Cymostachys thailandica
Fungal Planet description sheets

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**Cymostachys thailandica** Crous, sp. nov.

**Etymology.** Name refers to Thailand, the country where this fungus was collected.

**Classification.** *Stachybotryaceae, Hypocreales, Sordariomycetes.*

Conidiophores macronematous, mononematous, mostly in clusters, thin-walled, cymosely branched, erect, straight to flexuous, hyaline, 1–2-septate, smooth to slightly verruculose, 50–120 × 4–5 µm, bearing a whorl of 3–6 conidiogenous cells. Conidiogenous cells phialidic, clavate, olivaceous brown to dark brown at the apex, paler towards the base, smooth to slightly verruculose, 8–12 × 4–6 µm, with conspicuous collarette. Conidia acrogenous, aseptate, fabiform, dark brown, smooth to verruculose, (8–)9(–11) × (4–)5(–6) µm, rounded at ends, aggregating in mucoid mass.

**Culture characteristics.** Colonies spreading, with folded surface (MEA), sparse aerial mycelium and smooth, lobate margin, reaching 37 mm diam after 2 wk at 25 °C. On MEA surface pale olivaceous grey, reverse sienna. On PDA surface and reverse olivaceous grey. On OA surface isabelline.

**Typus.** **Thailand**, Ratchaburi Province, on leaves of unidentified vine, 2008, P.W. Crous, HPC 2252 (holotype CBS H-23773, culture ex-type CPC 34505 = CBS 145079, ITS, LSU, rpb2, tef1 and tub2 sequences GenBank MK047448.1, MK047498.1, MK047546.1, MK047566.1 and MK047582.1, MycoBank MB 828199).

Notes — *Cymostachys* was established for stachybotrys-like fungi characterised by irregularly cymosely, branched conidiophores and olivaceous brown to dark brown, fabiform conidia. *Cymostachys thailandica* is phylogenetically distinct, but related to *C. coffeicola*, which is known from leaves of Coffea arabica (Cuba), and *Poinsettia* sp. (Thailand) (Lombard et al. 2016). The genus presently includes four species. Based on a megablast search of NCBI’s GenBank nucleotide database, the closest hits using the ITS sequence had highest similarity to *Cymostachys coffeicola* (GenBank KU846052.1; Identities = 562/569 (99 %), 5 gaps (0 %)), *Cymostachys fabispora* (GenBank KU846054.1; Identities = 541/548 (95 %), 5 gaps (0 %)) and *Stachybotrys renispora* (GenBank KU144929.1; Identities = 543/551 (99 %), 6 gaps (1 %)). Closest hits using the LSU sequence are *Cymostachys coffeicola* (GenBank MH872746.1; Identities = 889/895 (99 %), 2 gaps (0 %)), *Stachybotrys nephrospora* (GenBank KP893314.1; Identities = 887/892 (99 %), 1 gap (0 %)) and *Mennoniella echinata* (GenBank MH866746.1; Identities = 877/895 (98 %), 3 gaps (0 %)). Closest hits using the rpb2 sequence had highest similarity to *Cymostachys coffeicola* (GenBank KU846081.1; Identities = 712/721 (99 %), no gaps), *Cymostachys fabispora* (GenBank KU846082.1; Identities = 695/721 (96 %), no gaps) and *Striatibotrys eucylindrospora* (GenBank KU846975.1; Identities = 650/750 (89 %), no gaps). Closest hits using the tef1 sequence had highest similarity to *Cymostachys coffeicola* (GenBank KU846097.1; Identities = 455/476 (96 %), 2 gaps (0 %)), *Cymostachys fabispora* (GenBank KU846098.1; Identities = 418/478 (87 %), 11 gaps (2 %)) and *Striatibotrys rabdospora* (GenBank KU847089.1; Identities = 232/263 (88 %), 5 gaps (1 %)). Closest hits using the tub2 sequence had highest similarity to *Cymostachys coffeicola* (GenBank KU846113.1; Identities = 336/343 (98 %), no gaps), *Cymostachys fabispora* (GenBank KU846114.1; Identities = 330/343 (96 %), 3 gaps (0 %)) and *Cymostachys garethjonesii* (GenBank KY124126.1; Identities = 274/286 (96 %), 3 gaps (1 %)).

**Colour illustrations.** Indigenous forest in Thailand; colony sporulating on oatmeal agar, conidiophores, conidiogenous cells and conidia. Scale bars = 10 µm.