

Talaromyces pulveris



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***Talaromyces pulveris* Crous, sp. nov.**

Etymology. Name refers to the bore dust (L = *pulvis*) of a beetle, from which it was isolated.

Classification — *Trichocomaceae*, *Eurotiales*, *Eurotiomycetes*.

Mycelium consisting of hyaline, smooth, branched, septate, 1.5–2 µm diam hyphae. *Conidiophores* dimorphic. *Microconidiophores* monoverticillate or as solitary phialides, short, 1–2-septate, arising from superficial hyphae, 15–25 × 2 µm. *Macroconidiophores* biverticillate, erect, subcylindrical, flexuous, penicillate, 70–300 × 2.5–3 µm, stipe smooth to slightly roughened, multiseptate. *Metulae* two to seven, subcylindrical, hyaline, smooth to slightly roughened, subcylindrical, aseptate, 8–12 × 2–3 µm; additional branches rarely observed. *Conidiogenous cells* phialidic, arranged in whorls of 2–6 per metula, acerose to subcylindrical with apical taper in upper third, 8–13 × 2–3 µm. *Conidia* arranged in long, unbranched chains, aseptate, green in masse, in basipetal chains, subglobose, thick-walled, smooth, 2–2.5 µm diam.

Culture characteristics — Colony diam, 7 d, in mm: CYA, 25 °C: Colonies restricted, non-sulcate, flat, thin; margin entire; mycelium white; sporulation absent or very sparsely produced; soluble pigments absent; exudates absent; reverse white. YES, 25 °C: Similar to CYA, though sporulation lacking. MEA, 25 °C: Colonies non-sulcate, moderately high; margin entire; mycelium white; sporulation sparse to strong; texture floccose to slightly funiculose; soluble pigments absent after 7 d, present after 2 wk, red; exudates absent; conidial colour *en masse* grey-green; reverse brown or dark brown. DG18, 25 °C: See CYA. OA, 25 °C: Similar to CYA, though sporulation poor to moderate; red soluble pigments produced after 2 wk. Colony diam, 7 d, in mm – CYA microcolonies to 5; CYA30°C microcolonies–5; CYA37°C no growth; CYAS no growth; DG18 3–6; MEA 7–10; OA 5–8; YES no growth or microcolonies; CREA no growth.

Typus. FRANCE, from bore dust of deathwatch beetle (*Xestobium rufovillosum*) infesting floorboards (*Quercus* wood), 2019, C.A. Decock (holotype CBS H-24417, culture ex-type CPC 38523 = MUCL pd8781 = DTO 432-H1 = CBS 146831, ITS, LSU, *cmdA*, *rpb2* and *tub2* sequences GenBank MW175345.1, MW175385.1, MW173099.1, MW173115.1 and MW173136.1, MycoBank MB837837).

Colour illustrations. Sampling site in France. Colony on MEA; conidiophores and conidiogenous cells giving rise to conidial chains. Scale bars = 10 µm.

Notes — *Talaromyces pulveris* represents a new species in section *Purpurei*, phylogenetically most closely related to *T. iowaense* (Samson et al. 2011, Yilmaz et al. 2014, Crous et al. 2018a, Guevara-Suarez et al. 2020). *Talaromyces rademirici* is a sister species of *T. pulveris* and *T. iowaense* (Samson et al. 2011, Yilmaz et al. 2014, Crous et al. 2018a, Guevara-Suarez et al. 2020, Houbraken et al. 2020). *Talaromyces iowaense*, *T. pulveris* and *T. rademirici* grow restrictedly on CYA and are unable to grow on CYA supplemented with 5 % NaCl. *Talaromyces pulveris* grows more restrictedly on MEA (7–10 mm) than *T. iowaense* (17–18 mm) and *T. rademirici* (14–15 mm). The production of subglobose conidia and inability of *T. pulveris* to grow on CYA incubated at 37 °C is shared with *T. iowaense*. In contrast, the conidia of *T. rademirici* are ellipsoidal and this species is able to grow on CYA incubated at 37 °C. *Talaromyces iowaense* grows on CREA, while *T. pulveris* and *T. rademirici* are unable to grow on this medium (Yilmaz et al. 2014, Crous et al. 2018a).

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Talaromyces pseudostromaticus* (strain AS3.16005, GenBank MT182956.1; Identities = 472/540 (87 %), 33 gaps (6 %)), *Talaromyces pittii* (strain CBS 139.84, GenBank MH861710.1; Identities = 472/540 (87 %), 33 gaps (6 %)), and *Talaromyces aculeatus* (strain BCC<THA> 88118, GenBank MH997879.1; Identities = 465/532 (87 %), 30 gaps (5 %)). Closest hits using the **LSU** sequence are *Talaromyces purpureus* (strain CBS 475.71, GenBank NG_064090.1; Identities = 787/807 (98 %), one gap (0 %)), *Talaromyces rademirici* (strain CBS 140.84, GenBank NG_064134.1; Identities = 815/837 (97 %), one gap (0 %)), and *Talaromyces dendriticus* (strain CBS 660.80, GenBank MH873068.1; Identities = 781/806 (97 %), one gap (0 %)). Closest hits using the **cmdA** sequence had highest similarity to *Talaromyces purpureus* (strain CBS 475.71, GenBank KJ885292.1; Identities = 354/410 (86 %), 16 gaps (3 %)), *Talaromyces ptychoconidium* (strain CV2807, GenBank JX140699.1; Identities = 443/550 (81 %), 50 gaps (9 %)), and *Talaromyces cecidicola* (strain CBS 101419, GenBank KJ885287.1; Identities = 285/336 (85 %), seven gaps (2 %)). Closest hits using the **rpb2** sequence had highest similarity to *Talaromyces rademirici* (strain CBS 140.84, GenBank KM023302.1; Identities = 697/760 (92 %), no gaps), *Talaromyces purpureus* (strain CBS 475.71, GenBank JN121522.1; Identities = 748/825 (91 %), no gaps), and *Talaromyces ptychoconidium* (strain DTO180F1, GenBank MK450880.1; Identities = 772/864 (89 %), no gaps). Closest hits using the **tub2** sequence had highest similarity to *Talaromyces rademirici* (strain CBS 140.84, GenBank KJ865734.1; Identities = 395/444 (89 %), nine gaps (2 %)), *Talaromyces iowaense* (as *Talaromyces* sp. GP-2018a; strain EMSL 2233, GenBank MH282578.1; Identities = 390/452 (86 %), 12 gaps (2 %)), and *Talaromyces ptychoconidium* (as *Penicillium* sp. CMV-2008; strain CV323, GenBank GU385735.1; Identities = 297/346 (86 %), 14 gaps (4 %)).