

Venturia paralias



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Venturia paralias G.C. Hunter, I. Zeil-Rolfe, M. Jourdan & L. Morin, *sp. nov.*

Etymology. Named after *Euphorbia paralias*, the *Euphorbia* species from which the fungus was isolated.

Classification — *Venturiaceae*, *Venturiales*, *Dothideomycetes*.

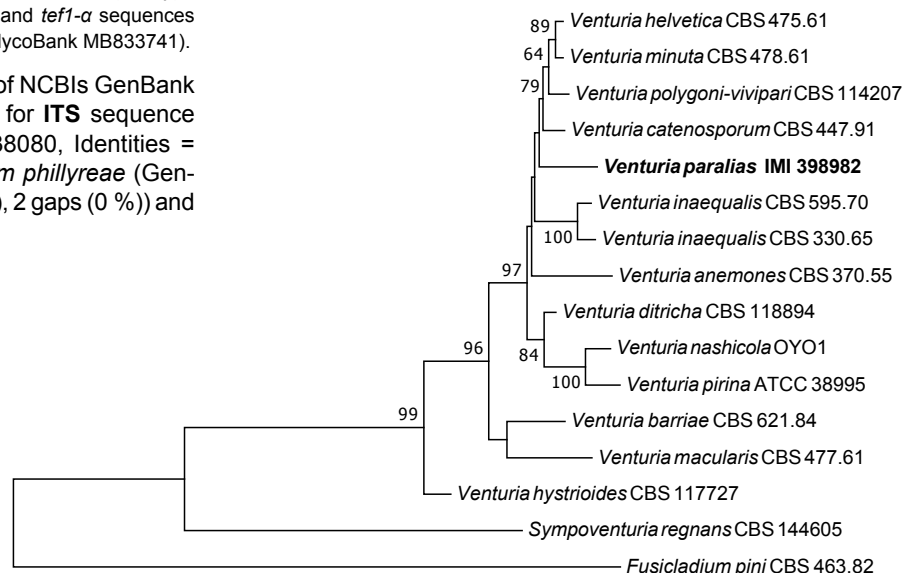
Lesions on leaves and stems, amphigenous, predominantly adaxial, circular to irregular, pale to dark brown, 2–8 mm diam, stem lesions pale to dark brown. **Mycelium** internal, 1.5–6 mm, subcuticular. **Stromata** oblong to subcircular, (49–)59–90(–110) × (29–)39–74(–103) μm, formed by swollen thick-walled cells. **Conidiophores** in loose to dense fascicles on stroma, unbranched, thin-walled, straight to slightly curved, pale brown and lighter towards the apex, occasionally thickened at the base, smooth, (16–)31–59(–81) × (2–)4–5(–6) μm, 0–3-septate. **Conidiogenous cells** integrated, terminal, one to several conidiogenous loci, slightly guttulate, proliferating sympodially, loci flat, hila convex and slightly thickened and darkened-refractive. **Conidia** solitary or catenate, fusiform, subcylindrical, obclavate, clavate, straight or slightly curved, (11–)17–29(–39) × (3–)4–6(–8) μm, 0–3-septate, slightly or not constricted at the septa, brown to pale brown, smooth to verruculose, thickened, apex obtuse, truncate or papillate.

Culture characteristics — Colonies on potato dextrose agar (PDA) flat to slightly raised, aerial mycelium feathery, circular to irregular with entire to undulate margin, 18 mm diam after 30 d at 20 °C under 12 h photoperiod. Outer edge of colony grey olivaceous, inner part olivaceous; reverse olivaceous to olivaceous black.

Typus. FRANCE, Gironde, Pyla-sur-Mer, Plage La Salie, on leaves of *Euphorbia paralias* (*Euphorbiaceae*), 1 July 2009, M. Jourdan (holotype IMI 398982, culture ex-type IMI 398982; ITS, LSU and *tef1-α* sequences GenBank MN864561, MN864538 and MT185924, MycoBank MB833741).

Notes — Based on a megablast search of NCBI's GenBank nucleotide database, the closest matches for ITS sequence were *Venturia oleaginea* (GenBank MN038080, Identities = 451/469 (96 %), 2 gaps (0 %)), *Fusicladium phillyrae* (GenBank EU035435, Identities = 451/469 (96 %), 2 gaps (0 %)) and

Venturia inaequalis (GenBank MN958659, Identities = 447/468 (96 %), 1 gap (0 %)). Closest similarities using the *tef1-α* partial gene sequence were to *Venturia polygoni-vivipari* (GenBank KF853984, Identities 330/358 (92 %), 4 gaps (1 %)), *Venturia ditricha* (GenBank KF853970, Identities = 327/357 (92 %), 2 gaps (0 %)) and *Venturia chlorospora* (GenBank KF 853969, Identities 327/357 (92 %), 2 gaps (0 %)). *Venturia paralias* was shown in pathogenicity tests to cause disease on *E. paralias* and *Euphorbia segetalis* (unpubl. data). *Venturia paralias* is morphologically similar to *Fusicladium euphorbiae* (Schubert et al. 2003), which has been recorded from *E. amygdaloides*, *E. cyparissias*, *E. esula*, *E. exigua*, *E. lamprocarpa*, *E. villosa* and *E. virgata* (Schubert et al. 2003). We were not able to obtain lectotype material of *F. euphorbiae* from LE for comparison. For taxonomic stability we have therefore described the fungus isolated from *E. paralias* as *V. paralias*. *Fusicladium fasciculatum* var. *fasciculatum*, *F. fasciculatum* var. *didymium* and *F. fautreyi* are also morphologically similar to *V. paralias*. *Venturia paralias* produces distinctive pale to dark brown elongated stem lesions, dense fasciculate conidiophores with conidiogenous loci that are less conspicuous or prominent than those of *F. fasciculatum* var. *fasciculatum* and *F. fasciculatum* var. *didymium* (Deighton 1967, Schubert et al. 2003). *Venturia paralias* is distinguished from *F. fautreyi* by its pale brown conidiophores, less conspicuous conidiogenous loci and 3-septate conidia (Deighton 1967).



Phylogenetic relationships of *Venturia* species based on combined *tef1-α* and ITS DNA sequences inferred using the Maximum Likelihood method based on the Tamura-Nei model (Tamura & Nei 1993) as implemented in MEGA v. 7 (Kumar et al. 2016). The phylogram is drawn to scale with branch lengths measured in the number of substitutions per site. Bootstrap support values (> 50 %) after 1 000 replicates are presented at nodes and the phylogeny is rooted with *Fusicladium pini* CBS 463.82.

Colour illustrations. *Euphorbia paralias* on a beach at La Salie, France. Colony on PDA after 1 mo at 20 °C; conidiophores, catenate and single conidia. Scale bars = 10 μm.

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