

*Gyrothrix encephalarti*



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

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

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

Culture sterile, morphology based on sporulation on dead leaf spots. *Mycelium* consisting of brown, smooth, septate, branched, 1.5–2 µm diam hyphae. *Setae* erect, 80–130 µm long, 3–4 µm diam, brown, multiseptate, thick-walled, verrucose, sub-cylindrical with apical taper, base bulbous, 5–6 µm diam, apex spirally twisted with twisted lateral branches in apical region. *Conidiophores* reduced to conidiogenous cells around base of setae, ampulliform to subcylindrical, pale brown, smooth, 6–10 × 3–4 µm, proliferating percurrently at apex. *Conidia* hyaline, smooth, aseptate, fusoid, inaequilateral, inner plane flat, outer plane convex, apex subobtuse, base truncate, (7–)10–12(–14) × 3(–3.5) µm.

*Culture characteristics* — Colonies flat, spreading, with moderate aerial mycelium and smooth, lobate margin, reaching 55 mm diam after 2 wk at 25 °C. On MEA surface buff, reverse cinnamon. On PDA surface buff, reverse rosy buff. On OA surface rosy buff.

*Typus.* SOUTH AFRICA, Northern Province, Tzaneen, on leaves of *Encephalartos* sp. (*Zamiaceae*), 2015, P.W. Crous, HPC 2486 (holotype CBS H-24364, culture ex-type CPC 35966 = CBS 146684; ITS, LSU and *tef1* sequences GenBank MT373376.1, MT373358.1 and MT375117.1, MycoBank MB835410).

*Notes* — *Gyrothrix encephalarti* is closely related to *G. eucalypti* (*Eucalyptus* sp., South Africa; conidia (8–)10–13(–15) × (2–)2.5 µm, setae 100–180 µm tall, 4–5 µm diam at base; Crous et al. 2019c), but has wider conidia and shorter setae. DNA sequences of *G. eucalypti* and *G. encephalarti* are related to the type sequence deposited for *Neoanthostomella viticola* (NG\_067792.1), which has a completely different asexual morph.

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Neoanthostomella viticola* (strain MFLUCC 16-0243, GenBank NR\_165511.1; Identities = 503/537 (94 %), 22 gaps (4 %)), *Gyrothrix eucalypti* (strain CPC 36066, GenBank NR\_166315.1; Identities = 540/581 (93 %), 8 gaps (1 %)), and *Calceomyces lacunosus* (strain CBS 633.88, GenBank KY610397.1; Identities = 524/588 (89 %), 22 gaps (3 %)). Closest hits using the **LSU** sequence are *Gyrothrix eucalypti* (strain CPC 35992, GenBank MN567618.1; Identities = 869/880 (99 %), no gaps), and *Torula ficus* (strain MFLUCC 18-0112, GenBank MH260322.1; Identities = 792/803 (99 %), no gaps). Closest hits using the **tef1** (second part) sequence had highest similarity to *Gyrothrix ramosa* (strain MUCL54061, GenBank KJ476975.1; Identities = 447/472 (95 %), no gaps), *Gyrothrix inops* (strain BE108, GenBank KJ476974.1; Identities = 447/472 (95 %), no gaps), and *Metarhizium globosum* (strain ARSEF 2596, GenBank EU248846.1; Identities = 438/470 (93 %), no gaps).

*Colour illustrations.* Leaves of *Encephalartos* sp. Setae and conidiogenous cells; conidia. Scale bars = 10 µm.

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