mycelium; surface dirty white to cream or pale luteous; covering the dish in 1 mo; sporulating with black conidiomata, oozing black spore masses.

Typus. SOUTH AFRICA, Mpumalanga, Buffelskloof Private Nature Reserve, latitude -25.302596656391604, longitude: 30.504741668701172, on leaves of *Protea roupelliae* subsp. *roupelliae* (*Proteaceae*), Sept. 2012, *M. van der Bank* (holotype CBS H-21435, culture ex-type CPC 21835 = CBS 136426, ITS sequence GenBank KF777162, LSU sequence GenBank KF777215, MycoBank MB805840).

Notes — Two species of *Harknessia* are known from *Proteaceae*, namely *H. leucospermi* (conidia (23–)25–27(–30) µm) and *H. protearum* (conidia (21–)23–24(–26) µm (Lee et al. 2004, Crous et al. 2012d, 2013b)). *Harknessia proteae* can be distinguished from these species by having larger, more fusoid-ellipsoid conidia.

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the LSU sequence are *Wuestneia molokaiensis* (GenBank JQ706246; Identities = 884/884 (100 %), no gaps), *Harknessia gibbosa* (GenBank JQ706226; Identities = 884/884 (100 %), no gaps) and *H. eucalypti* (GenBank JQ706215; Identities = 883/883 (100 %), no gaps). Closest hits using the ITS sequence had highest similarity to *H. ravenstreetina* (GenBank JQ706113; Identities = 428/431 (99 %), no gaps), *H. eucalypti* (GenBank JQ706089; Identities = 733/739 (99 %), Gaps = 4/739 (0 %)) and *H. globispora* (GenBank JQ706105; Identities = 687/693 (99 %), Gaps = 2/693 (0 %)).

Colour illustrations. *Protea roupelliae* subsp. *roupelliae* in Buffelskloof Private Nature Reserve, South Africa (photo credit: Olivier Maurin); conidioma on OA; macro- and microconidia. Scale bars = 10 µm.

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