

Extremopsis radicicola



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***Extremopsis* G. Delgado & Maciá-Vicente, gen. nov.**

Etymology. Named after its close phylogenetic relationship with the genus *Extremus*.

Classification — *Extremaceae*, *Mycosphaerellales*, *Dothi-deomycetes*.

Mycelium colonising root-associated soil and isolated on culture media from surface-sterilised roots of living plants. Chlamydo-spores present, terminal or intercalary, solitary, in chains or forming clusters, variable in shape, 0–1-septate.

Type species. *Extremopsis radicolica* G. Delgado & Maciá-Vicente
Mycobank MB 838931.

***Extremopsis radicolica* G. Delgado & Maciá-Vicente, sp. nov.**

Etymology. Name refers to the roots of the host plant from which the fungus was isolated.

Mycelium composed of hyaline, subhyaline to pale brown, branched, septate hyphae, 2–3.5 µm wide. *Chlamydo-spores* present, abundant, terminal or intercalary, solitary, in short chains of up to 8 or forming more or less dense clusters, globose, subglobose, ellipsoidal, pyriform or elongated, subhyaline to pale brown, smooth, thin-walled that may become brown, thick-walled, 0–1-septate and smooth to verruculose, dark brown when forming large clusters, (3–)4–11(–13) × 2.5–8(–10) µm.

Culture characteristics — Colonies on malt extract agar (MEA) slow growing, reaching 9–13 mm diam after 3 wk at 25 °C, velvety, grey to dark grey or blackish grey, raised 1–2 mm at the centre, with or without a concentric ring around the raised centre, margin entire, reverse black, no exudates. On potato dextrose agar (PDA) reaching 10–14 mm diam, dark grey olivaceous, slightly raised at the centre, margin slightly diffuse, reverse black olivaceous. On modified cellulose agar (MCA) very slow growing, reaching 6–8 mm diam, dark grey, grey at the centre, flat, margin irregular, diffuse, reverse black. Cultures sterile, chlamydo-spores abundant.

Typus. SPAIN, Ciudad Real, Cabañeros National Park, from root-associated soil in a wet heathland ('trampal'), N39°20'58.5" W4°21'38.6", 725 m a.s.l., isolated from surface-sterilised, asymptomatic roots of an *Arabidopsis thaliana* plant inoculated with soil and grown under controlled conditions, 19 Apr. 2018, coll. J.G. Maciá-Vicente, isol. 20 June 2018, J.G. Maciá-Vicente, P6446 (holotype stored in a metabolically inactive state CBS 147117, culture ex-type CBS 147117, ITS and LSU sequences GenBank MN310191 and MN308483, MycoBank MB 838946).

Notes — The family *Extremaceae* includes fungi that are ecologically highly diverse ranging from extremophilic, rock inhabiting and acidophilic members such as *Extremus*, the generic type, to lichenicolous, epiphyllous, endophytic, saprobic or plant pathogenic genera (Quaedvlieg et al. 2014). The new genus *Extremopsis* is introduced to accommodate sterile strains of a root endophyte isolated from surface-sterilised, asymptomatic roots of plants used as bait inoculated with root-associated soil. The three strains of *E. radicolica* did not sporulate in any of the different culture media used including MEA, PDA, MCA or Water Agar supplemented with wooden toothpicks, but they produced abundant chlamydo-spores in all media. Their ITS and partial LSU sequences were nearly

Colour illustrations. Wet heathland ('trampal') in the Cabañeros National Park, Ciudad Real, Spain. Colonies on MEA; chlamydo-spores solitary or in chains; cluster of chlamydo-spores; mycelium. Scale bars = 10 µm (chlamydo-spores), 5 µm (mycelium).

identical except for a single gap at position 128 of alignment in the case of the ITS of both CBS 147117 and P6514, and two bp differences in the LSU of the latter. Phylogenetically, they form a strongly supported monophyletic group in *Extremaceae* sister to the genus *Extremus* but with low support. Moreover, although originally identified as '*Devriesia*' sp., they group distant from *Devriesia* s.str. in *Teratosphaeriaceae* represented by *D. staurophora*, the generic type (Meng et al. 2017). Interestingly, two other strains also named '*Devriesia*' sp., NG_p52, isolated during a study of gene expression of fungal nitrate reductases in agricultural soils from Austria (Gorfer et al. 2011); and MI63, isolated from soil in Germany, grouped within the *Extremopsis* clade and seem conspecific with *E. radicolica*, expanding the known distribution of the genus from southern Spain to other localities across Europe.

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits of *Extremopsis radicolica* (CBS 147117) using the ITS sequence are '*Devriesia*' sp. NG_p52 (GenBank HQ115717.1; Identities = 232/232 (100 %), no gaps), '*Devriesia*' sp. MI63 (GenBank MW268825.1; Identities = 230/232 (99 %), no gaps) and a melanised limestone ascomycete CR-2004 TRN80 (GenBank AY559340.1; Identities = 222/232 (96 %), two gaps (0 %)). The closest hits using the LSU sequence are '*Devriesia*' sp. NG_p52 (GenBank: HQ115717.1; Identities = 488/490 (99 %), no gaps), *Extremus adstrictus* (GenBank KF310022.1; Identities = 527/539 (98 %), two gaps (0 %)) and '*Devriesia*' sp. OTU56 TS-2013 (GenBank AB808449.1; Identities = 521/535 (97 %), two gaps (0 %)).

Supplementary material

FP1250-1 Additional materials examined.

FP1250-2 Maximum likelihood (ML) phylogenetic tree inferred from concatenated ITS and LSU rDNA sequences of strains of *Extremopsis* and related genera showing their placement within *Extremaceae*. The new genus is enclosed in a coloured box and strains newly obtained in this study are in **bold**. ML and Bayesian analyses were performed using RAxML v. 8.2.12 (Stamatakis 2014) and MrBayes v. 3.2.7a (Ronquist & Huelsenbeck 2003), respectively, on the CIPRES Science Gateway server (Miller et al. 2010). Maximum likelihood analysis employed the rapid bootstrapping algorithm with the GTRCAT model and 1000 bootstrap iterations. Numbers above branches represent bootstrap support values ≥ 70 %. Bayesian inference consisted of two independent runs of 10 M generations sampled every 100th generation and the first 25 % of trees discarded as burn-in. Bayesian posterior probabilities ≥ 0.95 are indicated by thickened branches. *Myriangium hispanicum* (CBS 247.33) and *Elsinoe phaseoli* (CBS 165.31) were used as outgroup. The alignment and trees were deposited in TreeBASE (study 27826).

Gregorio Delgado, Eurofins EMLab P&K Houston, 10900 Brittmoore Park Dr. Suite G, Houston, TX 77041, USA;
e-mail: gregorio.delgado@eurofinset.com

Jose G. Maciá-Vicente, Plant Ecology and Nature Conservation, Wageningen University & Research,
P.O. Box 47, 6700 AA Wageningen, The Netherlands; e-mail: jose.maciavicente@wur.nl