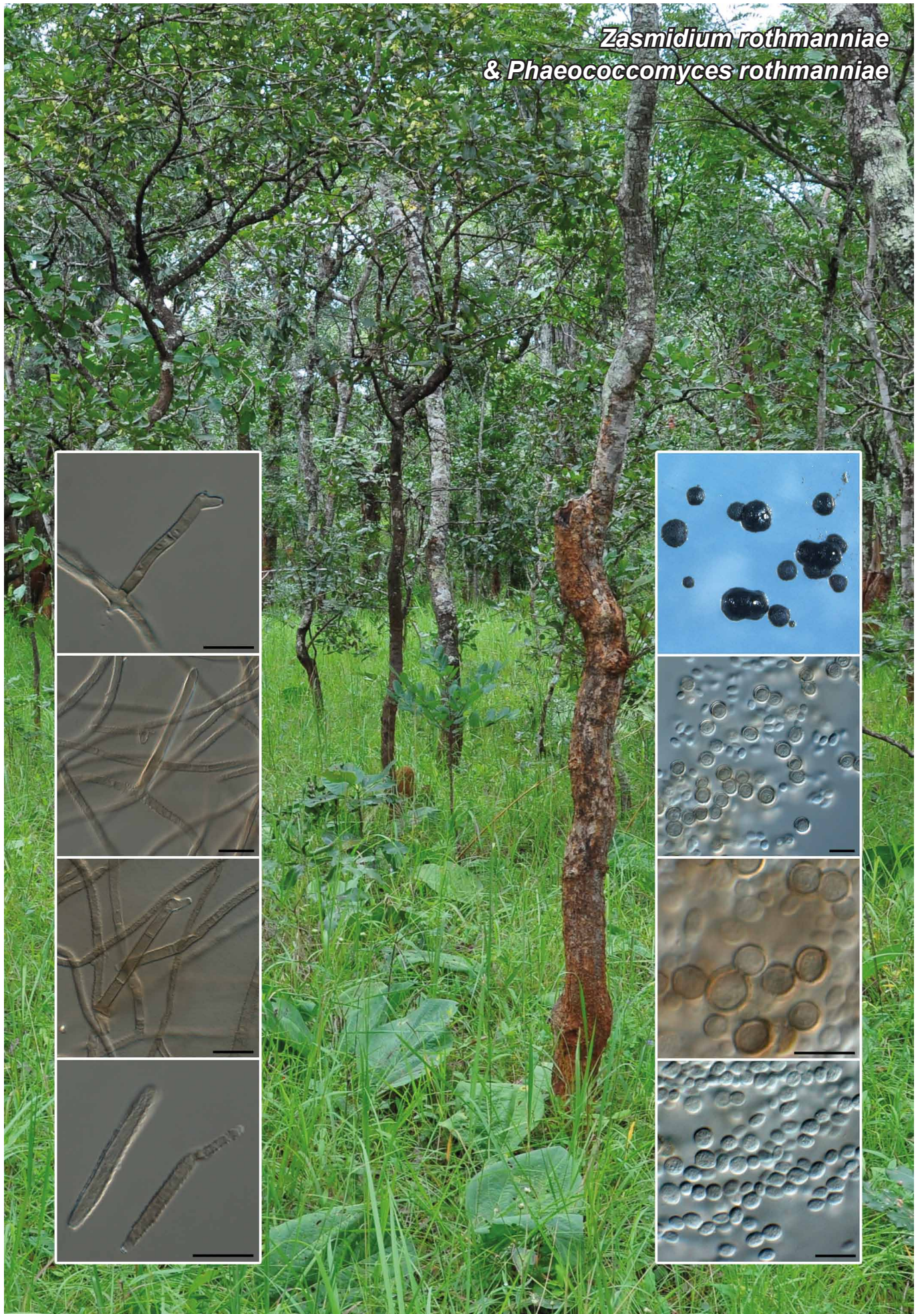


Zasmidium rothmanniae
& *Phaeococcomyces rothmanniae*



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***Zasmidium rothmanniae* Crous, sp. nov.**

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

Leaf spots brown, circular, amphigenous, up to 7 mm diam. On SNA. *Mycelium* consisting of septate, branched, brown, verruculose to warty, 3–4 µm diam hyphae. *Conidiophores* solitary on superficial mycelium, erect, medium brown, finely verruculose to smooth, subcylindrical, straight to once geniculate, 1–3-septate, 17–70 × 3–4 µm. *Conidiogenous cells* integrated, terminal, subcylindrical, medium brown, finely verruculose to smooth, proliferating sympodially, 10–20 × 3–3.5 µm; loci darkened, thickened and refractive, 2 µm diam. *Conidia* in branched chains, medium brown, verruculose, narrowly obclavate (subcylindrical in small conidia), apex subobtuse, base truncate, straight to curved, 1–6-septate, (25–)40–100(–150) × 2.5–3(–4) µm; loci thickened, darkened and refractive, 2 µm diam.

