

Cladosporium michoacanense

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Cladosporium michoacanense Iturrieta-González, Gené & Dania García, *sp. nov.*

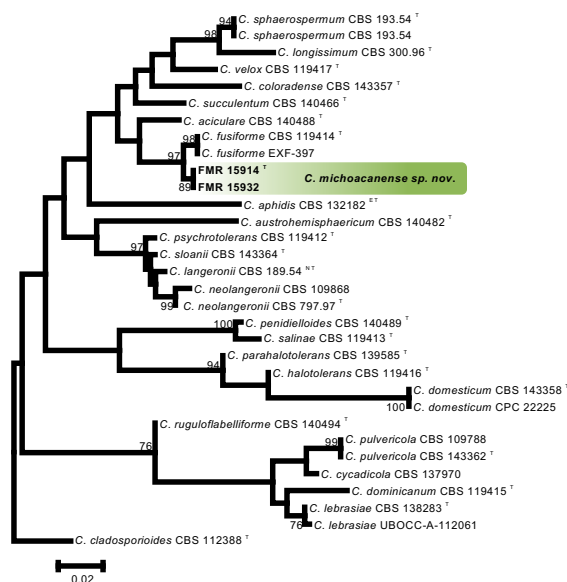
Etymology. Name refers to Michoacán, the geographical area where the fungus was collected.

Classification — *Cladosporiaceae*, *Capnodiales*, *Dothideomycetes*.

Colonies sporulating on synthetic nutrient-poor agar. *Mycelium* consisting of branched, septate, smooth, brown, 2–3 µm wide hyphae. *Conidiophores* macronematous, erect to slightly flexuous, 1–16-septate, branched or unbranched, pale to medium olivaceous brown, smooth, verruculose to tuberculate 24–552 × 3–3.5 µm. *Conidogenous cells* terminal, cylindrical, 14–20 × 2–3 µm, bearing 2–4 subdenticulate loci, 1 µm wide, thickened, darkened and refractive. *Primary ramoconidia* 0–1-septate, pale brown, smooth to somewhat tuberculate, cylindrical to subcylindrical, 11–31 × 2–3 µm, with up to three distal hila; hilum thickened, darkened and refractive. *Secondary ramoconidia* aseptate, pale brown, smooth, cylindrical to subcylindrical, 10–15 × 2–3 µm, with up to 4 distal hila. *Conidia* in branched chains, with up to 4 conidia in the terminal unbranched part, aseptate, pale brown, smooth, with protuberant and darkened hila; intercalary conidia, ellipsoidal and obovoid, 5–12.5 × 2–3.5 µm; small terminal conidia subglobose, obovoid, pyriform, ellipsoidal, occasionally fusiform, 2.5–6.5 × 1.5–2 µm.

Culture characteristics — (at 25 °C in 2 wk): Colonies on PDA up to 34 mm diam, slightly dusty to velvety, radially folded, olive to dull green (3F3/28E4) (Kornerup & Wanscher 1978), aerial mycelium scarce, margin regular; reverse dark green (28F8); exudate scarce, consisting of small colourless droplets on the colony surface. On OA, up to 23 mm diam, slightly dusty, flat, olive to dark green (2F4/29F8), aerial mycelium scarce, margin irregular; reverse dark green (29F8) to black. On SNA, up to 22 mm diam, slightly dusty, flat, olive (3F4–8), aerial mycelium scarce, margin regular; reverse olive (2F4).

Cardinal temperature for growth — Optimum 20 °C, maximum 30 °C, minimum 5 °C.



Colour illustrations. Villa Jiménez, Michoacán (Imagen Credit Marco A. Ambris), Mexico; colony sporulating on PDA after 2 wk at 25 °C; conidiophores and conidia on SNA after 7 d at 25 °C. Scale bars = 10 µm.

Typus. MEXICO, Michoacán, Villa Jiménez, from soil, Sept. 2016, leg. E. Rodríguez-Andrade (holotype CBS H-23245, cultures ex-type FMR 15914 = CBS 143588, ITS, LSU, *actA* and *tef1* sequences GenBank LT907958, LT934506.1, LT907961 and LT907945, MycoBank MB823063).

Additional material examined. MEXICO, Michoacán, Morelia, from soil, Sept. 2016, leg. E. Rodríguez-Andrade, FMR 15932, ITS, *actA* and *tef1* sequences GenBank LT907944, LT907960 and LT907959.

Notes — *Cladosporium michoacanense* belongs to the *C. sphaerospermum* complex (Bensch et al. 2018). Based on the combined analysis of ITS, *actA* and *tef1* markers, its closest relative is *C. fusiforme*. However, the lineage formed by the two isolates of *C. michoacanense* received a high statistical support and showed a phylogenetic distance of 1 % with respect to the lineage of the ex-type strain of *C. fusiforme* (CBS 119414). *Cladosporium fusiforme* differs from our novel species in several morphological aspects, such as in having shorter conidiophores (up to 200 µm long), larger primary (15–40 µm long) and secondary ramoconidia ((7–)8–24(–31) µm long), and terminal conidia commonly being fusiform (Zalar et al. 2007). *Cladosporium michoacanense* exhibits small conidia of varied shape (subglobose, ellipsoidal, obovoid, pyriform), but rarely fusiform.

Based on a megablast search of NCBI's GenBank nucleotide database using LSU sequences, the closest species were *C. sphaerospermum* (GenBank DQ780351.2; Identities = 840/844 (99 %), Gaps = 1/844 (0 %)), *C. longissimum* (GenBank DQ780352.2; Identities = 838/844 (99 %), Gaps = 1/844 (0 %)) and *C. langeronii* (GenBank DQ780380.2; Identities = 836/844 (99 %), Gaps = 1/844 (0 %)). The closest hits using ITS sequences were *C. cladosporioides* (GenBank JF911745.1; Identities 499/500 (99 %), Gaps = 0/500 (0 %)), *C. succulentum* (GenBank LN834434.1; Identities = 501/511 (98 %), Gaps = 5/511 (0 %)) and *C. crousii* (GenBank NR_148192.1; Identities = 500/511 (98 %), Gaps = 3/511 (0 %)). The closest hits using the *actA* sequences were *C. fusiforme* (GenBank KJ596640.1; Identities = 205/216 (95 %), Gaps = 4/216 (1 %)), *C. aciculare* (GenBank KT600607.1; Identities = 214/232 (92 %), Gaps = 0/232 (0 %)) and *C. velox* (GenBank KT600654.1; Identities = 202/225 (90 %), Gaps = 2/225 (0 %)). The closest hits with *tef1* sequences were *C. fusiforme* (GenBank KJ596595.1; Identities = 236/252 (94 %), Gaps = 3/252 (1 %)), *C. aciculare* (GenBank KT600509.1; Identities = 236/263 (90 %), Gaps = 1/262 (0 %)) and *C. velox* (GenBank KT600556.1; Identities = 216/258 (84 %), Gaps = 4/258 (1 %)).

Maximum likelihood tree obtained from the combined analysis of ITS, *actA* and *tef1* sequences of the *C. sphaerospermum* species complex (Bensch et al. 2018). Bootstrap support values above 70 % are indicated on the nodes. The alignment included 977 bp and was performed with ClustalW. The Kimura 2-parameter with Gamma distribution (G) was used as the best nucleotide substitution model. Both the alignment and tree were constructed with MEGA v. 6.0 (Tamura et al. 2013). The new species proposed herein is in the green box and ex-type, ex-epitype and ex-neotype strains are indicated with ^T, ^{ET} and ^{NT}, respectively.