Toxicocladosporium hominis
Toxicocladosporium hominis Sandoval-Denis, Gené & Deanna A. Sutton, sp. nov.

Etymology: Referring to the isolation source of the ex-type strain.

Classification — Cladosporiaceae, Capnodiales, Dothideomycetes.

Colonies sporulating on synthetic nutrient-poor agar. Mycelium branched, septate, smooth, subhyaline to pale brown, hyphae 1.5–3 μm wide. Conidiophores simple or branched, subcylindrical, erect, thickening toward the apex, dark brown, smooth- and thick-walled, 70–113 × 3–3.5 μm. Conidiogenous cells integrated, polyblastic, terminal, geniculate, dark brown, 13–30 × 3–4 μm; scars truncate, thickened and darkened, 1.5–2 μm wide. Primary ramoconidia cylindrical, dark brown, smooth- and thick-walled, 15–32 × 2–4 μm, 0–2-septate. Secondary ramoconidia subcylindrical to cylindrical, pale to dark brown, smooth- and thick-walled, 11–15 × 2.5–4 μm, 0–1-septate, sometimes constricted at the septum, giving rise to branched conidial chains; scars thickened, 0.5–1.5 μm diam. Intercalary conidia subcylindrical, brown, smooth- and thick-walled, 9–16 × 3–4 μm, 0–1-septate, usually constricted at the septum. Small terminal conidia ellipsoidal to clavate, brown, smooth-walled, 5.5–8 × 2.5–3.5 μm.


Notes — The genus Toxicocladosporium, typified by T. irritans, currently includes 12 species. Segregated from Cladosporium, Toxicocladosporium differs in the presence of conspicuous, dark septa in the conidiophores and conidia, and by having flat, thickened and refractive conidigenous scars in contrast to the coronate scars of Cladosporium (Crous et al. 2007b). Toxicocladosporium hominis is phylogenetically related and morphologically similar to T. strelitziae (Crous et al. 2012b), from which it differs in the production of larger conidigenous cells (13–30 × 3–4 μm) and intercalary conidia (9–16 × 3–4 μm) vs 10–15 × 2.5–3.5 μm and 10–12 × 2.5–2.5 μm, respectively, in T. strelitziae. In addition, the latter species has smooth to verruculose ramoconidia, secondary ramoconidia and intercalary conidia, without constrictions in the medial portion or at the septum.

Based on a megablast search of NCBI’s GenBank nucleotide database, the closest hit using the ITS sequence is T. strelitziae CBS 132535 (GenBank KM816684; Identities = 513/522 (98 %), Gaps = 2/522 (0 %)), followed by T. irritans CBS 185.58 (GenBank EU040243; Identities = 510/526 (97 %), Gaps = 4/526 (0 %)) and T. pini CPC 23639 (GenBank KJ869160; Identities = 505/527 (96 %), Gaps = 6/527 (1 %)). Closest hits using the LSU sequence were to T. strelitziae CBS 132535 (GenBank NG042687; Identities = 542/547 (99 %), Gaps = 2/547 (0 %)), T. irritans CBS 185.58 (GenBank EU040243; Identities = 542/547 (99 %), Gaps = 2/547 (0 %)) and Cladosporium sp. ATCC 28310 (GenBank KP780464; Identities = 539/547 (99 %), Gaps = 2/547 (0 %)).