

Myrmecridium thailandicum



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Myrmecridium thailandicum Crous & Cheew., *sp. nov.*

Etymology. Named after the country where this fungus was collected, Thailand.

On SNA *mycelium* consisting of hyaline, thin-walled, smooth, 2–3 µm diam hyphae. *Conidiophores* erect, unbranched, straight, medium brown, thick-walled, up to 300 µm tall, 3–4 µm wide, 3–15-septate, basal cell often inflated, 3–5 µm wide. *Conidiogenous cells* integrated, cylindrical, 12–30 µm long, medium brown, fertile region forming a rachis with pimple-like denticles arranged in whorls along the conidiogenous axis, less than 0.5 µm long, and 0.5 µm wide, unpigmented, slightly thickened scars. *Conidia* solitary, pale brown, thin-walled, finely verruculose, on MEA some conidia have a wing-like gelatinous sheath up to 0.5 µm thick, ellipsoid to obovoid or fusiform, (6–)7(–8) × (3–)3.5(–4) µm; tapering from obtuse apex to subtruncate base; hilum unthickened, 0.5 µm thick.

Culture characteristics — Colonies reaching 60 mm diam after 2 wk, flat, spreading, with sparse aerial mycelium and feathery margin. On MEA surface umber with patches of orange, in reverse orange; on PDA surface sienna, reverse umber; on OA centre umber, outer region luteous.

Typus. THAILAND, Chiang Mai, Boa Keaw Silvicultural Research Station, on reed litter next to pond, 29 Oct. 2012, *P.W. Crous* (holotype CBS H-21448, culture ex-type CPC 21696, 21694 = CBS 136551, ITS sequence GenBank KF777169, LSU sequence GenBank KF777222, MycoBank MB805854).

Notes — The genus *Myrmecridium* was established by Arzanlou et al. (2007) to accommodate taxa in the *Ramichloridium* complex that have hyaline to pale brown hyphae, relatively unpigmented pimple-like denticles and aseptate conidia with wing-like gelatinous sheaths. The genus is presently known from four species, including two varieties (Crous et al. 2011a, 2012c).

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the LSU sequence are *Myrmecridium banksiae* (GenBank JX069855; Identities = 865/885 (98 %), no gaps), *M. schulzeri* (GenBank EU041835; Identities = 866/887 (98 %), Gaps = 2/887 (0 %)) and *M. flexuosum* (GenBank EU041825; Identities = 865/887 (98 %), Gaps = 2/887 (0 %)). Closest hits using the ITS sequence had highest similarity to *M. flexuosum* (GenBank EU041768; Identities = 481/523 (92 %), Gaps = 7/523 (1 %)), *M. schulzeri* (GenBank EU041777; Identities = 514/560 (92 %), Gaps = 9/560 (1 %)) and *M. phragmitis* (GenBank JQ044425; Identities = 509/557 (91 %), Gaps = 6/557 (1 %)).

Colour illustrations. Reed litter next to pond at Chiang Mai, Boa Keaw Silvicultural Research Station; colony on OA; conidiophores and conidia. Scale bars = 10 µm.

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