

Nothoramichloridium perseae



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Anungitiomycetaceae Crous, *fam. nov.*

Etymology. Based on the genus *Anungitiomyces*.

Classification — *Anungitiomycetaceae*, *Xylariales*, *Sordariomycetes*.

Mycelium consisting of hyaline, smooth, septate, branched hyphae. *Conidiophores* solitary, erect, flexuous to geniculous-flexuous, subcylindrical, brown, smooth to finely verruculose, septate. *Conidiogenous cells* terminal, integrated, subcylindrical, upper part forming a rachis with tightly aggregated sym-

podial loci, truncate, flattened to subdenticulate, not thickened nor darkened. *Conidia* solitary, obclavate to clavate, hyaline to pale brown, guttulate, thick-walled, smooth to verruculose, apex obtuse, base truncate, not thickened nor darkened, septate.

Type genus. *Anungitiomyces* Crous.
MycoBank MB832876.

Genera included — *Anungitiomyces*, *Nothoramichloridium*, *Strelitzomyces*.

Nothoramichloridium Crous, *gen. nov.*

Etymology. Name reflects its morphological similarity to *Ramichloridium*.

Mycelium consisting of hyaline, smooth, septate, branched hyphae. *Conidiophores* solitary, erect, flexuous, subcylindrical, brown, finely verruculose, septate. *Conidiogenous cells* terminal, integrated, subcylindrical, straight to geniculous-sinuous; upper part forming a rachis with tightly aggregated sympodial

loci, truncate, subdenticulate, 1 µm diam, not thickened nor darkened. *Conidia* solitary, clavate, pale brown, guttulate, thick-walled, verruculose, straight, apex obtuse, base truncate, not thickened nor darkened, septate.

Type species. *Nothoramichloridium perseae* Crous.
MycoBank MB832877.

Nothoramichloridium perseae Crous, *sp. nov.*

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

Classification — *Phyllostictaceae*, *Botryosphaerales*, *Dothideomycetes*.

Mycelium consisting of hyaline, smooth, septate, branched, 1.5–2.5 µm diam hyphae. *Conidiophores* solitary, erect, flexuous, subcylindrical, brown, finely verruculose, 2–3-septate, 80–150 × 4–5 µm. *Conidiogenous cells* terminal, integrated, subcylindrical, straight to geniculous-sinuous, 40–70 × 4–5 µm; upper part forming a rachis with tightly aggregated sympodial loci, truncate, subdenticulate, 1 µm diam, not thickened nor darkened. *Conidia* solitary, clavate, pale brown, guttulate, thick-walled, verruculose, straight, apex obtuse, base truncate, 1 µm diam, not thickened nor darkened, 1(–2)-septate, with septa forming a protruding rift visible in conidial outline, (19–)21–23(–26) × 5(–6) µm.

Culture characteristics — Colonies erumpent, spreading, with moderate aerial mycelium and smooth, lobate margin, reaching 10 mm diam after 2 wk at 25 °C. On MEA surface rosy buff, reverse rosy buff to isabelline. On PDA surface buff to isabelline, reverse isabelline. On OA surface buff.

Typus. SOUTH AFRICA, Mpumalanga Province, Nelspruit, on leaves of *Persea americana* (*Lauraceae*), 9 Aug. 2014, P.W. Crous, HPC 2565 (holotype CBS H-24245, culture ex-type CPC 36383 = CBS 146048, ITS and LSU sequences GenBank MN562121.1 and MN567629.1, MycoBank MB832878).

Colour illustrations. Nelspruit Botanical Garden. Colony on synthetic nutrient poor agar; conidiophores with conidiogenous cells; conidia. Scale bars = 10 µm.

Notes — *Nothoramichloridium* is phylogenetically allied to *Anungitiomyces* and *Strelitzomyces*, and these genera represent an undescribed family in the *Xylariales* (Crous et al. 2019a).

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the ITS sequence had highest similarity to *Hypoxyylon lenormandii* (voucher EBS228, GenBank KM610287.1; Identities = 330/377 (88 %), 18 gaps (4 %)), *Rhinochlorella pyriformis* (strain CBS 469.94, GenBank MH862476.1; Identities = 393/449 (88 %), 14 gaps (3 %)), and *Anungitiomyces stellenboschiensis* (strain CPC 34726, GenBank MK876376.1; Identities = 374/428 (87 %), 15 gaps (3 %)). Closest hits using the LSU sequence are *Anungitiomyces stellenboschiensis* (strain CPC 34726, GenBank MK876415.1; Identities = 828/841 (98 %), 1 gap (0 %)), *Oxydothis gareth-jonesii* (strain MFLUCC 15-0287, GenBank KY206762.1; Identities = 827/863 (96 %), 4 gaps (0 %)), and *Arthrinium malaysianum* (strain CBS 102053, GenBank NG_042780.1; Identities = 826/864 (96 %), 4 gaps (0 %)).