**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*, Dothideomycetes.

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, doliform, 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, 3.6–6 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%)).