

Cladosporium fildesense



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***Cladosporium fildesense* C. Gil-Durán, Vaca & R. Chávez, sp. nov.**

Etymology. Name refers to Fildes Bay Area, King George Island, Antarctica, where the fungus was isolated.

Classification — *Cladosporiaceae*, *Capnodiales*, *Dothideo-mycetes*.

Conidiophores dimorphic, cylindrical or subcylindrical, solitary or in small groups, septate, erect, flexuous or straight, arising from the terminal or generally lateral hyphae, pale brown or pale olivaceous brown. Micronematous conidiophores much shorter, small and lateral, occasionally geniculate, subcylindrical to cylindrical-oblong, 6.3–8.1 × 2.3–3 µm, proliferating sympodially, with 1–3 conidiogenous loci. Macronematous conidiophores 50–79.8 × 4.5–5.8 µm. *Ramoconidia* 26–39 × 3.2–4.8 µm; secondary ramoconidia ellipsoid, subcylindrical, 11.10–18.08 × 3.88–4.58 µm, 0–1-septate, surface ornamentation verruculose with one or three distal hilum. Numerous catenate conidia in branched chains, 4.7–6.2 × 2.9–4.1 µm, obovoid, limoniform or subglobose, surface with pustulate ornamentation.

Culture characteristics — (after 2 wk at 20 °C in the dark): On potato dextrose agar colonies reach 29–32 mm diam, without the presence of diffusible pigments and/or exudates. The morphology of the colony seen on the back is characterised by a velvety mycelium immersed in the agar, radially furrowed, olive-green, while on the obverse of the plate the colony has a flat growth, with a somewhat elevated colony centre, velvety olive-black colour, and dense sporulation. In the outer part of the colony, there is an edge with a white filiform margin. On oatmeal agar the colony reaches 32–35 mm diam without presence of diffusible pigments and/or exudates. The colony has round shape, with abundant velvety olive-green aerial mycelium immersed in the agar, profuse sporulation, and presents filiform edges. On malt extract agar, the colony reaches 25–27 mm diam, and does not produce diffusible pigments and/or exudates. The colony seen on the back has a rounded shape, dark green colour and opaque texture. On the obverse of the plate, the colony has a flat growth with abundant aerial velvety mycelium of olive-yellow colour immersed in the agar, and filiform edges. On synthetic nutrient-poor agar, colonies reach 23–25 mm diam without presence of diffusible pigments and/or exudates. On the reverse of the plate, a flat round colony of dark green colour is observed. On the obverse of the plate, the colony has olive-green aerial mycelium and profuse sporulation mainly in the centre of the colony.

Cardinal temperature for growth — Optimum 20 °C, maximum 25 °C, minimum 5 °C.

Typus. ANTARCTICA, South Shetland archipelago, King George Island, Fildes Bay, from an unidentified marine sponge, 13 Dec. 2009, *I. Vaca* (holotype F09-T12-1, culture ex-type ChFC-554, ITS, LSU, *actA* and *tef1* sequences GenBank JX845290, MN245038, MN233632 and MN233633, MycoBank MB832139).

Colour illustrations. Picture taken during sampling showing typical landscape of Fildes Bay, King George Island, Antarctica. *Cladosporium fildesense* growing on oatmeal agar; conidiophores and conidium on SNA after 14 d at 20 °C. Scale bars = 10 µm (conidiophores), 2 µm (conidium).

Notes — Based on the combined analysis of ITS, *actA* and *tef1* markers, *Cladosporium fildesense* belongs to the *C. herbarum* complex (Bensch et al. 2015) and is phylogenetically related to *C. soldanellae*, *C. ossifragi* and *C. spinulosum*. *Cladosporium spinulosum* differs from our new species by the digitate ornamentation of conidia and the absence of secondary ramoconidia (Zalar et al. 2007). Regarding *C. soldanellae*, this species has stromatic cells and occasionally forms ramoconidia (Bensch et al. 2012) while *C. fildesense* does not show stromatic cells and ramoconidia were always observed. Finally, *C. ossifragi* differs from *C. fildesense* by having shorter conidiogenous cells (5–31 µm long), the muricate conidial ornamentation, and by lacking primary ramoconidia (Schubert et al. 2007).

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the ITS sequence are *Cladosporium ramotenellum* (GenBank MF473250.1; Identities 549/549 (100 %), no gaps), *Cladosporium cladosporioides* SLBB (GenBank JN565298.1; Identities 549/549 (100 %), no gaps), and *Cladosporium cucumerinum* (GenBank DQ681347.1; Identities 549/551 (99 %), 2 gaps (0 %)). The closest hits using the LSU sequence are *Cladosporium phlei* CBS 358.69 (GenBank MH877726.1; Identities 608/608 (100 %), no gaps), *Cladosporium herbarum* CBS 128892.69 (GenBank MH876581.1; Identities 608/608 (100 %), no gaps), and *Cladosporium cladosporioides* CBS 127051 (GenBank MH875838.1; Identities 608/608 (100 %), no gaps). The closest hits using the *actA* sequences were *Cladosporium spinulosum* CBS 102044 (GenBank EF679541.1; Identities 213/231 (92 %), 1 gap (0 %)), *Cladosporium ossifragi* CBS 842.91 (GenBank EF679535.1; Identities 212/233 (91 %), 4 gaps (1 %)), and *Cladosporium soldanellae* CPC 13153 (GenBank JN907001.1; Identities 207/231 (90 %), 4 gaps (1 %)). The closest hits with *tef1* sequences were *Cladosporium ramotenellum* (GenBank LN834482.1; Identities 214/245 (87 %), 6 gaps (2 %)), *Cladosporium soldanellae* CPC 13153 (GenBank JN906994.1; Identities 207/236 (88 %), 5 gaps (2 %)), and *Cladosporium ossifragi* CBS 843.91 (GenBank EF679460.1; Identities 204/236 (88 %), 5 gaps (2 %)).

Supplementary material

FP1006 Maximum likelihood (ML) phylogeny of *C. fildesense* and related species within *C. herbarum* complex was inferred from the combined analysis of ITS, *actA* and *tef1* sequences (Bensch et al. 2015). Alignments and ML analyses were performed with MegaX (Kumar et al. 2018). Model used was HKY + G + I. Bootstrap support values (> 50 %) are shown at the nodes (bootstrap iterations = 1000). The tree was rooted using combined ITS and *actA* sequences from *Toxicocladosporium banksiae* CBS 128215 (type strain).