

Tuber lucentum



Fungal Planet 1038 – 18 December 2019

***Tuber lucentum* Bordallo, sp. nov.**

Etymology. The epithet refers to Lucentum, the old Roman name for the city of Alicante (Spain), the locality where this species was found.

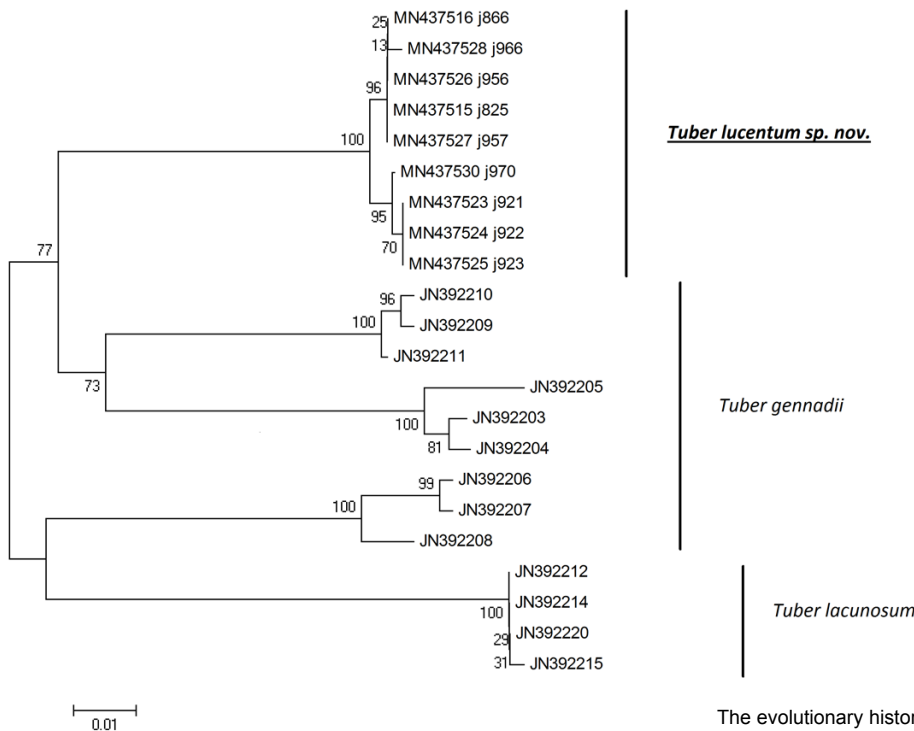
Classification — *Pezizaceae, Pezizales, Pezizomycetes.*

Ascomata hypogeous, very small globose, round, regular, < 1 cm diam in size. *Exoperidium* tomentose white to light cream and endoperidium pseudoparenchymatic (< 100 µm). *Gleba* hyaline, vitrea; forming neither isolated locules nor continuous labyrinthine loculated gleba. *Asci* clavate, containing mostly two spores. *Ascospores* globose to citriform (40–60 µm), by maturity ocher and ornamented with reticulum, mostly pentagonal or hexagonal, cells 3 µm high.

Habitat, Distribution & Season — Accompanying *Terfezia claveryi*, *T. crassiverrucosa*, and other desert truffles. Grows in calcareous, alkaline soils from eastern Spain, associated with *Cistaceae* plants: *Helianthemum violaceum*, *H. almeriense*, *H. syriacum*, *Fumana thymifolia*, etc. Collected in spring (Apr.–June).

Typus. SPAIN, Alicante, Moralet, 2017, J.J. Bordallo, (holotype MUB Fung-j825, ITS sequence GenBank MN437515, MycoBank MB832580); Paratype MUB Fung-j866, ITS sequence GenBank MN437516; Paratype MUB Fung-j921, ITS sequence GenBank MN437523; Paratype MUB Fung-j922, ITS sequence GenBank MN437524; Paratype MUB Fung-j923, ITS sequence GenBank MN437525; Paratype MUB Fung-j956, ITS sequence GenBank MN437526; Paratype MUB Fung-j957, ITS sequence GenBank MN437527; Paratype JJ Fung-j966, ITS sequence GenBank MN437528; Paratype JJ Fung-j970, ITS sequence GenBank MN437530.

Notes — *Tuber lucentum* is distinguished from *T. gennadii* and *T. lacunosum* based on its very small ascomata, its gleba lacking isolated locules or continuous labyrinthine locules, and ITS sequence identity.



Colour illustrations. Habitat with *Helianthemum violaceum*, *H. syriacum* and *Fumana thymifolia*. Ascocarps; gleba and mature ascospores (stain Acidic Fuchsina).

The evolutionary history of 22 taxa was inferred using the Maximum Parsimony and the Neighbour-Joining methods. The bootstrap consensus tree inferred from 500 replicates is taken to represent the evolutionary history of the taxa analysed. Branches corresponding to partitions reproduced in less than 50 % bootstrap replicates are collapsed. The percentage of replicate trees in which the associated taxa clustered together in the bootstrap test (500 replicates) are shown next to the branches. The MP tree was obtained using the Close-Neighbour-Interchange algorithm with search level 3. The evolutionary distances were computed using the Maximum Composite Likelihood method. All positions containing gaps and missing data were eliminated from the dataset (Complete Deletion option). There were a total of 487 positions in the final dataset, out of which 114 were parsimony informative. Maximum Parsimony and the Neighbour-Joining were similar in bootstrap support. Phylogenetic analyses were conducted in MEGA 4.