

Pyrenochaeta pinicola



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Pyrenochaeta pinicola* Crous, sp. nov.Etymology.* Named after the host genus from which it was isolated, *Pinus*.

Conidiomata immersed but becoming erumpent to superficial, brown, globose, up to 200 µm diam with prominent wide central ostiole, 40–60 µm diam, surrounded by a crest of brown setae, straight, flexuous, unbranched, septate with obtusely rounded ends, 50–150 µm long, 3–5 µm wide; conidiomatal wall of 3–4 layers of brown *textura angularis*. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* hyaline, smooth, ampulliform, lining the inner cavity, 4–6 × 3–4 µm, with prominent periclinal thickening. *Conidia* solitary, hyaline, smooth, thin-walled, guttulate, subcylindrical with obtuse ends, straight to slightly curved, allantoid, (4–)4.5–5.5(–6) × 2(–2.5) µm.

Culture characteristics — Colonies reaching 15 mm diam after 2 wk at 22 °C. On MEA erumpent, surface folded, with moderate aerial mycelium, and smooth, lobed margin. Surface dirty white, reverse salmon. On OA surface grey-olivaceous. On PDA surface and reverse dirty white with patches of smoke-grey.

Typus. FRANCE, Nice, L'aire d'Estérel petrol filling station, on needles of *Pinus* sp. (*Pinaceae*), 20 July 2013, P.W. Crous (holotype CBS H-21711, culture ex-type CPC 23455 = CBS 137997; ITS sequence GenBank KJ869152, LSU sequence GenBank KJ869209, ACT sequence GenBank KJ869230, TUB sequence GenBank KJ869249, MycoBank MB808934).

Notes — The genus *Pyrenochaeta* is characterised by having species with distinct, elongated, septate, acropleurogenous conidiophores produced in pycnidial conidiomata usually covered by long, brown setae (de Gruyter et al. 2010). Phylogenetically, *P. pinicola* is closely allied to *P. protearum* (Crous et al. 2011). Both species have brown, elongated setae and conidiophores reduced to conidiogenous cells. They differ in that *P. protearum* has smaller conidia, (3–)4–5(–6) × (2–)2.5(–3) µm (Crous et al. 2011) and colonies that tend to be more smoke-grey to olivaceous-grey on MEA and PDA in culture.

ITS. Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the ITS sequence are *Pyrenochaeta protearum* (GenBank JQ044434; Identities = 791/794 (99 %), Gaps = 1/794 (0 %)), *Pyrenochaeta unguis-hominis* (GenBank JX966641; Identities = 318/334 (95 %), Gaps = 4/334 (1 %)) and *Ochrocladosporium frigidarii* (GenBank FJ755255; Identities = 318/335 (95 %), Gaps = 8/335 (2 %)).

LSU. Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the LSU sequence are *Pyrenochaeta protearum* (GenBank JQ044453; Identities = 859/860 (99 %), no gaps), *Pyrenochaeta nobilis* (GenBank DQ678096; Identities = 834/845 (99 %), no gaps) and *Paraleptosphaeria orobanches* (GenBank JF740299; Identities = 855/868 (99 %), no gaps).

ACT. Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the ACT sequence are *Chalastospora gossypii* (GenBank JQ671625; Identities = 428/471 (91 %), Gaps = 9/471 (1 %)), *Embellisia phragmospora* (GenBank JQ671623; Identities = 428/471 (91 %), Gaps = 9/471 (1 %)) and *Macrospora scirpicola* (GenBank JQ671613; Identities = 428/471 (91 %), Gaps = 9/471 (1 %)).

TUB. Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the TUB sequence are *Phoma nigrificans* (GenBank AY749030; Identities = 265/302 (88 %), Gaps = 3/302 (0 %)), *Coniothyrium clematidis-rectae* (GenBank FJ515624; Identities = 249/284 (88 %), Gaps = 3/284 (1 %)) and *Phoma nebulosa* (GenBank GU237633; Identities = 257/294 (87 %), Gaps = 3/294 (1 %)).

Colour illustrations. *Pinus* sp. next to the roadside in France; conidiomata, setae, conidiogenous cells and conidia in culture. Scale bars = 10 µm.