

*Gymnostachys arthraeruae*

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***Cymostachys arthraeruae* Crous, sp. nov.**

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

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

*Mycelium* consisting of hyaline, smooth, irregular, 3–5 µm diam hyphae, at times forming swollen, thick-walled chains of chlamydospore-like structures, 7–9 µm diam. *Conidiophores* erect, solitary or in groups, unbranched, subcylindrical, 1(–2)-septate, 30–110 × 3–4 µm, upper cell becoming verruculose, and isabelline in colour, bearing a whorl of 3–6 conidiogenous cells. *Conidiogenous cells* clavate, phialidic, isabelline to dark brown and verruculose at apex, becoming paler so towards base, with minute collarettes. *Conidia* aseptate, guttulate, broadly ellipsoid to slightly obovoid (to subcylindrical on OA), finely verruculose, surface with continuously sigmoid striations, isabelline, apex obtuse, tapering to truncate hilum, 8–9(–11) × (6–)7–8(–10) µm.

*Culture characteristics* — Colonies flat, spreading, with sparse aerial mycelium and feathery, lobate margin, reaching 50 mm diam after 2 wk at 25 °C. On MEA surface sepia to hazel, reverse sepia; on PDA surface cinnamon with patches of isabelline, reverse cinnamon; on OA surface isabelline.

*Typus.* NAMIBIA, Walvis Bay, on *Arthraerua leubnitziae* (*Amaranthaceae*), 20 Nov. 2019, P.W. Crous, HPC 3127 (holotype CBS H-24549, culture ex-type CPC 39335 = CBS 147081, ITS, LSU, *rpb2*, *tef1* (first part) and *tef1* (second part) sequences GenBank MZ064454.1, MZ064511.1, MZ078211.1, MZ078235.1 and MZ078255.1, MycoBank MB 839540).

*Notes* — Morphologically, *Cymostachys arthraeruae* is closest to *C. coffeicola* (conidia fabiform, smooth to verruculose, (7–)7.5–8.5(–10) × (5–)5.5–6.5(–7) µm; Lombard et al. 2016), from which it is distinct in having larger conidia.

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Memnoniella oenanthes* (strain IBT 9473, GenBank KX690115.1; Identities = 489/498 (98 %), no gaps), *Cymostachys coffeicola* (strain CPC 25009, GenBank KU846053.1; Identities = 503/513 (98 %), three gaps (0 %)) and *Stachybotrys nephrospora* (strain Stanep1907, GenBank KF626486.1; Identities = 478/488 (98 %), one gap (0 %)). Closest hits using the **LSU** sequence are *Cymostachys coffeicola* (strain CBS 252.76, GenBank MH872746.1; Identities = 871/876 (99 %), one gap (0 %)), *Stachybotrys nephrospora* (strain LAMIC0040/07, GenBank KP893312.1; Identities = 871/876 (99 %), two gaps (0 %)) and *Cymostachys thailandica* (strain CBS 145079, GenBank NG\_066294.1; Identities = 871/877 (99 %), three gaps (0 %)). Closest hits using the **rpb2** sequence had highest similarity to *Cymostachys fabispora* (strain MUCL 39004, GenBank KU846082.1; Identities = 680/719 (95 %), no gaps), *Cymostachys thailandica* (strain CBS 145079, GenBank MK047546.1; Identities = 775/822 (94 %), no gaps) and *Cymostachys coffeicola* (strain CBS 252.76, GenBank KU846081.1; Identities = 677/719 (94 %), no gaps). Closest hits using the **tef1** (first part) sequence had highest similarity to *Cymostachys coffeicola* (strain CBS 252.76, GenBank KU846097.1; Identities = 272/325 (84 %), 23 gaps (7 %)), *Cymostachys thailandica* (strain CBS 145079, GenBank MK047566.1; Identities = 272/326 (83 %), 24 gaps (7 %)) and *Striatibotrys eucylindrospora* (strain CBS 949.72, GenBank KU847079.1; Identities = 258/311 (83 %), 17 gaps (5 %)). Closest hits using the **tef1** (second part) sequence had highest similarity to *Striatibotrys eucylindrospora* (as *Stachybotrys eucylindrospora*; strain UAMH 7122, GenBank DQ676617.1; Identities = 764/790 (97 %), two gaps (0 %)), *Stachybotrys microspora* (strain UAMH 7747, GenBank DQ676619.1; Identities = 759/790 (96 %), two gaps (0 %)) and *Stachybotrys chlorohalonata* (voucher MFLU 18-1638, GenBank MN200279.1; Identities = 753/789 (95 %), no gaps).

*Colour illustrations.* Namib Desert with long-lived, fog-dependent *Arthraerua leubnitziae* (pencil bush). Conidiophores; conidiogenous cells giving rise to conidia; conidia. Scale bars = 10 µm.

**Supplementary material**

Also see the phylogenetic tree provided with the supplementary material FP1194.

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