

Paecilomyces penicilliformis



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***Paecilomyces penicilliformis* Jurjević & Hubka, sp. nov.**

Etymology. Refers to the production of penicillium-like conidiophores.

Classification — *Thermoascaceae*, *Eurotiales*, *Eurotiomycetes*.

Micromorphology (on malt extract agar; MEA): *Hyphae* hyaline to pale yellow-brown, 2.5–11 µm diam, *Conidiophores* borne on the surface or from aerial hyphae, commonly 5–75 × (2.5–)3–5 µm diam; with smooth walls, bearing terminal whorls of verticillately arranged branches. *Phialides* 2–7 per branch, cylindrical, occasionally flask shaped, 10–16(–21) × 2.5–3.5(–5) µm diam, tapering abruptly toward a long cylindrical collula, up to 7 µm long and 1–2 µm diam, solitary phialides rarely present. *Conidia* in long divergent chains, ellipsoidal or cylindrical with conspicuously truncated ends, rarely subglobose, 3–5(–8) × 2–4.5(–5) µm diam. *Chlamydospores* very rare, smooth. *Sexual morph* was not observed even after prolonged incubation at 25 °C.

Cultural characteristics — (in darkness, 25 °C after 7 d): Colonies on MEA > 90 mm diam, colony texture, floccose, mycelium white to yellow-brown (deep colonial buff to honey yellow, R30; Ridgway (1912)), sporulation very good, conidia *en masse* light-buff to warm-buff (R15), exudate absent, soluble pigments absent, reverse mustard yellow to primuline yellow (R16). Colonies on Czapek yeast autolysate agar (CYA) 37–40 mm diam, colony texture floccose, mycelium white yellow ochre (R15), sporulation good, conidia *en masse* light buff to warm buff (R15), exudate absent, soluble pigments absent, reverse light buff to warm buff (R15). Colonies on potato dextrose agar (PDA) > 90 mm diam, colony texture floccose, mycelium deep colonial buff to honey yellow (R30), sporulation very good, conidia *en masse* light-buff to warm-buff (R15), exudate absent, soluble pigments absent, reverse amber yellow to primuline yellow (R16). Colonies on Czapek yeast agar with 20 % sucrose, (CY20S) 24–26 mm diam, colony texture floccose, mycelium white yellow ochre (R15), sporulation good, conidia *en masse* light buff to warm buff (R15), exudate absent, soluble pigments absent, reverse light buff to warm buff (R15). Colonies on Dichloran glycerol agar (DG18) 16–18 mm diam, colony texture light floccose, sporulation very good, mycelium white to cream colour (R16), reverse warm buff (R15). No growth on CYA supplemented with 5 % (w/v) NaCl (CYAS). Colonies on OA 65–67 mm diam, colony texture floccose, mycelium white to honey yellow (R30), sporulation very good, conidia *en masse* light-buff to warm-buff (R15), exudate absent, soluble pigments absent. Colonies on creatine sucrose agar (CREA) 2–3 mm diam, poor growth, no acid production, mycelium white, colony subsurface to submerged into the agar. Colony diam (in mm after 7 d) at 30 °C/37 °C; MEA > 90/7–12; CYA 38–41/4–5; PDA > 90/10–12; CY20S 42–45/3–4; DG18 30–31/3–4; OA > 90/9–11; CREA 9–11/ng; no growth at 41 °C.

