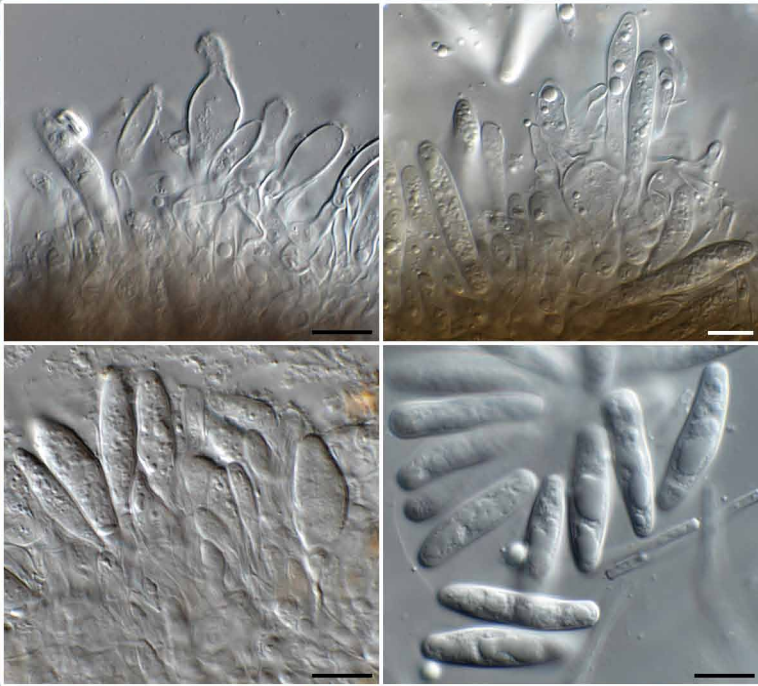


*Saccharata hakeigena*



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## *Saccharata hakeigena* Crous, *sp. nov.*

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

*Classification* — *Saccharataceae*, *Botryosphaeriales*, *Dothi-  
deomycetes*.

*Conidiomata* separate, pycnidial, globose, dark brown, 150–250 µm diam, with central ostiole; wall of 3–8 layers of brown *textura angularis*. *Conidiophores* 0–2-septate, subcylindrical, hyaline, smooth, branched or not, 20–30 × 5–6 µm. *Conidiogenous cells* mostly terminal, subcylindrical, hyaline, smooth, 15–20 × 3–4 µm, proliferating percurrently at apex. *Paraphyses* intermingled among conidiophores, subcylindrical, branched, up to 40 µm long, 3–5 µm diam. *Conidia* solitary, hyaline, smooth, guttulate, granular, aseptate, fusoid-ellipsoid, apex obtuse, base truncate, 4 µm diam, (25–)27–33(–35) × (6–)7–8 µm.

*Culture characteristics* — Colonies flat, spreading, with moderate aerial mycelium and feathery margins, reaching 30 mm diam after 2 wk at 25 °C. On MEA, PDA and OA surface smoke grey, reverse olivaceous grey.

*Typus.* AUSTRALIA, New South Wales, Nullica State Forest, on *Hakea sericea* (*Proteaceae*), 29 Nov. 2016, P.W. Crous (holotype CBS H-23296, culture ex-type CPC 32520 = CBS 143405, ITS, LSU, *rpb2* and *tef1* sequences GenBank MG386057, MG386110, MG386145 and MG386155, MycoBank MB823405).

*Notes* — Species of the genus *Saccharata* are commonly known to occur on species of *Proteaceae* and *Myrtaceae* in the southern hemisphere (Marincowitz et al. 2008). Two species are known from *Hakea*, namely *S. hakeicola* (conidia aseptate, (23–)27–29(–32) × (5–)5.5(–6) µm), and *S. hakeae* (conidia aseptate, (24–)28–31(–33) × (6.5–)7–8 µm). *Saccharata hakeigena* is morphologically similar to *S. hakeae*, but can be distinguished based on the presence of paraphyses (absent in *S. hakeae*), and its DNA phylogeny.

Based on a megablast search using the ITS sequence, the closest matches in NCBI's GenBank nucleotide database were *S. hakeae* (GenBank KY173452; Identities 538/558 (96 %), 3 gaps (0 %)), *Septorioides strobi* (GenBank KT884694; Identities 400/436 (92 %), 4 gaps (0 %)) and *S. eucalyptorum* (GenBank KY173451; Identities 514/561 (92 %), 20 gaps (3 %)). The highest similarities using the LSU sequence were *S. capensis* (GenBank KF766390; Identities 834/856 (97 %), 2 gaps (0 %)), *S. intermedia* (GenBank GU229889; Identities 830/854 (97 %), 2 gaps (0 %)) and *S. kirstenboschensis* (GenBank FJ372409; Identities 827/851 (97 %), 2 gaps (0 %)). The highest similarities using the *rpb2* sequence were *S. daviesiae* (GenBank KY173589; Identities 678/849 (80 %), 33 gaps (3 %)) and *Septorioides pini-thunbergii* (GenBank KX464075; Identities 385/496 (78 %), 15 gaps (3 %)). The highest similarities using the *tef1* sequence were *S. banksiae* (GenBank KY173596; Identities 173/217 (80 %), 14 gaps (6 %)) and *Septorioides proteae* (GenBank KF531789; Identities 148/181 (82 %), 9 gaps (4 %)).

*Colour illustrations.* *Banksia* sp. growing intermixed with *Hakea sericea*; conidiogenous cells and conidia. Scale bars = 10 µm.

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