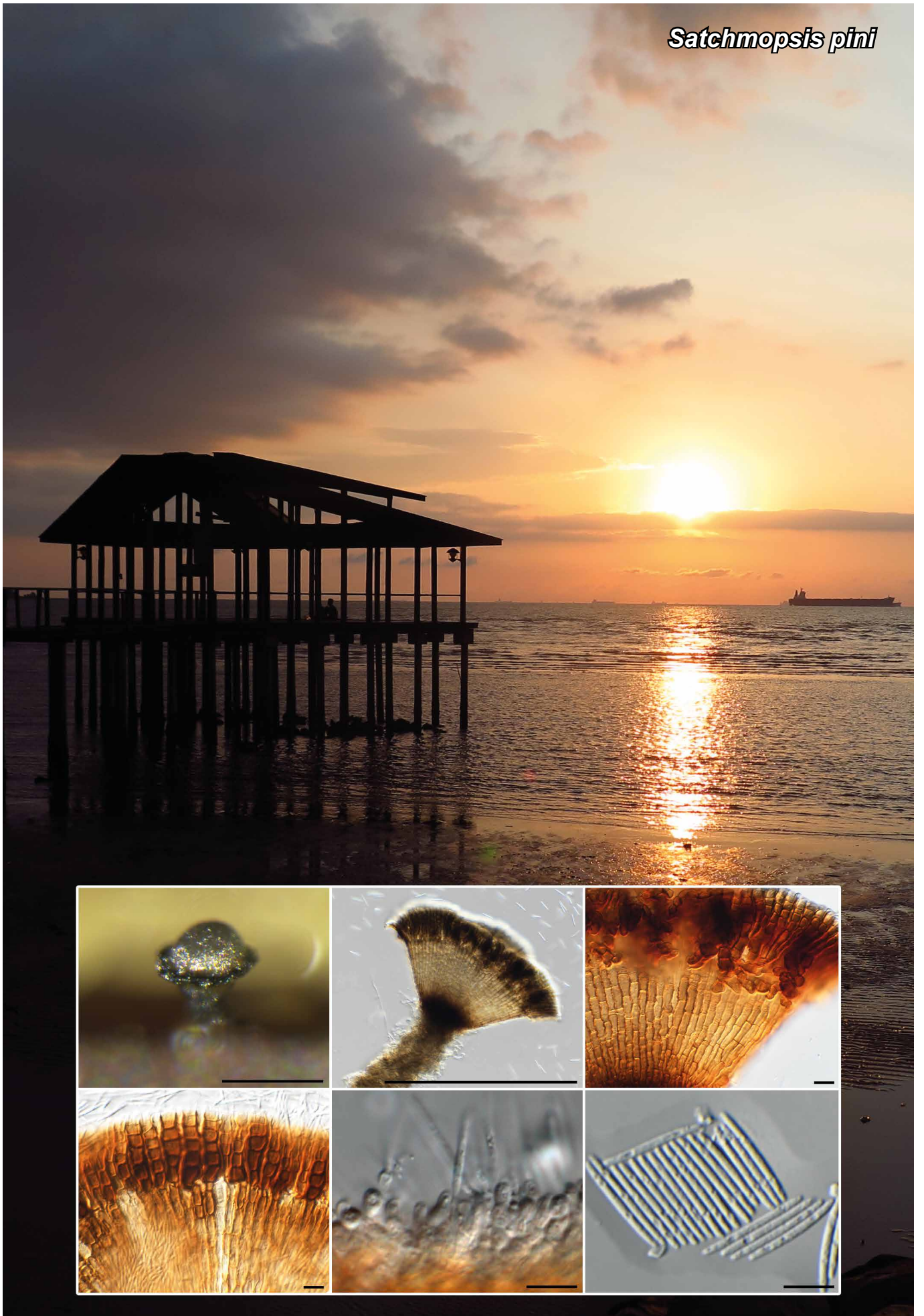


Satchmopsis pini



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Satchmopsis pini Crous, *sp. nov.*

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

Classification — *Cochlearomycetaceae*, *Leotiales*, *Leotiomycetes*.

