

Cladophialophora cabanerensis



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***Cladophialophora cabanerensis* Maciá-Vicente, sp. nov.**

Etymology. Named after the Cabañeros National Park in central Spain, where the soil sample was collected.

Classification — *Herpotrichiellaceae*, *Chaetothyriales*, *Eurotiomycetes*.

Mycelium consisting of hyaline, branched, septate hyphae, (0.5–) 0.7–1.3(–1.6) µm diam, forming hyphal strands. *Conidiophores* mostly single, sympodial, erect, subcylindrical, hyaline, smooth, bearing one phialide, often reduced to a conidiogenous cell. *Conidiogenous cells* phialidic, hyaline, smooth, fusiform with one locus at the apex that leaves a scar, (2.8–)3.6–6.2(–7.6) × (1.3–)1.7–2.6(–2.9) µm. *Conidia* aseptate, produced in mass, hyaline, smooth, globose with a scar, (1.7–)1.9–2.3(–2.4) µm diam (n = 40). *Chlamydospores* absent. *Sexual morph* unknown.

Culture characteristics — *Colonies* slow-growing, reaching 11–14 mm diam on malt extract agar (MEA), 13–17 mm diam on potato-dextrose agar (PDA), and 9–12 mm diam on cornmeal agar (CMA) after 7 d at 25 °C. Colonies velvety, white, becoming light earthy after 3–4 wk, with a compact and suede-like surface; reverse white-cream.

Typus. SPAIN, Ciudad Real, Cabañeros National Park, from rhizospheric soil from a wet heathland ('trampal'), N39.35 W4.36, 725 m asl, 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 (holotype FR 0214084, ex-type culture CBS 146718 = P6481; ITS and LSU sequences GenBank MN310213 and MN308512, MycoBank MB834845).

Additional materials examined. SPAIN, Ciudad Real, Cabañeros National Park, from rhizospheric soil from a wet heathland ('trampal'), N39.35 W4.36, 725 m asl, isolated from surface-sterilised, asymptomatic roots of an *A. 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, culture P6476; ITS and LSU sequences GenBank MT179621 and MN308507; Ciudad Real, Cabañeros National Park, from rhizospheric soil from a wet heathland ('trampal'), N39.35 W4.36, 725 m asl, isolated from surface-sterilised, asymptomatic roots of an *A. thaliana* plant inoculated with soil and grown under controlled conditions, coll. 19 Apr. 2018, J.G. Maciá-Vicente, isol. 20 June 2018, J.G. Maciá-Vicente, culture P6479; ITS and LSU sequences GenBank MN310212 and MN308510.

Colour illustrations. Wet heathland ('trampal') located in the Cabañeros National Park, Ciudad Real, Spain. Seven-day-old colonies growing at 25 °C on PDA; from top to bottom, overview of mycelium bearing conidiophores under phase-contrast microscopy; conidiophores under light microscopy; loose conidia under light microscopy. Scale bars = 10 µm (mycelium) and 5 µm (conidiophores and conidia).

Notes — The three isolates examined have identical morphologies and partial ITS and LSU sequences. Since they originate from the same soil sample, they likely represent clonal isolates. Based on a megablast search of NCBI's GenBank nucleotide database, the ITS sequence has low similarity with several unidentified *Chaetothyriales* strains (e.g., GenBank KX822488.1, identities 566/690 (82 %), 43 gaps (6 %); GenBank KF614863.1, identities 566/690 (82 %), 43 gaps (6 %); GenBank KF614863.1, identities 566/690 (82 %), 43 gaps (6 %)) and with *Cladophialophora immunda* (GenBank MH864254.1, identities 580/715 (81 %), 57 gaps (7 %)). However, the low identity values result from a long insert at the 3' end of the 18S rDNA gene, similarly to what has been found in other fungi (e.g., Tedersoo et al. 2015, Cross et al. 2017), but that is not present in most GenBank records. When analysing only the partial ITS1 region (nt 551–679) that is homologous to other sequences in GenBank, the megablast search yields highest similarity with 15 environmental sequences originating from a single study (e.g., GenBank MF793689.1, identities 129/129 (100 %), no gaps), and to two unidentified fungi (GenBank MG592689.1, identities 129/129 (100 %), no gaps; GenBank GQ996076.1, identities 127/129 (98 %), 1 gap (0 %)) and two *Cladophialophora* sp. isolates (GenBank LC189029.1, identities 129/129 (100 %), no gaps; and GenBank LC229675.1, identities 127/129 (98 %), 1 gap (0 %)). The closest hits using the LSU sequence are an unidentified fungus (GenBank GU552546.1, identities 675/676 (99 %), 1 gap (0 %)), *Cladophialophora* sp. (GenBank MF588895.1, identities 669/676 (99 %), 1 gap (0 %)), unidentified *Chaetothyriales* (GenBank KF614869.1, identities 666/676 (99 %), 1 gap (0 %)), and *Cladophialophora carrionii* (GenBank AF050262.1, identities 665/676 (98 %), 1 gap (0 %)).

The genus *Cladophialophora* is polyphyletic, including species that are commonly isolated from soil and living plants, but also found as causal agents of human infections. *Cladophialophora cabanerensis* is phylogenetically placed outside the *Carrionii* and *Bantiana* clades defined by Badali et al. (2008) that contain most species pathogenic to humans. All the closest hits in the megablast search using the insert-free ITS1 sequence originate from fungi associated with plant roots, like the type specimen of *C. cabanerensis*, suggesting a preference of the species toward this habitat

Supplementary material

FP1069 Maximum likelihood phylogenetic tree inferred from concatenated ITS and LSU rDNA sequences using RAxML v. 8.2.12 (Stamatakis 2014) with the GTR+I+G model.