

Venturia submersa

Fungal Planet 1040 – 18 December 2019

Venturia submersa* Iturrieta-González, Gené, Dania García, *sp. nov.*Etymology.* Referring to the fungus growing on submerged plant debris.Classification — *Venturiaceae*, *Venturiales*, *Dothideomycetes*.

Mycelium consisting of branched, septate, subhyaline to pale olivaceous, smooth-walled 2–5 µm diam hyphae. *Conidiophores* mononematous, growing laterally on hyphae, micronematous, reduced to a conidiogenous cell, or macronematous, erect, unbranched, more rarely branched, subcylindrical, pale olivaceous, smooth-walled, up to 30 µm long. *Conidiogenous cells* terminal, polyblastic, with up to three denticle-like conidiogenous loci, smooth-walled, pale olivaceous, 11–24 × 2–4 µm, forming conidia in simple or branched acropetal chains. *Ramoconidia* 0(–1)-septate, cylindrical, with truncate base, up to three terminal or subterminal conidiogenous loci, smooth-walled, pale olivaceous, 13–24 × 2–4 µm. *Conidia* fusiform, ellipsoidal or cylindrical, 0(–2)-septate, pale olivaceous, smooth-walled, 7–15 × 3–4(–5) µm. *Sexual morph* not observed.

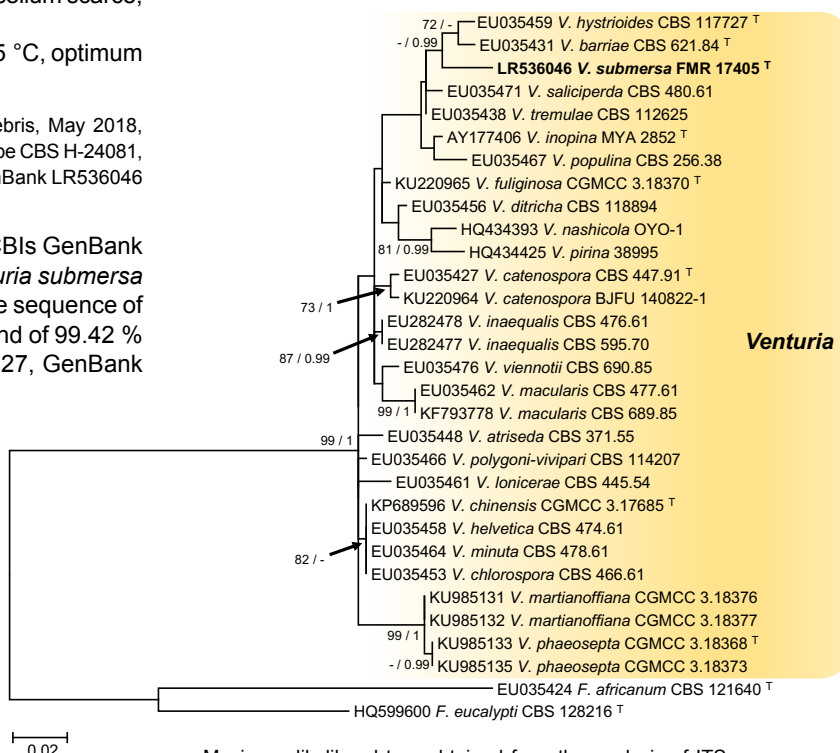
Culture characteristics at 25 °C in 2 wk — Colonies on potato dextrose agar (PDA) reaching 9 mm diam, grey (4F1), velvety, umbonate, aerial mycelium scarce, regular margin; reverse black. On potato carrot agar (PCA) reaching 8–10 mm, brownish grey (4F2), velvety, flat, aerial mycelium scarce, regular margin; reverse black. On oatmeal agar (OA) reaching 8–10 mm diam, grey (4F1), velvety, flat, aerial mycelium scarce, regular margin; reverse dark brown (6F8).

Cardinal temperature for growth — Minimum 5 °C, optimum 20 °C, maximum 25 °C.

Typus. SPAIN, Segovia, Riaza, on submerged plant debris, May 2018, I. Iturrieta-González, V. Magaña-Dueñas & D. García (holotype CBS H-24081, cultures ex-type FMR 17405; ITS and LSU sequences GenBank LR536046 and LR536048, MycoBank MB831789).

Notes — Based on a megablast search of NCBI's GenBank nucleotide database, the LSU sequence of *Venturia submersa* showed a similarity of 99.77 % (857/859) with the sequence of *V. barriae* (CBS 621.84, GenBank EU035431) and of 99.42 % (854/859) with that of *V. hystrioides* (CBS 117727, GenBank

EU035459); while the ITS sequence was 96.44 % (488/506) similar with that of the latter species (CBS 117727, GenBank EU035459) and 95.46 % (484/507) with *V. barriae* (CBS 621.84, GenBank EU035431). The phylogenetic reconstruction using ITS barcodes of different accepted *Venturia* species, including the type *V. inaequalis*, showed that the new species was located in an unsupported clade together with *V. barriae*, *V. hystrioides*, *V. inopina*, *V. populina*, *V. tremulae* and *V. saliciperda*, being closely related with the former two species. *Venturia barriae*, formerly *Fusicladium fagi*, and *V. hystrioides*, formerly *Capronia hystrioides*, were described from decaying leaves of *Fagus sylvatica* and from scar of cherry fruit, respectively (Dugan et al. 1995, Crous et al. 2007c, Rossman et al. 2015). Morphologically, our new species differs from *V. barriae* in having longer conidiophores (up to 30 µm long vs up to 15 µm long in *V. barriae*), commonly aseptate and shorter conidia (7–15 µm vs up to 40 µm in *V. barriae*), and slower growth on PDA after 4 wk in darkness (23 mm in *V. submersa* vs 50 mm at 25 °C in *V. barriae*). *Venturia hystrioides* differs from *V. submersa* in the absence of macronematous conidiophores, larger ramoconidia (up to 30 µm long) with more septa (0–3), and by its more rapid growth on PDA and OA (reaching 40 mm after 2 wk at 25 °C in dark) (Crous et al. 2007c).



Maximum likelihood tree obtained from the analysis of ITS sequences of the genus *Venturia*. The alignment included 502 bp and was performed with ClustalW. Both the alignment and tree for ML were constructed with MEGA v. 6 software (Tamura et al. 2013) and Bayesian Inference (BI) approaches under MrBayes v. 3.2.6 (Ronquist et al. 2012). Kimura 2-parameters with Gamma distribution (K2+G) was used as the best nucleotide substitution model for ML and Hasegawa-Kishino-Yano with Gamma distribution (HKY+G) for BI. Bootstrap support values for ML greater than 70 % and Bayesian posterior probabilities greater than 0.95 are given near nodes. The new species proposed in this study is indicated in **bold face**. A superscript ^T denotes ex-type cultures.

Colour illustrations. Riaza, Segovia, Spain. Colony sporulating on PCA after 2 wk at 25 °C; conidiophores and conidia after 10 d. Scale bars 10 mm (colony), 10 µm (microscopic structures).