Conidiomata cupulate, superficial, 140–200 µm diam, and 120–160 µm deep, dark brown, attached centrally to a brown stroma via a dark brown stalk, up to 150 µm tall, 50 µm wide; conidiomatal wall of two regions, the lower region of brown cells, the upper region of cylindrical cells with flat to obtuse edge, 3–7 × 4–7 µm; terminal 5–13 cell layers are prominently thick-walled, darker brown, and can give rise to hyphal outgrowths on outside of conidiomatal margin. *Conidiogenous cells* restricted to lower part of basal wall, 4–10 × 2–3 µm, doliform to lageniform, phialidic with periclinal thickening, hyaline with indistinct collarette. *Conidia* hyaline, smooth, aseptate, guttulate, subcylindrical, straight with obtuse ends, (11–)12–14(–15) × 1–1.5 µm.

Culture characteristics — Colonies flat, spreading, with sparse aerial mycelium and feathery, lobate margin, covering dish after 2 wk at 25 °C. On MEA, PDA and OA surface amber with patches of sepia, reverse umber.

Typus. MALAYSIA, on dead needles of *Pinus tecunumanii* (*Pinaceae*), 31 Oct. 2010, *M.J. Wingfield*, HPC 2657 (holotype CBS H-24360, culture ex-type CPC 36649 = CBS 146687; ITS, LSU, *actA*, *rpb2*, *tef1* and *tub2* sequences GenBank MT373378.1, MT373360.1, MT375096.1, MT375104.1, MT375112.1 and MT375123.1, MycoBank MB835412).

Additional material examined. MALAYSIA, on dead needles of *P. tecunumanii*, 31 Oct. 2010, *M.J. Wingfield*, HPC 2657, culture CPC 36729; ITS, *actA*, *rpb2* and *tef1* sequences GenBank MT373379.1, MT375097.1, MT375105.1 and MT375113.1.

Notes — *Satchmopsis pini* is morphologically distinct from *S. brasiliensis* and *S. metrosideri* in having cupulate conidiomata with a prominently thick-walled, darker brown upper region, giving rise to hyphal outgrowths on outside of conidiomatal margin. Furthermore, conidiomata are centrally attached to a brown stroma via a long, dark brown stalk, which is absent in *S. brasiliensis* and *S. metrosideri*.

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the ITS sequence had highest similarity to *Satchmopsis brasiliensis* (strain CBS 420.93, GenBank DQ195784.1; Identities = 507/507 (100 %), no gaps), *Massarina corticola* (strain 4607, GenBank FR668004.1; Identities = 420/451 (93 %), 9 gaps (1 %)), and *Capturomyces luteus* (strain CBS 144839, GenBank NR_165905.1; Identities = 473/510 (93 %), 11 gaps (2 %)). Closest hits using the LSU sequence are *Satchmopsis brasiliensis* (strain CBS 420.93, GenBank DQ195796.1; Identities = 873/873 (100 %), no gaps), *Cochlearomyces eucalypti* (strain CBS 142622, GenBank NG_059052.1; Identities = 840/877 (96 %), 4 gaps (0 %)), and *Pragmopora* cf. *bacillifera* (voucher G.M. 2019-04-30.1, GenBank MK900749.1; Identities = 843/883 (95 %), 10 gaps (1 %)). No significant hits were obtained when the *actA*, *rpb2*, *tef1* and *tub2* sequences were used in blastn and megablast searches. The ITS, *actA*, *rpb2* and *tef1* sequences of CPC 36649 and 36729 were identical; ITS: 507/507, *actA*: 596/596, *rpb2*: 879/879 and *tef1*: 405/405.

Colour illustrations. Beach area in Malaysia. Conidioma on OA; conidioma on SNA; conidiomatal wall; conidiogenous cells; conidia. Scale bars = 200 µm (conidiomata), 10 µm (all others).

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