

Pyrenochaeta protearum



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Pyrenochaeta protearum Crous, sp. nov.

Pyrenochaetae nobilis similis, sed conidiis minoribus, (3–)4–5(–6) × 2–2.5(–3) µm, discernitur.

Etymology. Named after the host genus from which it was collected, *Protea*.

Leaf spots not seen, presumed endophyte sporulating under moist conditions. On pine needle agar. **Mycelium** consisting of hyaline to pale brown, smooth, to finely verruculose 2–3 µm hyphae, forming intercalary chains of brown, ellipsoid chlamydo-spores, 8–15 µm diam. **Conidiomata** solitary, up to 300 µm diam, globose, brown, with central ostiole, surrounded by dark brown setae that are septate, straight, thick-walled, with obtuse ends, up to 100 µm tall, 4–5 µm diam. **Conidiogenous cells** phialidic, lining the cavity, hyaline, smooth, subcylindrical to ampuliform, 5–7 × 3–5 µm; apex 1–1.5 µm diam. **Conidia** hyaline, smooth, aseptate, guttulate or not, ellipsoid with obtuse ends, (3–)4–5(–6) × (2–)2.5(–3) µm.

Culture characteristics — (in the dark, 25 °C, after 2 wk): Colonies flat, spreading, with sparse aerial mycelium and even, lobate margins, reaching 25 mm diam after 2 wk. On oatmeal agar surface grey olivaceous. On malt extract agar olivaceous grey in centre, with patches of smoke-grey, olivaceous grey in reverse. On potato-dextrose agar olivaceous grey on surface and reverse.

Typus. SOUTH AFRICA, Western Cape Province, Hermanus, Fernkloof Nature Reserve, on leaves of *Protea mundii* (*Proteaceae*), 4 May 2010, P.W. Crous, holotype CBS H-20772, cultures ex-type CPC 18322 = CBS 131315, ITS sequence GenBank JQ044434 and LSU sequence GenBank JQ044453, MycoBank MB560706.

Notes — *Pyrenochaeta protearum* was isolated from asymptomatic leaves and is assumed to be endophytic. Morphologically it can be distinguished from *Phoma proteae* (conidia 4.5–7 × 2.5–3.5 µm) by having smaller conidia, and conidiomata with setae. A megablast search of the NCBI's GenBank nucleotide sequence database using the ITS sequence of *P. protearum* retrieves as closest hits *Pyrenochaetopsis microspora* (GenBank HM751085; Identities = 371/393 (94 %), Gaps = 17/393 (4 %)) and *Monodictys arctica* (GenBank EU686521; Identities = 378/425 (89 %), Gaps = 26/425 (6 %)), amongst others. Performing a similar search against the *Phoma* database present in Q-bank (www.q-bank.eu), retrieves high identity to *Pyrenochaeta dolichi* strain CBS 124143 (Identities = 362/398 (91 %), Gaps = 22/398 (6 %)). A megablast search of the NCBI's GenBank nucleotide sequence database using the LSU sequence of *P. protearum* retrieves as closest hits *Leptosphaeria macrospora* (GenBank DQ384092; Identities = 924/944 (98 %), Gaps = 2/944 (0 %)), *Phaeosphaeriopsis musae* (GenBank DQ885894; Identities = 922/944 (98 %), Gaps = 3/944 (0 %)) and *Coniothyrium obiones* (GenBank DQ678054; Identities = 903/920 (98 %), Gaps = 0/920 (0 %)), amongst others.

Colour illustrations. *Protea mundii* in the Fernkloof Nature Reserve, Hermanus, South Africa; conidiomata forming on oatmeal agar and malt extract agar; conidiomatal wall that tends to develop setae; conidiogenous cells; conidia. Scale bars = 10 µm.