

Trichophoma cylindrospora



Fungal Planet 1106 – 29 June 2020

***Trichophoma* Magaña-Dueñas, Cano & Stchigel, gen. nov.**

Etymology. From Greek τρίχες-, hairs, due to the abundant setae on the sporocarps.

Classification — *Sporormiaceae*, *Pleosporales*, *Dothideomycetes*.

Conidiomata pycnidial, solitary, subglobose to pyriform, ostiolate, covered by brown to dark brown, septate, nodose setae. *Conidioma* wall of *textura angularis*, composed of brown to dark

brown, flattened polygonal cells. *Conidiogenous cells* phialidic, hyaline, smooth walled, ampulliform. *Conidia* 0–1-septate, hyaline, guttulate, long cylindrical, with a narrowly flattened base and rounded at the end.

Type species. *Trichophoma cylindrospora* Magaña-Dueñas, Cano & Stchigel.

Mycobank MB833525.

***Trichophoma cylindrospora* Magaña-Dueñas, Cano & Stchigel, sp. nov.**

Etymology. From Greek κυλινδρικό-, cylindrical, due to the shape of the conidia.

Hyphae hyaline to brown, septate, branched, thin-walled, smooth to tuberculate, 1.5–2 µm wide. *Conidiomata* pycnidial, brown to blackish brown, immersed to semi-immersed, solitary, scattered, subglobose to pyriform, 300–390 × 300–410 µm, ostiolate, setose. *Conidioma* wall 4–6-layered, 15–30 µm thick, covered by a mass of interwoven, brown to dark brown hyphae, followed by an outer layer of *textura angularis*, composed of brown to dark brown, flattened polygonal cells of 5–8 µm diam, incrustated with a dark brown to carbonaceous material around the neck; neck dark brown to carbonaceous, cylindrical, 130–145 × 100–145 µm, covered by brown to dark brown, septate, erect, nodose, thick-walled setae 100–180 × 2–4.5 µm, tapering towards the apex, mainly disposed around the ostiole. *Conidiophores* absent. *Conidiogenous cells* phialidic, determinate, hyaline, smooth-walled, ampulliform, 3–5 × 8–14 µm. *Conidia* 0–1-septate, hyaline, smooth- and thin-walled, long cylindrical, 18–20 × 2–3 µm, guttulate, with a narrowly flattened base and rounded at the end.

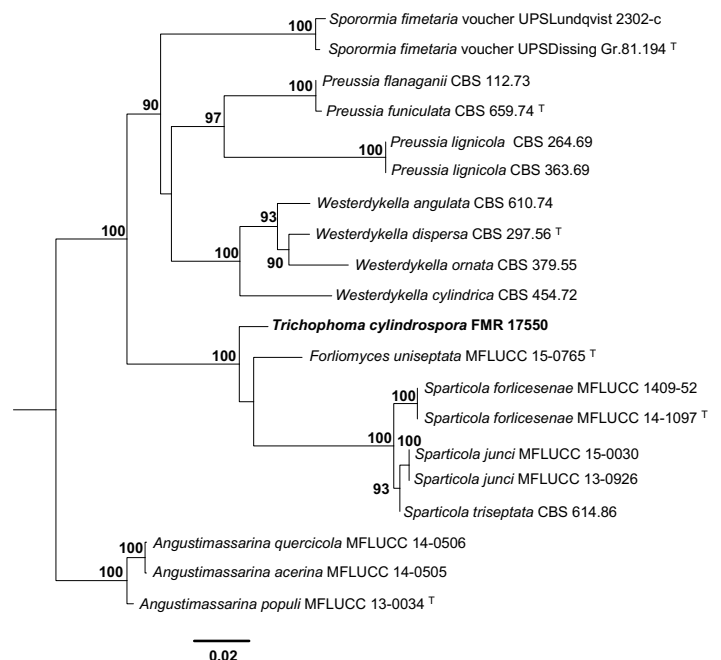
Culture characteristics — (7 d at 25 °C). Colonies on potato dextrose agar (PDA) reaching 24 mm diam, flattened, velvety, margins regular, yellowish white to reddish brown (M. 4A2 / 8D8; Kornerup & Wanscher 1978); reverse reddish brown to dark brown (M. 8E8 / 8F8), exopigment reddish brown to golden yellow (M. 8D8 / 5B7). Colonies on oatmeal agar (OA) reaching 40 mm diam, flattened, slightly floccose, margin regular, grey (M. 8F1); reverse grey (M. 8F1). Colonies on malt extract agar (MEA) 2 % reaching 25–29 mm diam, flattened, velvety to slightly floccose, margins lobate, dark brown to greyish yellow (M. 8F8 / 4C5); reverse greyish brown to greyish orange, with yellowish brown patches (M. 8F3 / 5B5 / 5F7).

Cardinal temperatures for growing — Optimum 30 °C, maximum 37 °C, minimum 15 °C.

Typus. SPAIN, Castilla y León community, Riaza, from plant debris, 4 May 2018, I.A. Iturrieta-González (holotype CBS H-24327; cultures ex-type CBS 146340 = FMR 17550; ITS, LSU and *tef-1α* sequences European Nucleotide Archive LR732023, LR732024 and LR732025, MycoBank MB833526).

Colour illustrations. Riaza, Spain. Colonies on PDA and OA after 14 d at 25 ± 1 °C; conidiomata; mycelial network on the pycnidial wall; conidiogenous cells and conidia. Scale bars = 50 µm (conidioma) and 10 µm (all others).

Notes — Based on the phylogenetic analysis of the ITS, LSU and *tef-1α* combined dataset, the closest relative of *T. cylindrospora* is *Forliomyces uniseptata*. *Forliomyces uniseptata* differs from *T. cylindrospora* in producing shorter and broader conidia (10–15 × 5–8 µm vs 18–20 × 2–3 µm), which are brown-coloured when mature (hyaline in *T. cylindrospora*) (Phukhamsakda et al. 2016). Based on a megablast search of NCBI's GenBank nucleotide database, the closest hit using the LSU sequence was *Forliomyces uniseptata* MFLUCC 15-0765 (GenBank NG_059659, Identities = 814/827 (98 %), no gaps); the closest hits using ITS was *Forliomyces uniseptata* MFLUCC 15-0765 (GenBank NR_154006, Identities = 440/458 (96 %), 3 gaps (0 %)); and the closest hits using the *tef-1α* sequence was *Forliomyces uniseptata* MFLUCC 15-0765 (GenBank KU27897, Identities = 420/438 (96 %), no gaps).



Maximum likelihood tree obtained from the combined DNA sequences dataset from three loci (ITS, LSU and *tef-1α*) of our isolate and sequences retrieved from the GenBank. Alignment and tree building were performed by MEGA v. 6.06 (Tamura et al. 2013). Type strains of the different species are indicated with T. The new taxon proposed in this study is indicated in bold. The RAxML bootstrap support values (> 70 %) are provided at the nodes. *Angustimassarina quercicola*, *Angustimassarina acerina* and *Angustimassarina populi* were used as outgroup.