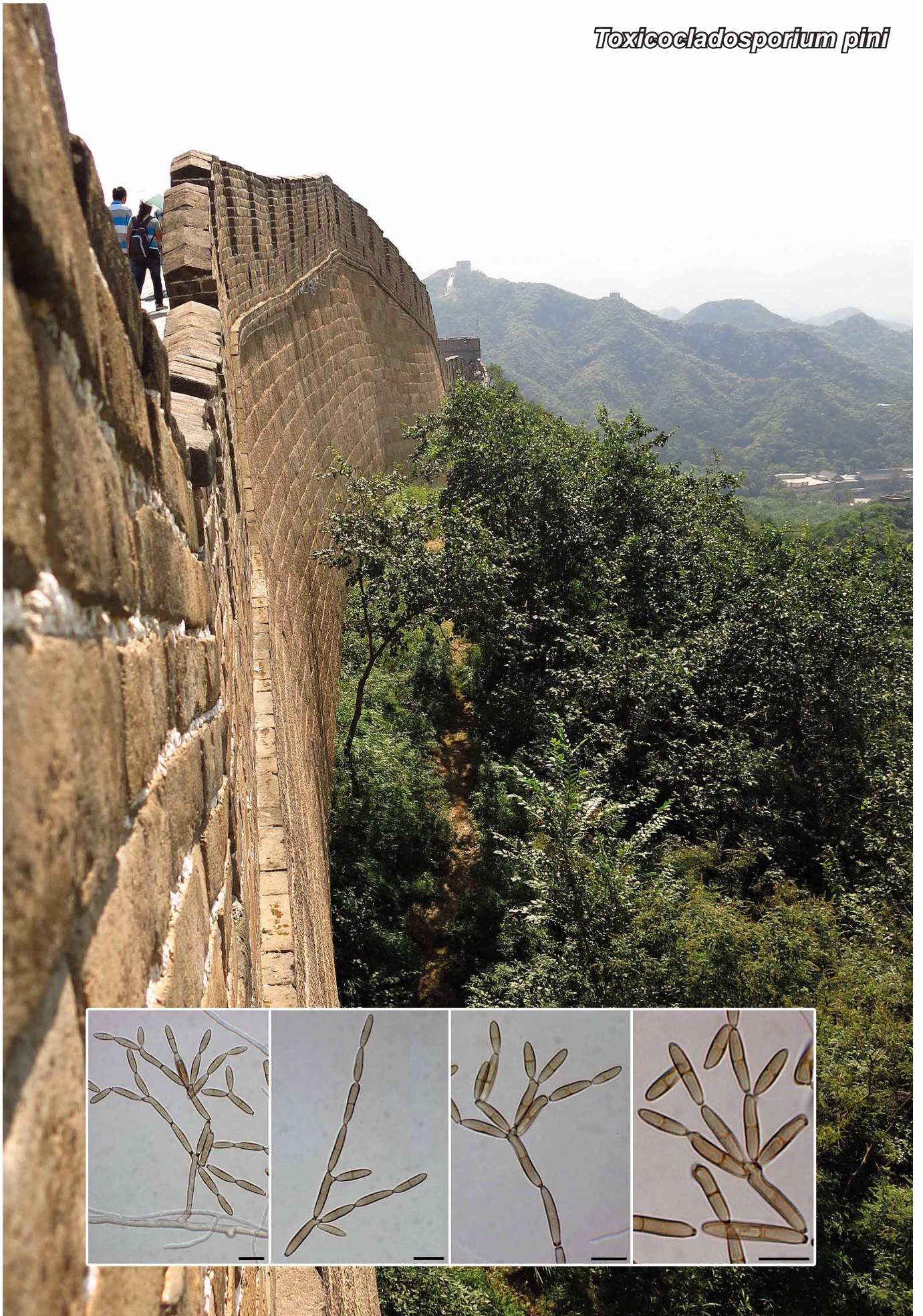


Toxicocladosporium pini



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***Toxicocladosporium pini* Crous & Y. Zhang ter, sp. nov.**

Etymology. Named after the host from which it was collected, *Pinus*.

