

*Coleophoma podocarpi*



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***Coleophoma podocarpi* Crous, sp. nov.**

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

*Classification* — *Dermateaceae*, *Helotiales*, *Leotiomyces*.

Associated with prominent brown leaf spots. *Conidiomata* pycnidial, grey-brown, 200–300 µm diam, with central ostiole. *Conidiophores* lining the inner cavity, intermingled among paraphyses, 0–2-septate, 20–35 × 5–7 µm, or reduced to conidiogenous cells, hyaline, smooth, guttulate, doliiform to ampulliform, 7–10 × 3–4 µm. *Paraphyses* intermingled among conidiophores, hyaline, smooth, cylindrical, aseptate, 3–4 (–6) µm diam, up to 30 µm long, with age becoming multiseptate and with intercalary conidiogenous cells. *Conidiogenous cells* hyaline, smooth, guttulate, doliiform to ampulliform, 7–10 × 3–4 µm, phialidic, with minute periclinal thickening. *Conidia* aseptate, hyaline, smooth, guttulate, subcylindrical to fusoid to irregular, straight to somewhat curved, apex subobtuse, base truncate, (9–)14–22 (–25) × (3.5–)4–5 (–7) µm.

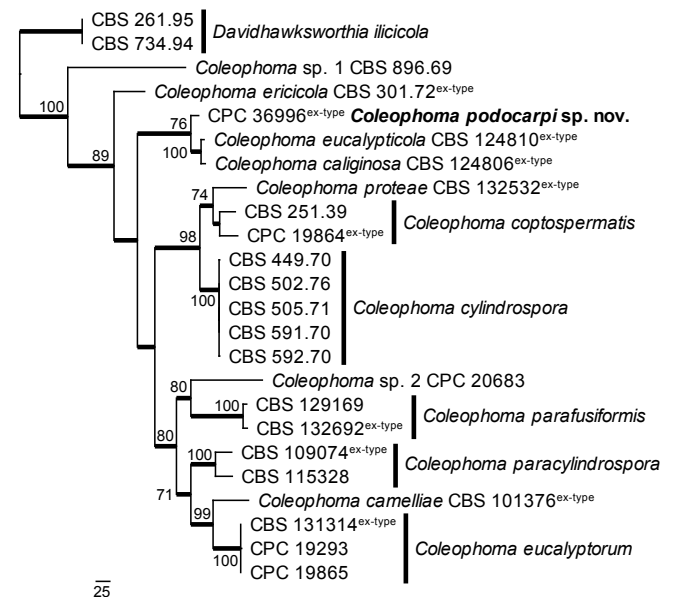
*Culture characteristics* — Colonies flat, spreading, with moderate aerial mycelium and feathery, lobate margin, reaching 30 mm diam after 2 wk at 25 °C. On MEA and PDA surface brick, reverse vinaceous with diffuse vinaceous pigment. On OA surface brick.

*Typus.* SOUTH AFRICA, Western Cape Province, Knysna, on leaf spots of *Podocarpus latifolius* (*Podocarpaceae*), Nov. 2018, F. Roets, HPC 2697 (holotype CBS H-24347, culture ex-type CPC 36996 = CBS 146625; ITS, LSU, *tef1* and *tub2* sequences GenBank MT373364.1, MT373347.1, MT375110.1 and MT375120.1, MycoBank MB835398).

*Notes* — *Coleophoma* includes species that are plant pathogenic or saprobic, occurring on a wide range of plant hosts (Crous et al. 2019b, 2020b). The genus was revised by Crous & Groenewald (2016), and shown to reside in the *Dermateaceae* (*Leotiomyces*), with morphologically similar taxa also clustering in *Dothideomycetes*.

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the ITS sequence had highest similarity to *Coleophoma parafusiformis* (strain CBS 132692, GenBank NR\_154807.1; Identities = 525/550 (95 %), 3 gaps (0 %)), *Coleophoma ericicola* (strain CBS 301.72, GenBank NR\_154805.1; Identities = 523/549 (95 %), no gaps), and *Coleophoma xanthosiae* (strain CPC 29214, GenBank NR\_154838.1; Identities = 512/543 (94 %), 2 gaps (0 %)). Closest hits using the LSU sequence are *Coleophoma paracylindrospora* (strain

CBS 109074, GenBank KU728531.1; Identities = 847/864 (98 %), no gaps), *Coleophoma parafusiformis* (strain CBS 132692, GenBank KU728534.1; Identities = 846/864 (98 %), no gaps), and *Coleophoma proteae* (strain CBS 132532, GenBank NG\_042679.1; Identities = 845/864 (98 %), no gaps). Closest hits using the *tef1* sequence had highest similarity to *Coleophoma ericicola* (strain CBS 301.72, GenBank KU728566.1; Identities = 428/500 (86 %), 22 gaps (4 %)), *Coleophoma parafusiformis* (strain CBS 132692, GenBank KU728573.1; Identities = 411/489 (84 %), 30 gaps (6 %)), and *Coleophoma eucalyptorum* (strain CPC 19865, GenBank KU728569.1; Identities = 402/483 (83 %), 31 gaps (6 %)). Closest hits using the *tub2* sequence had highest similarity to *Coleophoma xanthosiae* (strain CPC 29214, GenBank KY173598.1; Identities = 399/449 (89 %), 2 gaps (0 %)), *Coleophoma ericicola* (strain KU728605.1, GenBank KU728605.1; Identities = 383/439 (87 %), 5 gaps (1 %)), and *Coleophoma proteae* (strain CBS 132532, GenBank KU728613.1; Identities = 384/442 (87 %), 9 gaps (2 %)).



The first of two equally most parsimonious trees obtained from a phylogenetic analysis of the *Coleophoma* ITS/*actA/tef1/tub2* alignment (24 strains including the outgroup; 1 324 characters including alignment gaps analysed: 766 constant, 126 variable and parsimony-uninformative and 432 parsimony-informative). PAUP v. 4.0b10 (Swofford 2003) was used to analyse the data. The novel species was added to the alignment of Crous & Groenewald (2016), where also the GenBank accession numbers of the reference sequences can be found. The tree was rooted to two strains of *Davidhawksworthia illicicola* and the scale bar indicates the number of changes. Parsimony bootstrap support values higher than 70 % are shown at the nodes (PBS/NJBS) and the novel species is highlighted in bold. Type status is indicated in superscript. Branches present in the strict consensus tree are thickened. Tree statistics: TL = 1 501, CI = 0.640, RI = 0.745, RC = 0.477. The alignment and tree were deposited in TreeBASE (Submission ID S26166).

*Colour illustrations.* Knysna forest with waterfall. Conidiogenous cells giving rise to conidia; conidia. Scale bars = 10 µm.

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