

Myrmecridium banksiae



Fungal Planet 123 – 4 June 2012

***Myrmecridium banksiae* Crous, sp. nov.**

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

Colonies on synthetic nutrient-poor agar. *Hyphae submerged* and creeping, hyaline, thin-walled, 2–4 µm diam. *Conidiophores* arising vertically from creeping aerial hyphae, unbranched, straight, to geniculate-sinuuous, medium brown, not thick-walled, 1–5-septate, 15–90 µm tall, 3–5 µm diam. *Conidiogenous cells* integrated, cylindrical, 10–50 µm long, pale brown, forming a rachis with scattered pimple-shaped denticles less than 1 µm long and approx. 0.5 µm wide, apically pointed, pigmented, slightly thickened. *Conidia* solitary, aseptate, pale brown, thin-walled, smooth to verruculose in middle, granular to guttulate, surrounded by a wing-like gelatinous sheath in the middle, approx. 0.5 µm thick, ellipsoid to obovoid or fusoid, (9–)10–12(–14) × (2.5–)3–3.5 µm, tapering to a subtruncate hilum; hilum unpigmented, not darkened.

Culture characteristics — (in the dark, 25 °C after 3 wk): Colonies flat to erumpent, spreading, lacking aerial mycelium on PDA and OA, with moderate aerial mycelium on MEA, reaching 50 mm diam. On MEA surface grey olivaceous, outer region greyish sepia and cinnamon; on OA grey olivaceous with patches of cinnamon; on PDA cinnamon.

Typus. AUSTRALIA, Victoria, Melbourne, *Banksia* leaf litter (*Proteaceae*), 1 Aug. 2011, P.W. Crous, holotype CBS H-20967, cultures ex-type CPC 19853, 19852 = CBS 132537, ITS sequence GenBank JX069871 and LSU sequence GenBank JX069855, MycoBank MB800388.

Notes — The genus *Myrmecridium* was established by Arzanlou et al. (2007) on the basis of its hyaline mycelium, and pale to unpigmented, pimple-like denticles. Three species are presently known, namely *M. schulzeri* (var. *schulzeri* and var. *tritici*) (conidia 6–12 × 3–4 µm), *M. flexuosum* (conidia 5–9 × 3–4 µm), and *M. phragmitis* (conidia 6.5–9 × 2.5–3.5 µm; Crous et al. 2011b). *Myrmecridium banksiae* is easily distinguishable from known species by having larger conidia (9–14 × 2.5–3.5 µm).

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hit using the ITS sequence is *Myrmecridium schulzeri* (GenBank EU041778; Identities = 514/530 (97 %), Gaps = 5/530 (1 %)), followed by *Myrmecridium phragmitis* (GenBank JQ044425; Identities = 521/547 (95 %), Gaps = 6/547 (1 %)). Closest hits using the LSU sequence yielded highest similarity to *Myrmecridium schulzeri* (GenBank EU041835; Identities = 864/865 (99 %), Gaps = 0/865 (0 %)), *Myrmecridium phragmitis* (GenBank JQ044444; Identities = 869/884 (98 %), Gaps = 0/884 (0 %)) and *Myrmecridium flexuosum* (GenBank EU041825; Identities = 855/865 (99 %), Gaps = 0/865 (0 %)).

Colour illustrations. Coastal region along Great Ocean Road; colony sporulating on synthetic nutrient-poor agar; conidiophores, conidiogenous cells and conidia. Scale bars = 10 µm.