Harknessia communis
**Fungal Planet 586 – 20 June 2017**

**Harknessia communis** Crous, sp. nov.

*Etymology.* Name refers to the wider host range of this species.

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


*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 and reverse dirty white. On OA surface dirty white.

**Typus.** AUSTRALIA, Western Australia, Denmark, Mount Lindsay Walk Trail, on leaf litter of *Podocarpus* sp. (*Podocarpaceae*), 19 Sept. 2015, P.W. Crous (holotype CBS H-23101, culture ex-type CPC 29028 = CBS 142538, ITS, LSU, and cmdA sequences GenBank KY979778, KY979833, and KY979868, MycoBank MB620964).


*Notes.* — *Species of Harknessia* have a cosmopolitan distribution and are commonly associated with leaves and twigs of a wide range of plants, but they are especially common on *Myrtaceae* and *Proteaceae* (Crous et al. 2012b). Although they appear to be common endophytes, and several species are regarded as important foliar pathogens, the majority of species appear to be of little economic importance (Park et al. 2000). *Harknessia communis* 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), although it is morphologically distinct in having shorter and wider, broadly ellipsoid conidia. *Harknessia podocarpi* (on *Podocarpus parlatorei* from Argentina) has conidia that are 17.5–26 × 11–15 μm (Nag Raj 1993), thus larger than those of *H. communis* reported here. Based on a megablast search using the ITS sequence of the ex-type strain, the best matches were to numerous species of *Harknessia* with 99 % similarity, e.g. *H. ravenstreetina* (GenBank JQ706113; Identities = 429/431 (99 %), no gaps), followed by *H. spermatoidea* (GenBank JQ706120; Identities = 626/632 (99 %), 6 gaps (0 %)), and *H. uromycoides* (GenBank AY720740; Identities = 597/603 (99 %), 5 gaps (0 %)). However, based on a megablast search using the cmdA sequence of the ex-type strain, the best matches were equal to or less than 96 % similar to species of *Harknessia* in the NCBI's GenBank nucleotide database.

*Colour illustrations.* Mount Lindsay Walk Trail; conidiomata sporulating on PNA (scale bar = 250 μm); conidiogenous cells and conidia (scale bars = 10 μm).

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

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: t.burgess@murdoch.edu.au & g.hardy@murdoch.edu.au

© 2017 Naturalis Biodiversity Center & Westerdijk Fungal Biodiversity Institute