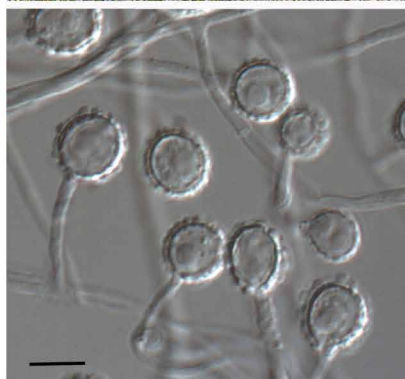
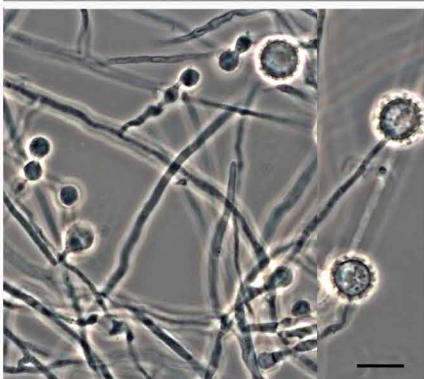
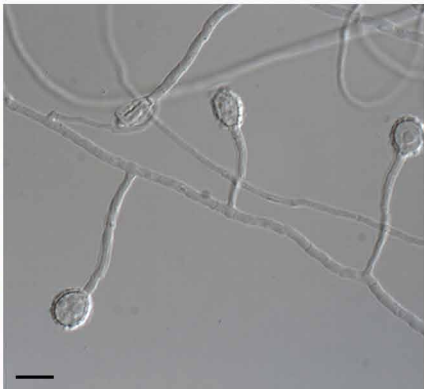
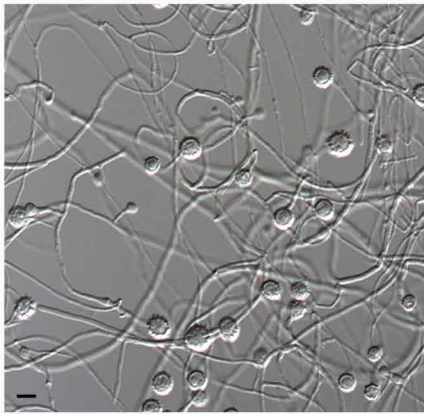
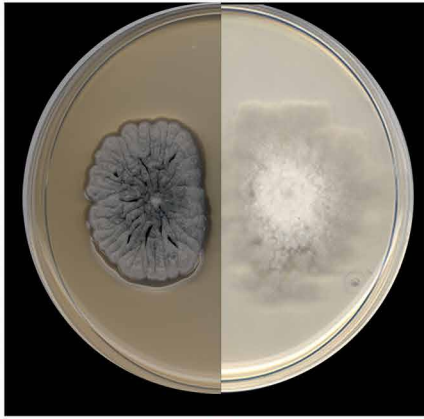


Emmonsiiellopsis tuberculata



Fungal Planet 1011 – 18 December 2019

***Emmonsiiellopsis tuberculata* Torres-Garcia, Guarro & Gené, sp. nov.**

Etymology. Name refers to the conidial ornamentation of the species.

Classification — *Ajellomycetaceae*, *Onygenales*, *Eurotiomycetes*.

On potato carrot agar (PCA) at 25 °C. *Mycelium* consisting of branched, septate, hyaline, smooth- and thin-walled 1–3 µm diam hyphae. *Conidiophores* unbranched, erect, cylindrical, 12–60 × 1–2 µm, bearing terminal conidia. *Conidia* solitary, more rarely in chains of 2–3, globose to subglobose, hyaline, verrucose to tuberculate, thick-walled, 6–9 × 6–8 µm. On malt extract agar (MEA) at 37 °C giant cells of 9–22.5 × 9–14.5 µm, and yeast-like cells of 7.5–11.8 × 7.5–9 were observed after 3 wk. *Sexual morph* absent.

Culture characteristics at 25 °C in 3 wk — Colonies on MEA reaching 17.5–19 mm diam, flat, yellowish white (4A2) to yellowish orange (4B7) (Kornerup & Wanscher 1978), velvety, margin lobulated; reverse yellowish orange (4B7); sporulation sparse. On potato dextrose agar (PDA) reaching 35–38 mm, felted, greenish white (282A), irregularly sulcate, margin lobulated; reverse dark green (28F7); sporulation sparse. On PCA reaching 44–49 mm diam, cottony, white, margin irregular; reverse colourless; sporulation abundant.

