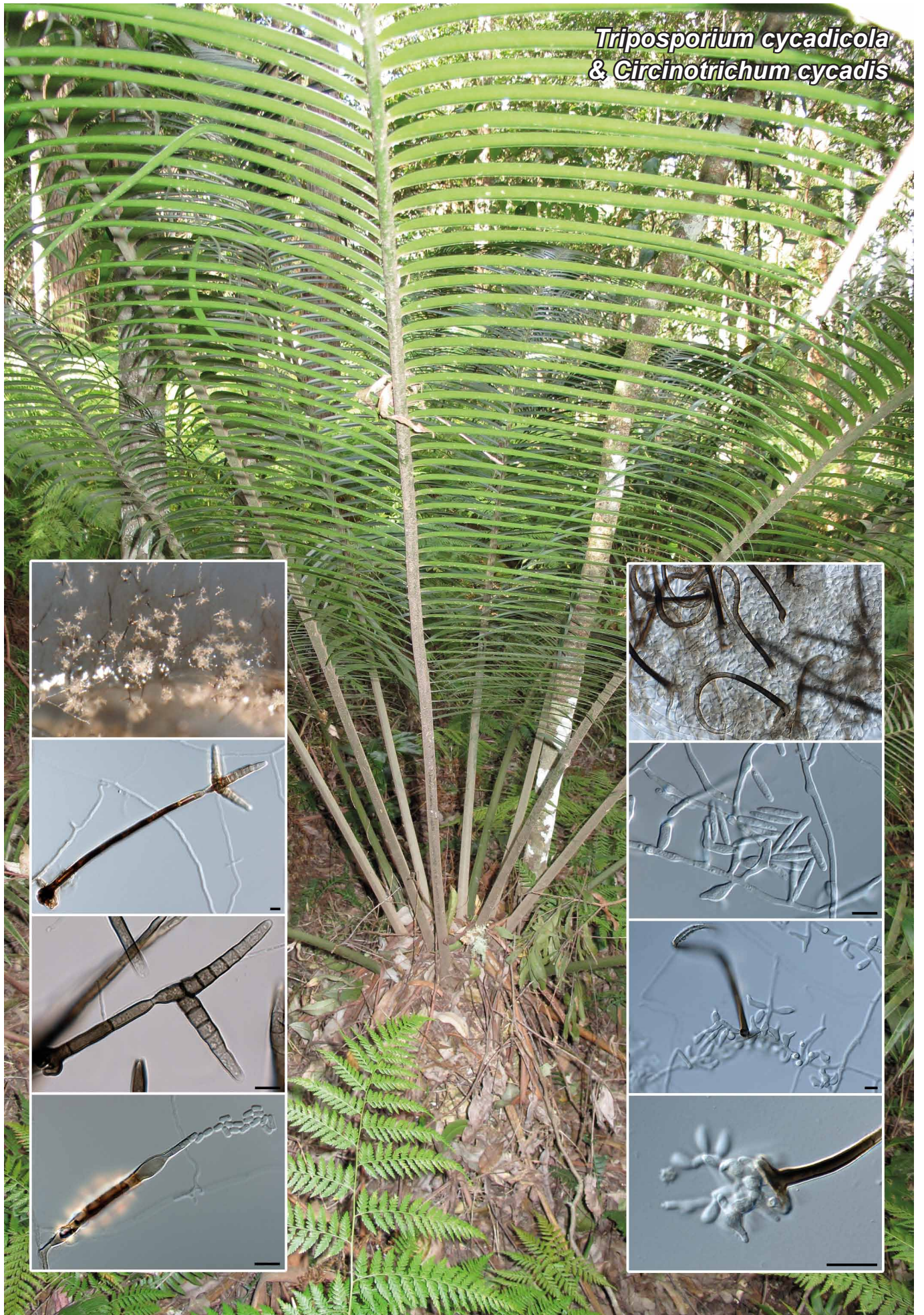


*Tripodosporium cycadicola*  
& *Circinotrichum cycadis*



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

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

**Mycelium** consisting of branched, septate, pale brown, 2–3 µm diam hyphae. **Conidiophores** dimorphic. **Macroconidiophores** erect, subcylindrical, flexuous, unbranched, 4–9-septate, 50–220 × 4–5 µm. **Conidiogenous cells** terminal, subcylindrical, brown, smooth, tapering towards a truncate holoblastic locus, 2–2.5 µm diam, 15–25 × 4–5 µm. **Conidia** solitary, brown, verruculose, thick-walled, guttulate, basal cell with truncate hilum, 2–2.5 µm diam, bearing 2–3 lateral arms, extending outwards; arms subcylindrical, tapering towards obtuse ends, 3–7-septate, (30–)55–65(–70) × (7–)8(–9) µm (including basal cell). **Synasexual morph** similar in morphology to macroconidiophores, but shorter, only up to 40 µm long, with terminal cell forming chalara-like conidiogenous cell, giving rise to chains of hyaline, aseptate, smooth microconidia, 3–6 × 2–3 µm.

**Culture characteristics** — Colonies reaching 20 mm diam after 2 wk at 22 °C, spreading with sparse aerial mycelium and even, smooth margins. On PDA surface umber, reverse grey-olivaceous. On OA surface umber. On MEA surface umber, reverse grey-olivaceous.