Mycelium consisting of smooth, hyaline, branched, septate, 1.5–2.5 µm diam hyphae. *Conidiophores* dimorphic. *Microconidiophores* erect, subcylindrical, straight to geniculate-sinuuous, 10–17 × 3–4 µm. *Macroconidiophores* brown, erect, finely verruculose, straight to geniculate-sinuuous, 2–8-septate, 30–90 × 3–4 µm. *Conidiogenous cells* integrated, terminal and lateral, 5–20 × 3–3.5 µm, subcylindrical, brown, finely verruculose; loci thickened and darkened, 1 µm diam. *Ramoconidia* subcylindrical, brown, finely verruculose, 0–1-septate, 12–17 × 3(–3.5) µm. *Intercalary conidia* brown, finely verruculose, 0–1-septate, fusoid-ellipsoid, 12–14 × 3 µm. *Terminal conidia* brown, finely verruculose, 0–1-septate, fusoid-ellipsoidal, 8–10(–11) × 2.5(–3) µm; loci thickened and darkened, 1 µm diam.

Culture characteristics — Colonies reaching 10 mm diam after 2 wk at 22 °C. On MEA surface erumpent, with sparse aerial mycelium and even, lobed margins. Surface and reverse olivaceous-grey, similar on OA and PDA.

Typus. CHINA, Beijing, Badaling, N40°20'45.1" E116°00'48.3", on needles of *Pinus* sp. (*Pinaceae*), 1 Sept. 2013, P.W. Crous & Y. Zhang (holotype CBS H-21719, culture ex-type CPC 23639 = CBS 138005; ITS sequence GenBank KJ869160, LSU sequence GenBank KJ869217, MycoBank MB808944).

Notes — The genus *Toxicocladosporium* was introduced for a cladosporium-like genus with dimorphic conidiophores, and conidia having hila that are slightly darkened, thickened and refractive (Crous et al. 2007b, Bensch et al. 2012). Phylogenetically, *T. pini* is most similar to *T. pseudoveloxum* (ramoconidia 0–1-septate, broadly ellipsoid to subcylindrical, 8–15 × 2.5–4 µm; intermediate and terminal conidia ellipsoid, (6–)7–10(–11) × (2–)2.5(–3) µm; Crous et al. 2011) and *T. protearum* (ramoconidia 0–1-septate, subcylindrical, 15–20 × 2.5–3.5 µm; intermediate and terminal conidia subcylindrical to narrowly fusoid-ellipsoidal, (9–)11–13(–16) × (2–)2.5(–3) µm; Crous et al. 2010). Although *T. pini* can be distinguished from *T. protearum* based on conidial dimensions, it is very similar to *T. pseudoveloxum* and can only be distinguished based on DNA data.

ITS. Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the ITS sequence are *Toxicocladosporium pseudoveloxum* (GenBank JF499847; Identities = 572/580 (99 %), Gaps = 3/580 (0 %)), *Toxicocladosporium protearum* (GenBank HQ599586; Identities = 539/547 (99 %), Gaps = 2/547 (0 %)) and *Toxicocladosporium veloxum* (GenBank FJ790288; Identities = 516/524 (98 %), Gaps = 1/524 (0 %)).

LSU. Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the LSU sequence are *Toxicocladosporium pseudoveloxum* (GenBank JF499868; Identities = 878/878 (100 %), no gaps), *Toxicocladosporium chlamydosporium* (GenBank FJ790302; Identities = 875/875 (100 %), no gaps) and *Toxicocladosporium veloxum* (GenBank FJ790306; Identities = 874/875 (99 %), no gaps).

Colour illustrations. Scenic view from next to the Great Wall in China; conidiophores and conidia in culture. Scale bars = 10 µm.

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