

*Myrmecridium phragmiticola*



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## *Myrmecridium phragmiticola* Crous & Akulov, *sp. nov.*

*Etymology.* Name refers to the host genus *Phragmites* from which it was isolated.

*Classification* — *Myrmecridiaceae*, *Myrmecridiales*, *Sordariomycetes*.

On SNA: *Mycelium* consisting of hyaline, smooth, branched, septate, 2–3 µm diam hyphae. *Conidiophores* unbranched, erect, straight, medium brown, thick-walled, 2–4-septate, up to 70 µm tall, 3–3.5 µm diam; basal cell 4–6 µm diam. *Conidigenous cells* terminal, integrated, subcylindrical, 25–35 µm long, pale brown, forming a rachis with pimple-shaped denticles less than 1 µm long and 0.5 µm diam; slightly thickened. *Conidia* solitary, aseptate, pale brown, thin-walled, smooth, guttulate, with or without a wing-like gelatinous sheath, ellipsoid to fusoid, (7–)8–9 × (2.5–)3 µm; hilum unthickened nor darkened, 0.5 µm diam.

*Culture characteristics* — Colonies flat, spreading, with moderate aerial mycelium and smooth, lobate margin, reaching 30 mm diam after 2 wk at 25 °C. On MEA surface isabelline, reverse hazel. On PDA surface and reverse greyish sepia. On OA surface isabelline.

*Typus.* UKRAINE, Sumy region, bank of Vorskla river, NNP Hetmanskyi, Klymentove village, on leaves of *Phragmites australis* (*Poaceae*), 5 Aug. 2018, A. Akulov, HPC 2554, AS 6809 (holotype CBS H-24351, culture ex-type CPC 36367 = CBS 146628; ITS and LSU sequences GenBank MT373366.1 and MT373349.1, MycoBank MB835400).

*Notes* — Arzanlou et al. (2007) established the genus *Myrmecridium* to accommodate taxa with hyaline mycelium, pigmented, solitary conidiophores with pimple-like denticles, and 0–1-septate, ellipsoid conidia with a mucoid sheath. *Myrmecridium phragmiticola* should be compared to *M. phragmites* (*Phragmites australis*, Netherlands), which has 0–1-septate conidia, (6.5–)7–8(–9) × (2.5–)3(–3.5) µm (Crous et al. 2011). Although the conidia are similar in size, those of *M. phragmiticola* are aseptate.

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Myrmecridium phragmitis* (strain CBS 131311, GenBank NR\_137782.1; Identities = 531/552 (96 %), 6 gaps (1 %)), *Myrmecridium spartii* (strain CBS 140006, GenBank NR\_155376.1; Identities = 523/543 (96 %), 4 gaps (0 %)), and *Myrmecridium banksiae* (strain CBS 132536, GenBank NR\_111762.1; Identities = 522/546 (96 %), 4 gaps (0 %)). Closest hits using the **LSU** sequence are *Myrmecridium schulzeri* (strain CBS 188.96, GenBank EU041829.1; Identities = 855/860 (99 %), no gaps), *Myrmecridium banksiae* (strain CBS 132536, GenBank NG\_042684.1; Identities = 862/870 (99 %), no gaps), and *Myrmecridium flexuosum* (strain CBS 398.76, GenBank EU041825.1; Identities = 852/860 (99 %), no gaps).

*Colour illustrations.* *Phragmites australis* along the bank of the Vorskla river. Conidiophores with conidigenous cells; conidia. Scale bars = 10 µm.

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