



Fungal Planet 661 – 20 December 2017

Saccharata acaciae Crous, *sp. nov.*

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

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

Conidiomata solitary or aggregated, brown, globose, 100–200 µm diam, pycnidial with central ostiole; wall of 6–10 layers of pale brown *textura angularis*. *Paraphyses* intermingled among conidiophores, septate, hyaline, smooth, hyphae-like with obtuse ends, 2.5–3.5 µm diam. *Conidiophores* lining the inner cavity, hyaline, smooth, reduced to conidiogenous cells, or with a supporting cell. *Conidiogenous cells* hyaline, smooth, dolii-form, 5–15 × 4–7 µm, proliferating percurrently at apex. *Conidia* solitary, aseptate, hyaline, smooth, prominently guttulate to granular, thin-walled, subcylindrical to fusoid-ellipsoid, apex obtuse, tapering in lower third to truncate base, 3–6 µm diam, with minute marginal frill, (25–)27–33(–42) × (6.5–)7–8(–9) µm.

Culture characteristics — Colonies erumpent, spreading, with sparse aerial mycelium and uneven surface and margin, reaching 15 mm diam after 2 wk at 25 °C. On MEA, PDA and OA surface olivaceous grey, and reverse iron-grey.

Typus. AUSTRALIA, New South Wales, Fitzroy Falls, Morton National Park, on leaves of *Acacia* sp. (*Fabaceae*), 26 Nov. 2016, P.W. Crous (holotype CBS H-23264, culture ex-type CPC 32181 = CBS 143167, ITS and LSU sequences GenBank MG386028 and MG386083, MycoBank MB823368).

Notes — The genus *Saccharata* clusters in the *Saccharataceae* in the *Botryosphaeriales* (Slippers et al. 2013), and is commonly associated with members of *Myrtaceae* and *Proteaceae*. *Saccharata acaciae* is phylogenetically closely related to *S. hakeae*, which is known from *Hakea baxteri* in the Stirling Range National Park in Western Australia. Morphologically, the conidia of *S. hakeae* are similar in range, (24–)28–31(–33) × (6.5–)7–8 µm to those of *S. acaciae*. However, conidiomata of *S. acaciae* (100–200 µm diam) are smaller though than those of *S. hakeae* (200–300 µm diam), which lack paraphyses, and have larger conidiophores, being 0–1-septate, 10–25 × 2.5–3.5 µm (Crous et al. 2016a).

Based on a megablast search using the ITS sequence, the closest matches in NCBI's GenBank nucleotide database were *S. hakeae* (GenBank KY173454; Identities 546/548 (99 %), 1 gap (0 %)), *S. banksiae* (GenBank KY173449; Identities 518/556 (93 %), 9 gaps (1 %)) and *S. petrophiles* (GenBank KY173463; Identities 513/554 (93 %), 9 gaps (1 %)). The highest similarities using the LSU sequence were *S. hakeae* (GenBank KY173542; Identities 827/830 (99 %), no gaps), *S. proteae* (GenBank EU552145; Identities 837/860 (97 %), 2 gaps (0 %)) and *S. intermedia* (GenBank GU229889; Identities 832/855 (97 %), 2 gaps (0 %)).

Colour illustrations. Symptomatic leaves of *Acacia* sp. at Fitzroy Falls; conidiomata sporulating on OA, 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@westerdijkinstituut.nl & e.groenewald@westerdijkinstituut.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: tburgess@murdoch.edu.au & g-hardy@murdoch.edu.au