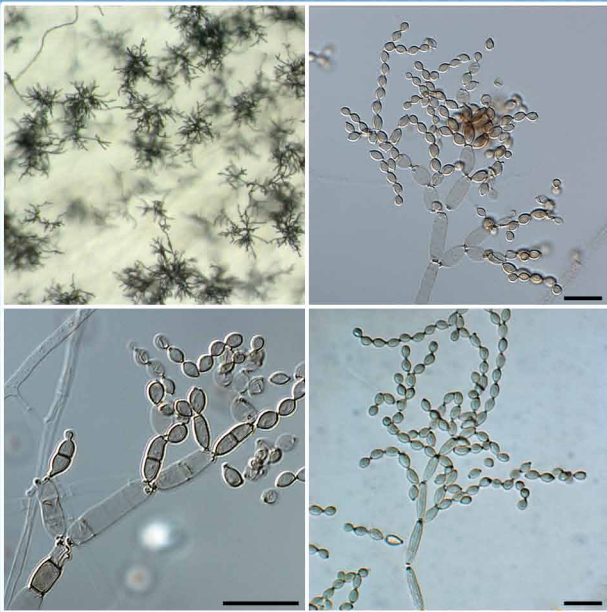


*Cladosporium cycadicola*



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***Cladosporium cycadicola* Crous & R.G. Shivas, sp. nov.**

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

*Mycelium* consisting of branched, septate, smooth, brown, 2–3 µm diam hyphae. *Conidiophores* erect, flexuous, subcylindrical, unbranched, 30–70 × 3–4 µm, 2–5-septate, giving rise to a conidiogenous apparatus with chains of branched conidia. *Primary ramoconidia* subcylindrical, pale brown, smooth, 0–1-septate, 17–27 × 2.5–3 µm; hila thickened, darkened and refractive, 0.5–1.5 µm diam. *Secondary ramoconidia* subcylindrical to fusoid-ellipsoidal, 7–14 × 1.5–3 µm. *Intercalary* and small *terminal conidia* in branched chains (–15), brown, smooth, ellipsoid, pale brown, guttulate, (4–)5(–6) × 2.5(–3) µm; hila thickened, darkened, refractive, 0.5 µm diam.

*Culture characteristics* — Colonies reaching 30 mm diam after 2 wk at 22 °C, spreading, folded, with sparse aerial mycelium and smooth, even margins. On PDA olivaceous-grey, reverse iron-grey. On OA surface iron-grey. On MEA surface and reverse olivaceous-grey.

*Typus.* AUSTRALIA, Queensland, Cairns Botanical Garden, S16°53'57.1" E145°44'48.7", on *Cycas media* (*Cycadaceae*) leaves, 12 Aug. 2009, P.W. Crous & R.G. Shivas (holotype CBS H-21681, culture ex-type CPC 17251 = CBS 137970; ITS sequence GenBank KJ869122, LSU sequence GenBank KJ869179, ACT sequence GenBank KJ869227, TEF sequence GenBank KJ869236, MycoBank MB808896).

*Notes* — Two species of *Cladosporium* have been described from *Cycas*, namely *C. apicale* and *C. cycadis* (Bensch et al. 2012). *Cladosporium cycadicola* can be distinguished from both species by being more allied to the *C. sphaerospermum* species complex (Zalar et al. 2007), having ramoconidia that are subcylindrical to fusoid-ellipsoid, 0–1-septate and intercalary and terminal conidia in long chains that are smaller than those in *C. apicale* and *C. cycadis*.

*ITS.* Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the ITS sequence are *Cladosporium sphaerospermum* (GenBank EU570256; Identities = 635/647 (98 %), Gaps = 5/647 (0 %)), *Cladosporium cucumerinum* (GenBank HM148071; Identities = 632/644 (98 %), Gaps = 5/644 (0 %)) and *Cladosporium lignicola* (GenBank AF393709; Identities = 607/619 (98 %), Gaps = 5/619 (0 %)).

*LSU.* Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the LSU sequence are *Cladosporium sphaerospermum* (GenBank JN938884; Identities = 867/875 (99 %), Gaps = 1/875 (0 %)), *Cladosporium langeronii* (GenBank DQ780380; Identities = 863/876 (99 %), Gaps = 1/876 (0 %)) and *Cladosporium perangustum* (GenBank JF499856; Identities = 894/910 (98 %), Gaps = 1/910 (0 %)).

*ACT.* Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the ACT sequence are *Cladosporium dominicanum* (GenBank EF101368; Identities = 171/190 (90 %), no gaps), *Cladosporium exile* (GenBank HM148580; Identities = 200/235 (85 %), Gaps = 15/235 (6 %)) and *Cladosporium psychrotolerans* (GenBank EF101366; Identities = 162/191 (85 %), Gaps = 9/191 (4 %)).

*TEF.* Based on a megablast search of NCBI's GenBank nucleotide database, the closest hit using the complete TEF sequence is *Cladosporium dominicanum* (GenBank JN906986; Identities = 361/421 (86 %), Gaps = 19/421 (4 %)) with partial hits of the last exon with *Cladosporium angustisporum* (GenBank HM148236; Identities = 184/190 (97 %), no gaps) and *Cladosporium cladosporioides* (GenBank HM148267; Identities = 186/194 (96 %), no gaps).

*Colour illustrations.* Brisbane, Australia; conidiophores and conidia in culture. Scale bars = 10 µm.

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