

Penicillium vallebormidaense



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***Penicillium vallebormidaense* Houbraken & Di Piazza, sp. nov.**

Etymology. Latin, name refers to Valle Bormida, the region from which the type specimen was collected.

Classification — *Aspergillaceae*, *Eurotiales*, *Eurotiomycetes*.

Conidiophores monoverticillate; stipes non-vesiculate, smooth, short, 13–25(–35) × 1.5–2.5 μm; phialides ampulliform, 3–6 per conidiophore, 7–8.5(–10) × 2–2.5(–3) μm. **Conidia** smooth, globose to subglobose, 2–2.5(–3) μm. **Ascomata** or sclerotia not observed.

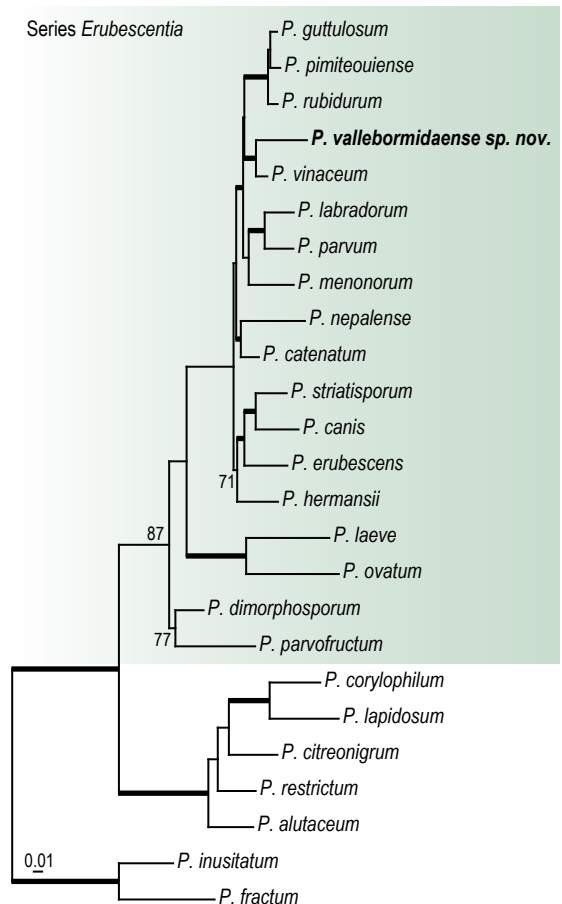
Culture characteristics (25 °C, 7 d) — Czapek yeast extract agar (CYA): Colonies non-sulcate, elevated in centre; margin slightly irregular; mycelium pale yellow; texture velvety; sporulation absent; soluble pigments brown, moderately produced; exudates absent; reverse brown. Malt extract agar (MEA): Colonies non-sulcate, slightly elevated in centre; margin slightly irregular; mycelium pale yellow; texture floccose; sporulation poor in centre, profuse in a ring between centre and edge, absent at edge; soluble pigments absent; exudates absent; conidia *en masse* pale grey green; reverse brown, pale brown at edge. Yeast extract sucrose agar (YES): Colonies randomly sulcate (radial and concentric), slightly elevated; margins slightly irregular; mycelium pale yellow; texture floccose in centre, velvety at edge; sporulation absent; soluble pigment absent; exudates absent; reverse pale brown. Dichloran 18 % glycerol agar (DG18): Colonies non-sulcate, plane, raised at the centre; margins entire; mycelium pale yellow in centre, white at edge; texture velvety; sporulation absent; soluble pigments absent; exudates absent; reverse pale yellow-brown. Oatmeal agar (OA): Colonies non-sulcate, plane, low; margins slightly irregular; mycelium yellow; texture velvety; sporulation absent; soluble pigments present, pale brown, poorly produced; exudates absent. Creatine agar (CREA): poor growth, acid production absent, base production absent. Colony diam, after 7 d, in mm — CYA 18–22; CYA 30 °C 22–26; CYA 37 °C 16–20; MEA 18–22; DG18 20–23; YES 21–25; OA 18–22; CREA 9–11.

Typus. ITALY, Savona, Valle Bormida, Ferrania (Cairo Montenotte), from compost 18 d in maturation, 26 June 2018, S. Di Piazza (holotype CBS H-24527, culture ex-type CBS 147064 = DTO 402-H5; ITS, LSU, *BenA*, *CaM* and *RPB2* sequences GenBank MT316359, MW092765, MW115862, MW115863 and MW115864; MycoBank MB837659).

Notes — A BLAST search of *BenA*, *CaM* and *RPB2* sequences of *P. vallebormidaense* CBS 147064 against an in-house reference sequence database containing data of all accepted *Penicillium* species (Houbraken et al. 2020), did not retrieved any high similarity hits. A homology search with the ITS sequence retrieved *P. pimateouiense* (99.2 %), *P. guttulosum* (99.0 %) and *P. vinaceum* (98.9%) as most similar species.

Colour illustrations. Compost pile during ripening process. Colonies (7 d, 25 °C), left to right, first row: CYA, MEA, second row: CYA reverse, YES observe; conidiophores; conidia. Scale bars = 10 μm.

Based on the phylogenetic analysis, *P. vallebormidaense* belongs to series *Erubescens* of section *Exilicaulis*. *Penicillium vallebormidaense* grows rather slowly on CYA, MEA, DG18 and YES, is able to grow at 37 °C and produces short, monoverticillate conidiophores. These features are shared with many other species in series *Erubescens* (Houbraken et al. 2020), confirming the results of the phylogenetic analysis. The new species is phylogenetically most closely related to NRRL 739, the ex-type of *P. vinaceum*. The sequence similarity scores with this strain are: *BenA* 95.0 % (identities = 459/478), *CaM* 90.6 % (identities = 444/490) and *RPB2* 93.8 % (identities = 837/892). *Penicillium vinaceum* is characterised by the (copious) production of ruby or vinaceous exudates on CYA and other media. In contrast, no exudate production is observed in *P. vallebormidaense*. Furthermore, the mycelium of *P. vallebormidaense* is pale yellow coloured, while the mycelium in *P. vinaceum* is white (Pitt 1980).



Maximum likelihood tree of *Penicillium* strains belonging to section *Exilicaulis* series *Erubescens* based on 1871 aligned nucleotides (combined *BenA*, *CaM* and *RPB2* sequences). Strain and GenBank accession numbers used in the analysis can be found in Houbraken et al. (2020). Analysis performed using RAxML v. 8.2.12 (Stamatakis 2014). Bootstrap 1000 re-samplings; only bootstrap support values above 70 % are presented at the nodes and branches of > 95 % are thickened. *Penicillium fractum* and *P. inusitatum* were used as outgroup. The scale bar indicates the number of substitutions per site.