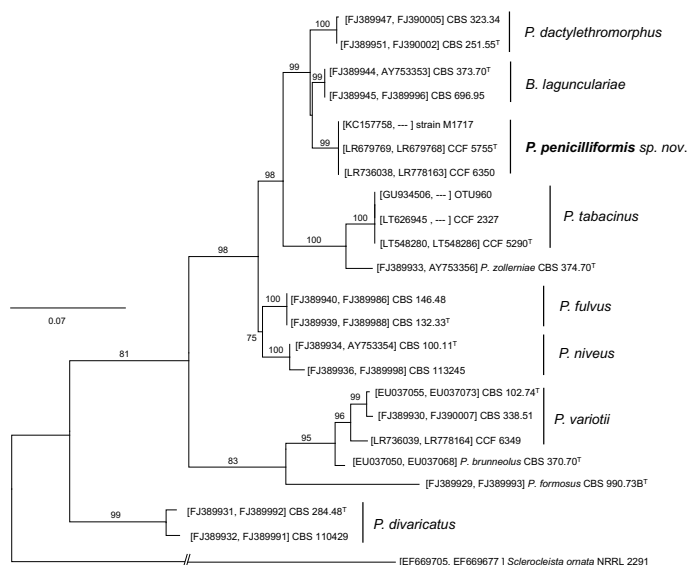
Typus. USA, Wisconsin, Menasha, pharmacy, air, 17 Mar. 2016, Ž. Jurjević (holotype BPI 911216, cultures ex-type CCF 5755 = CBS 146003 = EMSL 3392; ITS, LSU, β-tubulin and calmodulin sequences GenBank LR679769, LR679770, LR679768 and LR778299, MycoBank MB834874).

Colour illustrations. Inside of the pharmacy. Seven-day-old cultures of *Paecilomyces penicilliformis* on MEA (top to bottom 25 °C, 30 °C, 37 °C); conidia and conidiophores on MEA. Scale bars = 10 µm.

Additional material examined. USA, Massachusetts, Taunton, peach-mango juice, 25 Sept. 2018, Ž. Jurjević, CCF 6350 = EMSL 4943; ITS-LSU, β-tubulin and calmodulin sequences GenBank LR736038, LR778163 and LR778165.

Notes — BLAST analysis with the ITS, β-tubulin and calmodulin sequences of *P. penicilliformis* showed greatest similarity with *P. dactylethromorphus* (syn. *P. saturatus*) (98.8 %, 92.7 % and 93.1 %, respectively), *Byssoschlamys lagunculariae* (98.8 %, 95.4 % and 96.3 %, respectively), *P. niveus* (98.4 %, 89.6 % and 91.4 %, respectively) and *P. fulvus* (98.2 %, 89.4 % and 90.3 %, respectively).

Paecilomyces penicilliformis produces predominantly long cylindrical conidia with conspicuously truncated ends, 3–5(–8) × 2–4.5(–5) µm compared to smaller and predominantly globose conidia with flattened base produced by the closely related *B. lagunculariae*, 2.7–4.5 × 2.2–3.3 µm (Samson et al. 2009). In addition, *B. lagunculariae* produces a sexual morph in culture (homothallic) and grows faster on MEA at 37 °C (25–55 mm after 7 d) (Samson et al. 2009). *Paecilomyces penicilliformis* is similar to *P. dactylethromorphus* by its cylindrical or ellipsoidal conidia and regularly branched conidiophores (penicillium-like). These species can be distinguished by wider conidia, 2–4.5(–5) µm produced by *P. penicilliformis* compared to *P. dactylethromorphus*, 1.7–3.4 µm wide (Samson et al. 2009).



A best scoring maximum likelihood tree based on the ITS region and the β-tubulin gene sequences shows the relationships of *P. penicilliformis* with other *Paecilomyces* and *Byssoschlamys* species. The dataset contained 23 taxa and a total of 1056 characters of which 345 were variable and 234 parsimony-informative. Partitioning scheme and substitution models for analyses were selected using PartitionFinder v. 2 (Lanfear et al. 2017); the GTR+I+G model was proposed for the ITS1, ITS2 and β-tubulin gene exons; JC model for the 5.8S region; and K80+I model for the β-tubulin gene introns. The tree was constructed with IQ-TREE v. 1.4.4 (Nguyen et al. 2015). Support values at branches were obtained from 1000 bootstrap replicates. Only bootstrap support values ≥ 70 % are shown; ex-type strains are indicated by † and the novel species in **bold** text. The tree is rooted with *Sclerocleista ornata* NRRL 2291.