

*Satchmopsis metrosideri*



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***Satchmopsis metrosideri* Crous, sp. nov.**

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

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

*Conidiomata* cupulate, superficial, 100–140 µm diam at apex, 130–180 µm deep, dark brown, attached to a basal stroma of dark brown cells that occupy the stomatal chamber; wall consisting of two regions, the lower region having thick-walled dark brown cells up to 5 layers thick; upper region on thin-walled paler cells, cylindrical, 10–17 × 3–4 µm, with even, smooth flat edge. In culture conidiomata are paler in colour and much larger, flattened, cupulate, and margins have cells that are lobate due to expanding growth (not flat as *in vivo*). *Conidiogenous cells* restricted to lower part of basal wall, 3–7 × 2–3 µm, doliform to lageniform, phialidic with periclinal thickening, hyaline with indistinct collarette. *Conidia* hyaline, smooth, aseptate, guttulate, subcylindrical, predominantly straight with obtuse ends, (15–)16–17(–19) × 1–1.5 µm.

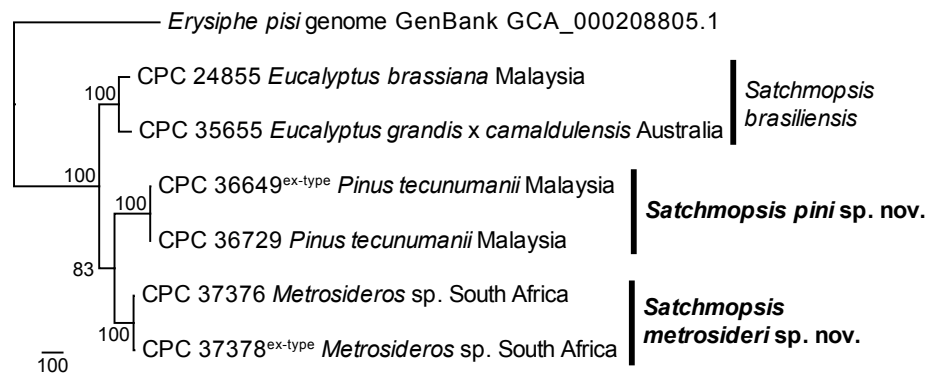
*Culture characteristics* — Colonies flat, spreading, with sparse aerial mycelium and feathery, lobate margin, reaching 60 mm diam after 2 wk at 25 °C. On MEA, PDA and OA surface umber with patches of sepia, reverse umber.

*Typus.* SOUTH AFRICA, Eastern Cape Province, Haga Haga, Amathole, on leaf litter of *Metrosideros excelsa* (*Myrtaceae*), 2015, *M.J. Wingfield*, HPC 2754 (holotype CBS H-24359, culture ex-type CPC 37378 = CBS 146686; ITS, LSU, *actA*, *rpb2*, *tef1* and *tub2* sequences GenBank MT373377.1, MT373359.1, MT432194.1, MT375103.1, MT375111.1 and MT375122.1, MycoBank MB835411).

*Additional material examined.* SOUTH AFRICA, Eastern Cape Province, Haga Haga, Amathole, on leaf litter of *M. excelsa*, 2015, *M.J. Wingfield*, HPC 2754, culture CPC 37376; ITS, *actA*, *rpb2*, *tef1* and *tub2* sequences GenBank MT432187.1, MT432188.1, MT432189.1, MT432190.1 and MT432190.1.

*Notes* — The genus *Satchmopsis*, based on *S. brasiliensis* (*Eucalyptus paniculata*, Brazil; conidia 11.5–15.5 × 1–1.5 µm) (Sutton 1975) was introduced for a genus of cupulate coelomycetes with aseptate conidia. *Satchmopsis* is commonly isolated from eucalypt leaf litter in South America (Crous et al. 2006). The present collection, from *Metrosideros excelsa* leaf litter collected in South Africa, differs from *S. brasiliensis* in being phylogenetically distinct, and also having longer conidia.

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 CPC 11017, GenBank DQ195786.1; Identities = 506/507 (99 %), no gaps), *Capturomyces luteus* (strain CBS 144839, GenBank NR\_165905.1; Identities = 474/511 (93 %), 12 gaps (2 %)), and *Capturomyces funiculosus* (strain CBS 144840, GenBank NR\_165904.1; Identities = 471/512 (92 %), 13 gaps (2 %)). Closest hits using the LSU sequence are *Satchmopsis brasiliensis* (strain CPC 11017, GenBank DQ195798.1; Identities = 857/858 (99 %), no gaps), *Cochlearomyces eucalypti* (strain CBS 142622, GenBank NG\_059052.1; Identities = 828/862 (96 %), 4 gaps (0 %)), and *Pallidophorina paarla* (strain GLMC 791, GenBank MK314612.1; Identities = 824/863 (95 %), 10 gaps (1 %)). Closest hits using the *rpb2* sequence had highest similarity to *Chlorociboria spathulata* (strain D1822, GenBank JN985530.1; Identities = 695/887 (78 %), 8 gaps (0 %)), *Moellerodiscus lentus* (strain 10544, GenBank MH729344.1; Identities = 693/887 (78 %), 18 gaps (2 %)), and *Microscypha ellisii* (voucher KUS-F52489, GenBank JN086863.1; Identities = 687/890 (77 %), 16 gaps (1 %)). No significant hits were obtained when the *actA*, *tef1* and *tub2* sequences were used in blastn and megablast searches. The ITS, *actA*, *rpb2* and *tef1* sequences of CPC 37378 and 37376 were identical; ITS: 508/508, *actA*: 644/644, *rpb2*: 911/911, and *tef1*: 552/552; and *tub2* almost identical: 695/701.



The single most parsimonious tree obtained from a phylogenetic analysis of the *Satchmopsis* ITS/*actA*/*rpb2*/*tef1*/*tub2* alignment (7 strains including the outgroup; 3220 characters including alignment gaps analysed: 1911 constant, 935 variable and parsimony-uninformative and 374 parsimony-informative). PAUP v. 4.0b10 (Swofford 2003) was used to analyse the data. The tree was rooted to *Erysiphe pisi* (genome GenBank GCA\_000208805.1) and the scale bar indicates the number of changes. Parsimony bootstrap support values higher than 49 % are shown at the nodes and the novel species are highlighted in **bold**. Type status is indicated in superscript. Tree statistics: TL = 1572, CI = 0.964, RI = 0.880, RC = 0.849. The alignment and tree were deposited in TreeBASE (Submission ID S26166).

*Colour illustrations.* Beach area in Haga Haga, with *Metrosideros* in background. Conidioma on OA; conidioma on SNA; conidiomatal wall; conidia. Scale bars = 140 µm (conidiomata), 10 µm (all others).

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