

Exophiala embothrii



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Exophiala embothrii Sand.-Den. & Giraldo López, *sp. nov.*

Etymology. Named after the plant genus on whose rhizosphere the fungus was isolated, *Embothrium*.

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

Mycelium consisting of hyaline to pale brown, smooth, branched, septate, 1–3 µm diam hyphae, torulose hyphae seldom present. **Conidiophores** short, erect, cylindrical, septate, poorly differentiated 18–50 µm long, 1–2.5 µm wide at the widest portion, often reduced to conidiogenous cells born laterally on the hyphae. **Conidiogenous cells** terminal or lateral on conidiophores and hyphae, subcylindrical to doliiform, 3.5–12.5 × 1–3 µm, or more commonly as lateral pegs borne terminal or intercalary on undifferentiated hyphae, 0.5–1.5 × 0.5–1 µm. **Conidia** aseptate, (sub)hyaline, ellipsoidal to cylindrical, (2.5–)4.5–6(–7) × 1.5–2.5 µm, often forming palisades alongside the hyphae or small heads on the tip of conidiophores. **Chlamydospores** and **budding cells** not observed.

Culture characteristics — Colonies on malt extract agar (MEA) dull green to olivaceous grey, velvety to cottony, slightly raised to umbonate, margin entire. Reverse olivaceous black without diffusible pigment.

Typus. CHILE, Los Lagos Region, Osorno, from rhizosphere of *Embothrium coccineum* (*Proteaceae*), 1 Jan. 2019, A. Giraldo & N. Sandoval-Giraldo (holotype CBS H-24520, culture ex-type CBS 146558, ITS, LSU, *tef1* and *tub2* sequences GenBank MW045817, MW045821, MW055980 and MW055976, MycoBank MB837535).

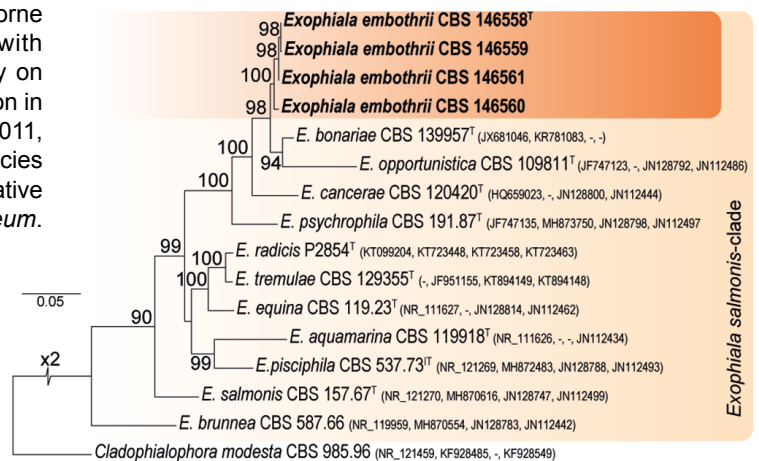
Additional materials examined. CHILE, Los Lagos Region, Osorno, from rhizosphere of *Embothrium coccineum*, 1 Jan. 2019, A. Giraldo & N. Sandoval-Giraldo, CBS 146559 ITS, LSU, *tef1* and *tub2* sequences GenBank MW045818, MW045822, MW055981 and MW055977; *ibid.*, CBS 146560, ITS, LSU, *tef1* and *tub2* sequences GenBank MW045819, MW045823, MW055982 and MW055978; *ibid.*, CBS 146561, ITS, LSU, *tef1* and *tub2* sequences GenBank MW045820, MW045824, MW055983 and MW055979.

Notes — *Exophiala embothrii* clusters within the salmonis-clade of *Exophiala*. This clade includes typically waterborne mesophilic species, some of which are associated with superficial and in some cases invasive infections mostly on cold-blooded animals, but also including agents of infection in humans and other homeothermic animals (De Hoog et al. 2011, Najafzadeh et al. 2018, Garzon et al. 2019). The new species described here was isolated from the rhizosphere of a native South American *Proteaceae* species, *Embothrium coccineum*.

Colour illustrations. *Embothrium coccineum* ('Notro' or 'Chilean firetree') with the Osorno volcano on the background (photo by Samuel Troncoso Sandoval, from Wikimedia Commons, license CC BY-SA 3.0). Conidiophores; conidiogenous cells; conidia. Scale bars = 5 µm.

Similarly, two other genetically related *Exophiala* species of the salmonis-clade, *E. radicans* and *E. tremulae*, are known to inhabit plant roots of *Microthlaspi perfoliatum* (*Brassicaceae*) and *Populus tremula* (*Salicaceae*), respectively (Crous et al. 2011, Maciá-Vicente et al. 2016). A four-gene phylogeny based on ITS, LSU, *tef1* and *tub2* sequences showed that *E. embothrii* is phylogenetically closely related to *E. opportunistica* and *E. bonariae*. However, *E. embothrii* differ by its consistently more elongated conidia and phialides, the absence of budding cells and the scarce presence of moniliform hyphae.

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the ITS sequence had highest similarity to *Exophiala opportunistica* (strain CBS 637.69, GenBank JF747121.1; Identities = 549/549 (100 %), 0 gaps), and *Exophiala opportunistica* (strain CBS 122269, GenBank JF747124.1; Identities = 549/549 (100 %), 0 gaps). Closest hits using the LSU sequence are *Exophiala psychrophila* (strain CBS 191.87, GenBank MH873750.1; Identities = 812/815 (99 %), no gaps), *Exophiala bonariae* (strain CCFFEE 5899, GenBank KR781082.1; Identities = 812/815 (99 %), no gaps), and *Exophiala cancerae* (strain CBS 115142, GenBank MH874540.1; Identities = 814/816 (99%), 1 gap (0%)). Closest hits using the *tef1* sequence had highest similarity to *Exophiala opportunistica* (strain CGMCC:3.17515, GenBank KP347908.1; Identities = 192/201 (96 %), no gaps), *Exophiala opportunistica* (strain CGMCC:3.17507, GenBank KP347907.1; Identities = 192/201 (96 %), no gaps), and *Exophiala cancerae* (strain CBS 117491, GenBank JN128799.1; Identities = 173/201 (86 %), 3 gaps (1 %)). Closest hits using the *tub2* sequence had highest similarity to *Exophiala opportunistica* (strain CBS 112269, GenBank JN112487.1; Identities = 408/408 (100 %), no gaps), and *Exophiala opportunistica* (CBS 637.69, GenBank JN112490.1; Identities = 405/408 (99 %), no gaps).



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