

Nothoseiridium podocarpi



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Nothoseiridium Crous, gen. nov.

Etymology. Name refers to the fact that it is related to *Seiridium*, but morphologically distinct from that genus.

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

Plant pathogenic. *Conidiomata* black, round, flattened, acervular; wall of several layers of brown *textura epidermoidea*. *Conidiophores* reduced to conidiogenous cells, arising from basal

layers of stroma, hyaline, smooth, subcylindrical to ampulliform, annellidic. *Conidia* fusoid, slightly curved, smooth-walled, guttulate, pale brown, unequally 4-euseptate; basal cell obconic with truncate hilum, hyaline; median cells pale brown; apical cell obtuse, hyaline; apical and basal appendage filiform, flexuous, unbranched, excentric.

Type species. *Nothoseiridium podocarpi* Crous.
MycoBank MB835396.

Nothoseiridium podocarpi Crous, sp. nov.

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

Associated with brown leaf spots. *Conidiomata* (on *Podocarpus* leaves and on SNA), black, round, flattened, acervular, 300–400 µm diam; wall of several layers of brown *textura epidermoidea*, splitting open all along outer margin, appearing saucer-shaped on leaf. *Conidiophores* reduced to conidiogenous cells, arising from basal layers of stroma, hyaline, smooth, subcylindrical to ampulliform, annellidic, 5–10 × 2.5–3 µm. *Conidia* fusoid, slightly curved, smooth-walled, guttulate, pale brown, unequally 4-euseptate; basal cell obconic with truncate hilum, hyaline; median cells pale brown; apical cell obtuse, hyaline. Apical cell 2.5–4 µm long; second cell 2.5–4 µm long; third cell 4–5 µm long; fourth cell 12–14 µm long; basal cell 3–4 µm long; conidia (22–)24–25(–27) × (2.5–)3 µm; apical appendage filiform, flexuous, unbranched, excentric, 7–10 µm long; basal appendage filiform, flexuous, unbranched, excentric, 6–7 µm long.

Culture characteristics — Colonies spreading, with moderate aerial mycelium and smooth, lobate margin, covering dish after 2 wk at 25 °C. On MEA surface smoke grey, reverse olivaceous grey. On PDA surface and reverse olivaceous grey. On OA surface pale olivaceous grey.

Typus. SOUTH AFRICA, Western Cape Province, Knysna, on leaf spots of *Podocarpus latifolius* (*Podocarpaceae*), Nov. 2018, M.J. Wingfield, HPC 2710 (holotype CBS H-24362, culture ex-type CPC 36967 = CBS 146690; ITS, LSU, *rpb2*, *tef1* and *tub2* sequences GenBank MT373363.1, MT373346.1, MT375099.1, MT375109.1 and MT375119.1, MycoBank MB835397).

Notes — *Seimatosporium* and allied genera have recently been revised (Bonthond et al. 2018, Liu et al. 2019), with 23 genera being accepted in *Sporocadaceae*. *Nothoseiridium podocarpi* is allied to *Seiridium* (5-septate, appendaged conidia) and *Nonappendiculata* (3-septate, non-appendaged conidia), but is distinct in having 4-septate, fusoid conidia with unbranched, excentric apical and basal appendages. *Nothoseiridium* is further characterised by forming submerged acervuli

Colour illustrations. Leaf spot on *Podocarpus latifolius* with *Nothoseiridium podocarpi* and *Coleophoma podocarpi*. Conidioma on PNA; conidioma on OA; conidiogenous cells; conidia. Scale bars: conidiomata = 400 µm, all others = 10 µm.

that break through the epidermis with a saucer-like appearance, being associated with prominent leaf spots. It is not possible to distinguish *Nothoseiridium* from *Seiridium* based on LSU sequence data.

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Seimatosporium lichenicola* (as *Discostroma fuscellum*; strain GSAA-0182, GenBank JF320818.1; Identities = 542/571 (95 %), 7 gaps (1 %)), *Sporocadus rosarum* (as *Seimatosporium pseudorosarum*; strain MFLUCC 14-0466, GenBank KT284775.1; Identities = 561/592 (95 %), 4 gaps (0 %)), *Seimatosporium lichenicola* (strain CBS 160.25, GenBank MH854829.1; Identities = 561/592 (95 %), 6 gaps (1 %)) and *Millesimomyces rhoicissi* (strain CPC 35297, GenBank NR_166350.1; Identities = 566/598 (95 %), 12 gaps (2 %)). Closest hits using the **LSU** sequence are *Seiridium unicorn* (strain CBS 320.51, GenBank MH868398.1; Identities = 870/870 (100 %), no gaps), *Seiridium pseudocardinale* (strain CBS 122613, GenBank MH554206.1; Identities = 834/834 (100 %), no gaps), and *Seiridium phyllicae* (strain CPC 19962, GenBank NG_042759.1; Identities = 870/871 (99 %), 1 gap (0 %)). Closest hits using the **rpb2** sequence had highest similarity to *Seiridium cardinale* (strain CPC 23791, GenBank LT853119.1; Identities = 721/838 (86 %), no gaps), *Seiridium unicorn* (strain CBS 143873, GenBank MK058478.1; Identities = 636/741 (86 %), no gaps), and *Seiridium aquaticum* (voucher MFLU 18-1627, GenBank MN156531.1; Identities = 642/748 (86 %), no gaps). Closest hits using the **tef1** sequence had highest similarity to *Seiridium marginatum* (strain CBS 140403, GenBank LT853199.1; Identities = 344/417 (82 %), 30 gaps (7 %)), *Seiridium papillatum* (strain CBS 340.97, GenBank LT853200.1; Identities = 332/404 (82 %), 22 gaps (5 %)), and *Seiridium podocarpi* (strain CBS 137995, GenBank LT853198.1; Identities = 331/403 (82 %), 31 gaps (7 %)). Closest hits using the **tub2** sequence had highest similarity to *Seiridium cupressi* (strain CBS 224.55, GenBank LT853230.1; Identities = 652/791 (82 %), 46 gaps (5 %)), *Seiridium papillatum* (strain CBS 340.97, GenBank LT853250.1; Identities = 636/771 (82 %), 31 gaps (4 %)), and *Seiridium podocarpi* (strain CBS 137995, GenBank LT853248.1; Identities = 638/777 (82 %), 39 gaps (5 %)).

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