

*Gyrothrix eucalypti*



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## *Gyrothrix eucalypti* Crous, sp. nov.

*Etymology.* Name refers to the host genus *Eucalyptus* from which it was isolated.

*Classification* — *Incertae sedis*, *Xylariales*, *Sordariomycetes*.

*Mycelium* internal and external, consisting of branched, septate, hyaline to pale brown, 2–3 µm diam hyphae. *Setae* erect, straight to geniculate-sinuous, dark brown, thick-walled, verruculose to warty, 100–180 µm tall, 4–5 µm wide at base, 4–10-septate, branched, forming 2–6 lateral branches. *Conidiophores* reduced to conidiogenous cells (rarely with a supporting cell), arranged on hyphae around bases of setae, smooth, olivaceous, ampulliform, 5–10 × 3–4 µm, giving rise to conidia via conspicuous annellations. *Conidia* forming in a slimy mass, hyaline, smooth, falcate, aseptate, with excentric hilum, 0.5–1 µm diam, (8–)10–13(–15) × (2–)2.5 µm.

*Culture characteristics* — Colonies flat, spreading, with sparse aerial mycelium folded surface, and smooth, lobate margin, reaching 35 mm diam after 2 wk at 25 °C. On MEA, PDA and OA surface buff, reverse cinnamon to honey.

*Typus.* SOUTH AFRICA, Limpopo Province, Tzaneen, near turnoff coach road, on leaves of *Eucalyptus* sp. (*Myrtaceae*), 2010, *P.W. Crous*, HPC 2472 (holotype CBS H-24163, culture ex-type CPC 36066 = CBS 146023, ITS, LSU and *tef1* sequences GenBank MN562109.1, MN567617.1 and MN56832.1, MycoBank MB832866).

*Additional material examined.* SOUTH AFRICA, Limpopo Province, Tzaneen, on *Eucalyptus dunnii*, 2010, *P.W. Crous*, HPC 2469, culture CPC 35992 = CBS 146022, ITS and LSU sequences GenBank MN562110.1 and MN567618.1.

*Notes* — *Gyrothrix* is characterised by producing brown, branched, sterile setae that arise from superficial hyphae, and lageniform conidiogenous cells that form hyaline, aseptate, cylindrical to falcate, straight to slightly curved conidia. *Gyrothrix* is close to *Circinotrichum*, but distinguished based on its branched setae (Ellis 1971). *Gyrothrix eucalypti* is distinguished from *G. circinata* (setae 80–180 µm, conidia 12–15 × 1.5–1.8 µm) and *G. podosperma* (setae 120–260 µm, conidia 8–16 × 1.5–2 µm) by the dimensions of its setae and conidia (Ellis 1971).

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the ITS sequence of CPC 36066 had highest similarity to *Lopadostoma lechatii* (strain CBS 133694, GenBank NR\_132032.1; Identities = 373/412 (91 %), 16 gaps (3 %)), *Calceomyces lacunosus* (strain CBS 633.88, GenBank KY610397.1; Identities = 516/583 (89 %), 18 gaps (3 %)), *Anthostomella* sp. DAD-2016a (strain MFLUCC 16-0243, GenBank KX505957.1; Identities = 487/540 (90 %), 19 gaps (3 %)), and *Ceratocladium microspermum* (strain CBS 126092, GenBank MH864077.1; Identities = 529/600 (88 %), 35 gaps (5 %)). The ITS sequences of CPC 35992 and 36066 differ at a single position (576/577 bases similar). Closest hits using the LSU sequence of CPC 36066 are *Torula ficus* (strain MFLUCC 18-0112, GenBank MH260322.1; Identities = 791/803 (99 %), no gaps), *Circinotrichum papakurae* (strain CBS 101373, GenBank KR611897.1; Identities = 874/891 (98 %), 3 gaps (0 %)), and *Gyrothrix ramosa* (strain MUCL 54061, GenBank KC775722.1; Identities = 797/816 (98 %), 4 gaps (0 %)). The LSU sequences of CPC 35992 and 36066 are identical (894/894 bases). Closest hits using the *tef1* sequence of CPC 36066 had highest similarity to *Furfurella luteostiolata* (strain CE3, GenBank MK523302.1; Identities = 431/476 (91 %), 2 gaps (0 %)), *Gyrothrix inops* (strain BE108, GenBank KJ476974.1; Identities = 429/475 (90 %), no gaps), and *Gyrothrix ramosa* (strain MUCL 54061, GenBank KJ476975.1; Identities = 428/475 (90 %), no gaps).

*Colour illustrations.* *Eucalyptus* leaves *Gyrothrix eucalypti* was isolated from. Conidiogenous cells; conidia; setae. Scale bars = 10 µm.

Pedro W. Crous & Johannes Z. Groenewald, Westerdijk Fungal Biodiversity Institute, P.O. Box 85167, 3508 AD Utrecht, The Netherlands; e-mail: p.crous@wi.knaw.nl & e.groenewald@wi.knaw.nl  
Michael J. Wingfield, Department of Biochemistry, Genetics and Microbiology, Forestry and Agricultural Biotechnology Institute (FABI), Faculty of Natural and Agricultural Sciences, University of Pretoria, Private Bag X20, Hatfield 0028, Pretoria, South Africa; e-mail: mike.wingfield@fabi.up.ac.za