Pseudoacremonium sacchari
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**Pseudoacremonium Crous, gen. nov.**

**Etymology.** Name derived from pseudo- (false-), in Greek) and the genus name Acremonium.

*Mycelium* consisting of hyaline, septate, branched hyphae, developing brown zones with solitary brown, globose chlamydospores. *Conidiophores* erect, subcylindrical, rarely branched, 1–3-septate, up to 80 µm tall, 3–3.5 µm diam, hyaline, smooth, but with age brown, verruculose and warty. *Conidiogenous cells* terminal, integrated (Type III phialides sensu Mostert et al. 2006), either elongate-ampulliform or navicular, tapering towards apex, with prominent periclinal thickening and inconspicuous collarette, hyaline, smooth, becoming brown and verruculose to warty. *Conidia* in unbranched chains, ellipsoid, aseptate, smooth, hyaline, thin-walled, becoming brown, verruculose, guttulate, with scar at each end, somewhat darkened and refractive; older conidia brown and verruculose, appearing flaky when mounted in lactic acid or water.

**Type species.** *Pseudoacremonium sacchari.* MycoBank MB808925.

**Pseudoacremonium sacchari** Crous, sp. nov.

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

*Mycelium* consisting of hyaline, septate, branched, 2–3 µm diam hyphae, developing brown zones with solitary brown, globose, 5–7 µm diam chlamydospores. *Conidiophores* erect, subcylindrical, rarely branched, 1–3-septate, up to 80 µm tall, 3–3.5 µm diam, hyaline, smooth, but with age brown, verruculose and warty. *Conidiogenous cells* terminal, integrated (Type III phialides sensu Mostert et al. 2006), either elongate-ampulliform or navicular, tapering towards apex, 25–30 × 2.5–4 µm, apex 1–1.5 µm diam, with prominent periclinal thickening and inconspicuous collarette, hyaline, smooth, becoming brown and verruculose to warty. *Conidia* in unbranched chains, ellipsoid, aseptate, smooth, hyaline, thin-walled, becoming brown, verruculose, guttulate, with scar at each end, 0.5–1 µm diam, somewhat darkened, and refractive, (6–)7–8(–9) × 2.5(–3) µm; older conidia brown and verruculose, appearing flaky when mounted in lactic acid or water.

Culture characteristics — Colonies reaching 7 mm diam after 2 wk at 22 °C, with sparse aerial mycelium and even, smooth margins. On PDA surface and reverse dirty white. On OA surface pale olivaceous-grey. On MEA surface cinnamon, reverse cinnamon with patches of vinaceous, with a diffuse brick pigment in agar.

**Typus.** VIETNAM, Dong Nai Province, Cat Tien National Park, Nam Cat Tien Sector, on leaves of *Saccharum spontaneum* (Poaceae), in association with *Pyncicula contorta*, 3 Mar. 2013, A. Alexandrova & O. Descherevskaya (holotype CBS H-21704, culture ex-type CPC 23155 = CBS 137990; ITS sequence GenBank HQ232014, LSU sequence GenBank KJ869201, MycoBank MB808926).

Notes — The acremonium-like morphology and pigmented conidia are reminiscent of the genus *Pseudogliomastix*, which clusters outside the *Hypocreales* (Rehner & Samuels 1995), and is thus unavailable to accommodate this taxon, for which the new genus *Pseudoacremonium* is established. *Pseudoacremonium* is characterised by forming chlamydospore, and having mycelium that turns brown with age, and unbranched conidial chains that become brown (encrusted, flaky) with slightly darkened scars at each end of the conidia.

**ITS.** Based on a megablast search of NCBI’s GenBank nucleotide database, the closest hits using the ITS sequence are *Acremonium cerealis* (GenBank AB540571; Identities = 560/663 (88 %), Gaps = 31/633 (4 %)), *Acremonium persicinum* (GenBank AB540575; Identities = 555/634 (88 %), Gaps = 30/634 (4 %)) and *Stromatonectria caraganae* (GenBank HQ112288; Identities = 694/799 (87 %), Gaps = 41/799 (5 %)).

**LSU.** Based on a megablast search of NCBI’s GenBank nucleotide database, the closest hits using the LSU sequence are *Lasionectria mantuana* (GenBank GQ505994; Identities = 826/843 (98 %), no gaps), *Acremonium cerealis* (GenBank HQ232014; Identities = 815/832 (98 %), Gaps = 1/832 (0 %)) and *Hydropisphaera erubescens* (GenBank AY545726; Identities = 841/859 (98 %), Gaps = 2/859 (0 %)).

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