**Typus.** AUSTRALIA, Queensland, Brisbane Forest Park, S27°17'36.2" E152°44'42.0", on *Cycas* sp. (*Cycadaceae*) leaves, 15 July 2009, P.W. Crous & R.G. Shivas (holotype CBS H-21679, culture ex-type CPC 17215 = CBS 137968; ITS sequence GenBank KJ869119, LSU sequence GenBank KJ869177, TEF sequence GenBank KJ869235, MycoBank MB808894); CPC 17217, ITS sequence GenBank KJ869120.

***Circinotrichum cycadis* Crous & R.G. Shivas, sp. nov.**

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

**Mycelium** consisting of brown, septate, smooth, 1.5–2.5 µm diam hyphae. **Setae** erect, dark brown, 4–7-septate, stalk dark brown, thick-walled, upper curled part medium brown, thin-walled, warty, tapering to obtusely rounded apex, foot cell arising from hyphae, lacking rhizoids, stalk 25–40 × 2–3 µm, apical curled part with 1–2 loops. **Conidiophores** reduced to conidiogenous cells, arranged in clusters around setae, pale olivaceous, smooth, ampulliform, 8–20 × 3–4 µm, proliferating inconspicuously percurrently at apex. **Conidia** hyaline, smooth, fusoid-ellipsoid, straight, apex obtuse, base truncate, (8–)9–11(–13) × 2(–2.5) µm; hilum truncate, not thickened nor darkened, 0.5 µm diam.

**Culture characteristics** — Colonies reaching up to 5 mm diam after 2 wk at 22 °C, spreading, erumpent, with sparse aerial mycelium and feathery margins. On PDA surface and reverse olivaceous-grey. On OA surface iron-grey. On MEA dirty white, with sienna margin, reverse umber.

**Typus.** AUSTRALIA, Queensland, Brisbane Forest Park, S27°17'36.2" E152°44'42.0", on *Cycas* sp. (*Cycadaceae*) leaves, 15 July 2009, P.W. Crous & R.G. Shivas (holotype CBS H-21680, culture ex-type CPC 17285 =

**Colour illustrations.** Brisbane Forest Park, Queensland, Australia; conidiophores and conidia of *Triposporium cycadicola* in culture (left column); setae, conidiogenous cells and conidia of *Circinotrichum cycadis* in culture (right column). Scale bars = 10 µm.

**Notes** — The genus *Triposporium* differs from the morphologically similar *Actinocladium* and *Ceratosporella* by having stauriform conidia composed of a short basal cylindrical stalk, and 3–4-septate arms. However, the branches of the type species of *Triposporium*, *T. elegans*, morphologically differ from that of *T. cycadicola* in that they are more conical and have swollen apical cells (Seifert et al. 2011). The chalara-like synanamorph produced here in culture, also appears to be a unique record for the genus. Further collections are required, however, to resolve the phylogeny of *Triposporium* s.str.

**ITS.** Based on a megablast search of NCBI GenBank nucleotide database, the closest hits using the ITS sequence are *Phialea strobilina* (GenBank EF596821; Identities = 630/692 (91 %), Gaps = 12/692 (1 %)), *Scleropezicula alnicola* (GenBank AF141168; Identities = 630/694 (91 %), Gaps = 17/694 (2 %)) and *Xenopolyscytalum pinea* (GenBank HQ599581; Identities = 573/653 (88 %), Gaps = 21/653 (3 %)).

**LSU.** Based on a megablast search of NCBI GenBank nucleotide database, the closest hits using the LSU sequence are *Phialea strobilina* (GenBank EF596821; Identities = 886/903 (98 %), Gaps = 1/903 (0 %)), *Rhytisma acerinum* (GenBank AF356696; Identities = 826/845 (98 %), Gaps = 2/845 (0 %)) and *Chalara acuaría* (GenBank FJ176248; Identities = 831/853 (97 %), Gaps = 6/853 (0 %)).

CBS 137969; ITS sequence GenBank KJ869121, LSU sequence GenBank KJ869178, MycoBank MB808895).

**Notes** — The genus *Circinotrichum* is characterised by having unbranched, brown, solitary, sterile setae, surrounded at the base by clusters of aseptate, hyaline conidiogenous cells. It is distinguished from *Gyrothrix* in that the latter has branched setae (Seifert et al. 2011). The conidiogenesis is obscure in both genera due to the minute dimensions of the conidiogenous cell apices, and more studies are required to resolve this aspect. *Circinotrichum cycadis* is presently the only species known from *Cycas*.

**ITS.** Based on a megablast search of NCBI GenBank nucleotide database, the closest hits using the ITS sequence are *Gibberella moniliformis* (GenBank JN232129; Identities = 430/496 (87 %), Gaps = 20/496 (4 %)), *Fusarium oxysporum* (GenBank JN232179; Identities = 424/488 (87 %), Gaps = 20/488 (4 %)) and *Calceomyces lacunosus* (GenBank JX658530; Identities = 413/464 (89 %), Gaps = 26/464 (5 %)). An identification using MycoID on MycoBank yielded a similarity of 549/586 (94 %) and Gaps = 6/586 (1 %) with *Circinotrichum olivaceum* strain CBS 101185.

**LSU.** Based on a megablast search of NCBI GenBank nucleotide database, the closest hits using the LSU sequence are *Anthostomella conorum* (GenBank EU552099; Identities = 865/897 (96 %), Gaps = 2/897 (0 %)) and *Barrmaelia macrospora* (GenBank KC774566; Identities = 856/897 (95 %), Gaps = 4/897 (0 %)).

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