

Seiridium syzygii



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***Seiridium syzygii* Crous, sp. nov.**

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

Classification — *Sporocadaceae*, *Xylariales*, *Sordariomycetes*.

Conidiomata stromatic, separate, globose, immersed to erumpent, black, up to 300 µm diam, unilocular; walls of 3–6 layers of brown *textura angularis*. *Conidiophores* lining the inner cavity, subcylindrical, unbranched or branched below, hyaline, 1–3-septate, smooth, up to 40 µm long. *Conidiogenous cells* discrete, integrated, subcylindrical, 7–13 × 2.5–3 µm, with several percurrent proliferations near apex. *Conidia* fusoid, wall smooth, not constricted at septa, 5-septate with central pore, guttulate, (24–)25–28(–31) × 8(–10) µm, wall 1.5 µm thick, with appendages; basal cell obconic, subhyaline to pale brown with a single, unbranched central appendage, 5–12 µm; apical cell broadly conical to bluntly rounded, subhyaline to pale brown with central appendage, unbranched, 5–12 µm.

Culture characteristics — Colonies flat, spreading, with moderate aerial mycelium and lobate, smooth margin, reaching 35 mm diam after 2 wk at 25 °C. On MEA surface pale grey olivaceous, reverse sienna in middle, umber in outer region; on PDA surface and reverse grey olivaceous; on OA surface olivaceous grey.

Typus. SOUTH AFRICA, Mpumalanga, Mbombela, Lowveld Botanical Garden, on twigs of *Syzygium cordatum* (*Myrtaceae*), Nov. 2018, *P.W. Crous*, HPC 3149 (holotype CBS H-24543, culture ex-type CPC 39149 = CBS 147078, ITS and LSU sequences GenBank MZ064444.1 and MZ064501.1, MycoBank MB 839533).

Additional material examined. SOUTH AFRICA, Mpumalanga, Mbombela, Lowveld Botanical Garden, on twigs of *Syzygium cordatum* (*Myrtaceae*), Nov. 2018, *P.W. Crous*, HPC 3149 (CBS H-24482, culture CPC 38822 = CBS 146970, ITS, LSU, *tef1* (first part) and *tub2* sequences GenBank MZ064445.1, MZ064502.1, MZ078231.1 and MZ078271.1).

Colour illustrations. Leaves of *Syzygium cordatum*. Conidiomata on OA; conidiogenous cells giving rise to conidia; conidia. Scale bars = 300 µm (conidiomata), 10 µm (all others).

Notes — *Seiridium syzygii* has conidia that are similar to those of *S. podocarpi* (on *Podocarpus latifolius*, South Africa, (23–)25–28(–30) × (8–)9–10 µm; Crous et al. 2014a, Bonthond et al. 2018), but it has shorter conidiophores and conidiogenous cells, and is also phylogenetically distinct from the latter species.

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence of CPC 39149 had highest similarity to *Seiridium podocarpi* (strain CBS 137995, GenBank NR_156589.1; Identities = 584/588 (99 %), no gaps), *Seiridium camelliae* (strain MFLUCC 12-0647, GenBank NR_158886.1; Identities = 525/534 (98 %), three gaps (0 %)) and *Seiridium cancrinum* (strain CBS 226.55, GenBank NR_160577.1; Identities = 567/597 (95 %), nine gaps (1 %)). The ITS sequences of CPC 39149 and 38822 differ by a single substitution (586/587 (99 %)). Closest hits using the **LSU** sequence of CPC 39149 are *Seiridium cardinale* (strain CBS 172.56, GenBank MH869107.1; Identities = 877/877 (100 %), no gaps), *Seiridium neocupressi* (strain CBS 142625, GenBank MH554329.1; Identities = 834/834 (100 %), no gaps) and *Nothoseiridium podocarpi* (strain CPC 36967, GenBank MT373346.1; Identities = 869/870 (99 %), no gaps). The LSU sequences of CPC 39149 and 38822 are identical (849/849 (100 %)). Closest hits using the **tef1** sequence of CPC 38822 had highest similarity to *Seiridium podocarpi* (strain CBS 137995, GenBank LT853198.1; Identities = 501/540 (93 %), five gaps (0 %)), *Seiridium eucalypti* (strain CBS 343.97, GenBank LT853196.1; Identities = 474/545 (87 %), 23 gaps (4 %)) and *Seiridium kartense* (as *Seiridium* sp. GB-2017a; strain CBS 142629, GenBank LT853197.1; Identities = 468/542 (86 %), 18 gaps (3 %)). Closest hits using the **tub2** sequence of CPC 38822 had highest similarity to *Seiridium podocarpi* (strain CBS 137995, GenBank LT853248.1; Identities = 667/710 (94 %), six gaps (0 %)), *Seiridium cupressi* (strain CMW18607, GenBank DQ926979.1; Identities = 290/312 (93 %), two gaps (0 %)) and *Seiridium personiae* (strain CBS 143445, GenBank MG386163.1; Identities = 367/403 (91 %), four gaps (0 %)).

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