

Cladosporium arenosum



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***Cladosporium arenosum* C. Gil-Durán & L. Sanhueza, sp. nov.**

Etymology. *arenosum* means sandy, referring to substrate (sea sand) from which the fungus was isolated.

Classification — *Cladosporiaceae*, *Cladosporiales*, *Dothi-deomycetes*.

Mycelium scarcely submerged and superficial; hyphae sinuous, unbranched, smooth, 1.8–3 µm wide, septate, not constricted at septa, subhyaline to olive brown. *Conidiophores* smooth, occasionally geniculate, multiseptate, erect to slightly flexuous, oblong, proliferating sympodially; macronematous conidiophores arising terminally or laterally from hyphae, up to 80 µm long, 3.1–4 µm wide; semimacronematous conidiophores arising terminally or laterally from hyphae, 1.3–1.6 µm wide, pale olive brown, with a single apical scar; micronematous conidiophore arising laterally from hyphae, 3.1–3.5 µm wide. *Ramoconidia* straight, smooth, concolourous, subcylindrical, 7.0–13.2 × 2.9–4.3 µm, 1-septate. *Secondary ramoconidia* ellipsoid to subcylindrical, smooth, 7.2–12 × 3.1–4.2 µm, 0–1-septate in the middle, with 2–3 distal hila, proliferating sympodially. *Conidia* numerous, catenated, dichotomously branched in all directions, straight, smooth, with up to 7 conidia; small terminal conidia obovoid, 2.5–5.8 × 1.4–2.8 µm; intercalary conidia ovoid or limoniform, 6–8.2 × 2.3–4.1 µm; microcyclic conidiogenesis not observed.

Culture characteristics — (after 2 wk at 20 °C in the dark): On potato dextrose agar (PDA), colonies reach 44–47 mm diam, round shape, flat, dark olive green, dusty, aerial mycelium absent, profuse sporulation, margin white and glabrous, exudates (blackish droplets) produced mainly on the outermost colony surface; reverse olive green to olive black. On malt extract agar (MEA), colonies reach 40–43 mm diam, irregular flat growth, elevated centre, dusty, olive green to yellowish green, aerial mycelium absent, exudates absent, white filiform margin; reverse, irregular olive-black. On synthetic nutrient-poor agar (SNA), colonies reach a 28–30 mm diam, irregular flat growth, dusty, olive-green, profuse sporulation mainly in the centre of the colony, exudates absent; reverse olive grey with white filiform margin. On oatmeal agar (OA), colonies reach 40–45 mm diam, round shape, flat, olive-green, abundant velvety aerial mycelium, absent on the outermost colony surface, profuse sporulation, exudates absent, margin grey-green, narrow and glabrous.

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

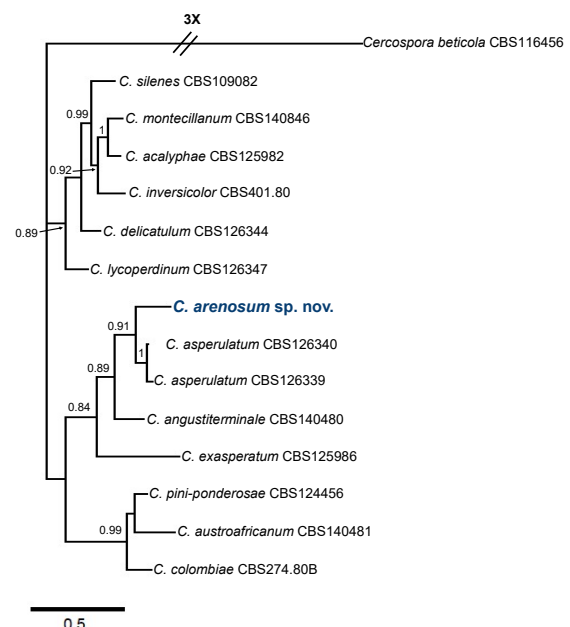
Typus. ANTARCTICA, South Shetland archipelago, King George Island, Fildes Bay, from marine sediment sand, 24 Feb. 2018, L. Sanhueza LS-2 (holotype CHFC-EA 566 stored in a metabolically inactive state in Chilean Fungal Collection; ITS, LSU, *actA* and *tef1* sequences GenBank MN879328, MT015967, MN890008 and MN890011, MycoBank MB834383).

Notes — Based on the combined analysis of ITS, *actA* and *tef1* markers, *Cladosporium arenosum* belongs to the *C. cladosporioides* complex (Bensch et al. 2015) and is phylogenetically related to *Cladosporium asperulatum*. However, *C. asperulatum* exhibits asperulate surface ornamentation of its conidia, conidiophores and mycelium (Bensch et al. 2010), characters not found in *C. arenosum*. In addition, *C. asperulatum* has longer

Colour illustrations. Sea shore of Fildes Bay, Antarctica, where the sample was taken. *Cladosporium arenosum* growing on PDA and MEA; conidiophores and conidium on SNA after 14 d at 20 °C. Scale bars = 10 µm.

conidiophores ((15–)45–210(–360) × (2–)3–4(–5) µm) and ramoconidia (15–50 × 3–4 µm) (Bensch et al. 2010). Finally, *C. arenosum* produces exudates on PDA, limoniform conidia, and its colonies have a characteristic yellowish green colour after 2 wk at 20 °C on MEA, characters not found in *C. asperulatum* (Bensch et al. 2010).

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the ITS sequence are *Cladosporium perangustum* ID58 (GenBank MN511354.1; Identities 551/551 (100 %), no gaps), *Cladosporium globisporum* DTO 220-D4 (GenBank KP701967.1; Identities 551/551 (100 %), no gaps), and *Cladosporium asperulatum* UTHSC DI-13-216 (GenBank LN834357.1; Identities 551/551 (100 %, no gaps). The closest hits using the LSU sequence are *Cladosporium cladosporioides* CBS 129108 (GenBank MH876646.1; Identities 608/608 (100 %, no gaps), *Cladosporium herbarum* CBS 129088 (GenBank MH876640.1; Identities 608/608 (100 %, no gaps), and *Cladosporium tenuissimum* CBS 125995 (GenBank MH876286.1; Identities 608/608 (100 %, no gaps). The closest hits using the *actA* sequence are *Cladosporium asperulatum* UTHSC DI-13-216 (GenBank LN834541.1; Identities 218/227 (96 %), 1 gap (0 %)), *Cladosporium myrtacearum* CBS 126350 (GenBank HM148606.1; Identities 204/227 (90 %), 4 gaps (1 %)), and *Cladosporium longicatenatum* CPC 17189 (GenBank KT600598.1; Identities 202/224 (90 %), 5 gaps (2 %)). The closest hits with *tef1* sequence are *Cladosporium asperulatum* BP312 (GenBank KU605784.1; Identities 242/242 (100 %, no gaps), *Cladosporium angustiterminale* CPC 15564 (GenBank KT600476.1; Identities 222/243 (91 %), 5 gaps (2 %)), and *Cladosporium lycoperdinum* CBS 126347 (GenBank HM148356.1; Identities 213/245 (87 %), 3 gaps (1 %)).



Phylogram obtained by combined analysis of ITS, *actA* and *tef1* sequences of *C. arenosum* and related species from the *C. cladosporioides* complex (Bensch et al. 2018). Analyses were done in MrBayes v. 3.2.6 (Huelsenbeck & Ronquist 2001) under GTR + G model for 5 M generations. Posterior probabilities values > 0.84 are shown at the nodes. *Cercospora beticola* CBS 116456 was used as outgroup.

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