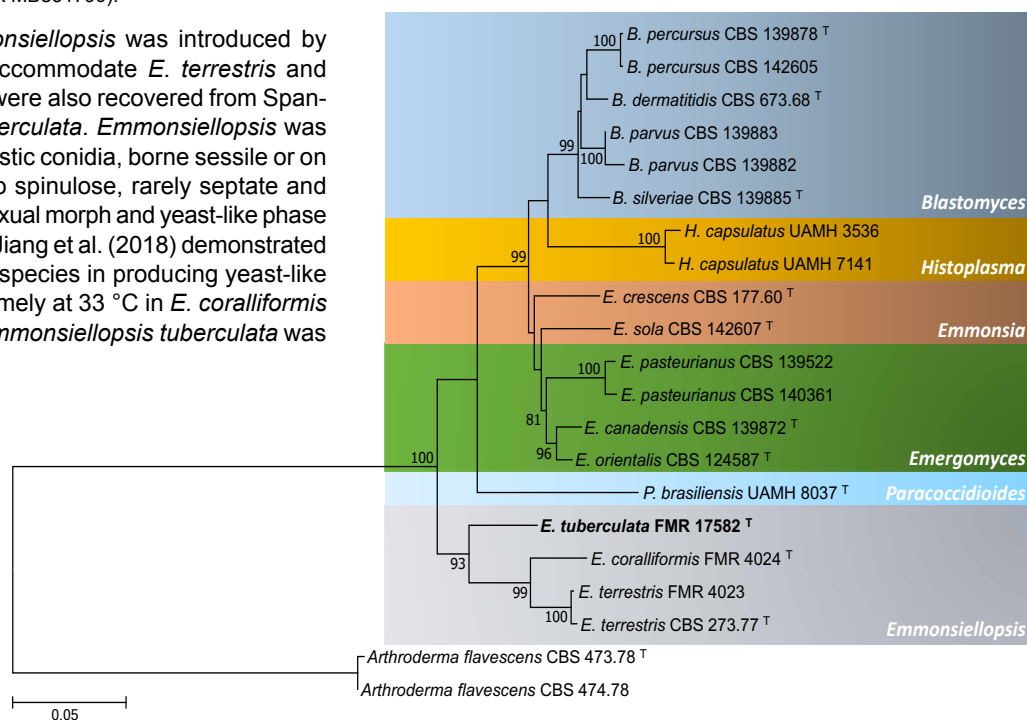
Cardinal temperatures for growth — Minimum 15 °C, optimum 30 °C, maximum 37 °C.

Typus. SPAIN, Aragón, Huesca, Remáscaro stream, fluvial sediments, Sept. 2018, *D. Torres-Garcia* (holotype CBS H-24082, culture ex-type CBS 145944 = FMR 17582; LSU, ITS and *BenA* sequences GenBank LR598891, LR598892 and LR599029, MycoBank MB831790).

Notes — The genus *Emmonsiiellopsis* was introduced by Marin-Felix et al. (2015) to accommodate *E. terrestris* and *E. coralliformis*, both of which were also recovered from Spanish fluvial sediments as *E. tuberculata*. *Emmonsiiellopsis* was characterised by producing blastic conidia, borne sessile or on pedicels, smooth, verrucose to spinulose, rarely septate and intercalary, and by the lack of sexual morph and yeast-like phase (Marin-Felix et al. 2015). Later Jiang et al. (2018) demonstrated the ability of *Emmonsiiellopsis* species in producing yeast-like cells after 4–5 wk on MEA, namely at 33 °C in *E. coralliformis* and at 37 °C in *E. terrestris*. *Emmonsiiellopsis tuberculata* was

able to produce the yeast morph at 37 °C as in *E. terrestris*, but with a faster conversion time (3 wk). Besides, our species differs from the other two by its verrucose to tuberculate conidia, the lack of sessile and intercalary conidia, and colonies with a dark green in reverse when growing on PDA at 25 °C. Colony reverse on PDA in *E. coralliformis* was pale yellow to olive brown and in *E. terrestris* yellowish white to pale yellow (Marin-Felix et al. 2015).

Our phylogenetic reconstruction with the barcodes LSU, ITS and *BenA* places *E. tuberculata* in a basal lineage distant from the clade formed by the other species of *Emmonsiiellopsis*. A megablast search in the NCBI GenBank nucleotide database using LSU sequences showed that *E. tuberculata* was 98.83 % (675/683) similar with *E. terrestris* (CBS 273.77; GenBank KT155190.1) and 97.85 % (684/699) with *E. coralliformis* (CBS 137500; GenBank NG_059238.1), whereas the similarity using ITS sequences was 90.80 % (533/587) with *E. terrestris* (CBS 273.77; GenBank NR_153965.1) and 92.98 % (503/541) with *E. coralliformis* (CBS 137500; GenBank NR_153996.1), respectively. *BenA* sequences showed a similarity of 80.17 % (380/474) between *E. tuberculata* and *E. terrestris* (CBS 273.77; GenBank KT155526.1) and of 79.33 % (330/416) between *E. tuberculata* and *E. coralliformis* (CBS 137500; GenBank KY710967.1).



Maximum likelihood tree obtained from the concatenated analysis of LSU, ITS and *BenA* sequences of *Emmonsiiellopsis* and related genera of the family *Ajellomycetaceae*. Bootstrap support values above 70 % are indicated on the nodes. The alignment included 1443 bp and was performed using Tamura-Nei with Gamma distribution with Invariant sites (G+I) as the best nucleotide substitution model. Both the alignment and tree were constructed with MEGA v. 6 software (Tamura et al. 2013). The new species proposed in this study is indicated in **bold face**. A superscript T denotes ex-type cultures.

Colour illustrations. Cerler, Aragón, Spain. Colony on PDA and PCA after 3 wk at 25 °C; conidiophores and conidia after 14 d at 25 °C; yeast-like cells from MEA after 3 wk at 37 °C. Scale bars = 10 µm.