Culture characteristics — Colonies reaching 20 mm diam after 2 wk at 22 °C, erumpent, folded, with sparse to moderate aerial mycelium and even margin. On PDA surface olivaceous-grey, reverse iron-grey; on OA olivaceous-grey. On MEA surface and reverse iron-grey.

Typus. ZAMBIA, OM4106, on *Rothmannia engleriana* (Rubiaceae), 21 Feb. 2013, M. van der Bank (holotype CBS H-21695, culture ex-type CPC 22656 = CBS 137983; ITS sequence GenBank KJ869135, LSU sequence GenBank KJ869192, MycoBank MB808914).

Notes — The genus *Zasmidium* is characterised by having pigmented, verruculose mycelium and conidiophores, and chains of verruculose conidia with darkened, thickened and refractive scars (Crous et al. 2007a, Braun et al. 2013). This morphology has, however, evolved several times within the *Mycosphaerellaceae*, rendering *Zasmidium* paraphyletic (Crous et al. 2009a). As far as we could establish, no cercosporoid fungi have thus far been described from *Rothmannia* and hence *Z. rothmanniae* is introduced as a new taxon.

ITS. Based on a megablast search of NCBI GenBank nucleotide database, the closest hits using the ITS sequence are *Ramichloridium strelitziae* (GenBank EU041803; Identities = 518/557 (93 %), Gaps = 10/557 (1 %)), *Mycosphaerella pseudovespa* (GenBank DQ530216; Identities = 478/514 (93 %), Gaps = 11/514 (2 %)) and *Stenella queenslandica* (GenBank EU514295; Identities = 484/521 (93 %), Gaps = 14/521 (2 %)).

LSU. Based on a megablast search of NCBI GenBank nucleotide database, the closest hits using the LSU sequence are *Zasmidium anthuriicola* (GenBank KF251785; Identities = 594/604 (98 %), no gaps), *Zasmidium suregadae* (GenBank KC677939; Identities = 594/604 (98 %), no gaps) and *Zasmidium anthuriicola* (GenBank FJ839662; Identities = 594/604 (98 %), no gaps).

***Phaeococcomyces rothmanniae* Crous, sp. nov.**

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

Colonies lacking mycelium but consisting of a globular mass of chlamydospore-like cells; cells aseptate, brown (hyaline when young), 4–6 µm diam, covered in mucus, globose, thin-walled, verruculose, remaining attached to one another, giving rise to younger conidia via budding, ellipsoid to globose, hyaline, thin-walled, covered in mucus, smooth, 3–5 × 2–3 µm.

Culture characteristics — Colonies reaching 10 mm diam after 2 wk at 22 °C, surface folded, spreading, lacking aerial mycelium, with even, smooth margins. On PDA, OA and MEA black.

Typus. ZAMBIA, OM4106, on *Rothmannia engleriana* (Rubiaceae), 21 Feb. 2013, M. van der Bank (holotype CBS H-21696, culture ex-type CPC 22668 = CBS 137984; ITS sequence GenBank KJ869136, LSU sequence GenBank KJ869193, MycoBank MB808915).

Notes — The genus *Phaeococcomyces* represents a genus of black yeasts with slimy, folded, slow-growing colonies that lack aerial mycelium. The genus *Phaeococcomyces* presently contains eight species (Crous et al. 2013b, Moreno-Rico et al. 2014). Compared to the presently known species, *P. rothmanniae* is phylogenetically closely allied to *P. nigricans* (conidia globose to broadly ellipsoidal, 4–6.5 × 4–5 µm; de Hoog 1979), though it has somewhat smaller conidia.

ITS. Based on a megablast search of NCBI GenBank nucleotide database, the closest hits using the ITS sequence are *Phaeococcomyces nigricans* (GenBank AF050278; Identities = 508/541 (94 %), Gaps = 4/541 (0 %)) and *Phaeococcomyces* aff. *nigricans* (GenBank JX188194; Identities = 362/397 (91 %), Gaps = 13/397 (3 %)).

LSU. Based on a megablast search of NCBI GenBank nucleotide database, the closest hits using the LSU sequence are *Phaeococcomyces nigricans* (GenBank AF050278; Identities = 807/815 (99 %), no gaps), *Phaeococcomyces eucalypti* (GenBank KC005791; Identities = 791/816 (97 %), Gaps = 2/816 (0 %)) and *Phaeococcomyces mexicanus* (GenBank KJ152786; Identities = 791/816 (97 %), Gaps = 4/816 (0 %)).

Colour illustrations. *Rothmannia engleriana* in Zambia (photo: John Burrows); conidiophores and conidia of *Zasmidium rothmanniae* (left column) in culture; colonies and conidia of *Phaeococcomyces rothmanniae* (right column) in culture. Scale bars = 10 µm.

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