Paraphysalospora Crous, gen nov.

Etymology. Named refers to Physalospora, a morphologically similar genus.

Classification — Clypeophysalosporaceae, Xylariales, Sordariomycetes.


Type species. Paraphysalospora eucalypti Crous. MycoBank MB823380.

Paraphysalospora eucalypti Crous, sp. nov.

Etymology. Name refers to Eucalyptus, the host genus from which this fungus was collected.

Single ascospores shot onto MEA, but ascomata not traced on leaf tissue. Ascospores hyaline, smooth, limoniform with cylindrical appendage at each end, 45–50 × 15–20 µm. Conidiomata sporodochial on OA and SNA, up to 400 µm diam, with buff, slimy conidial mass. Conidiophores subcylindrical, pale brown, smooth, branched, septate, up to 80 µm tall. Conidiogenous cells terminal and intercalary, subcylindrical, pale brown, smooth, 10–20 × 2.5 µm, phialidic with prominent periclinal thickening. Conidia solitary, hyaline, smooth, aseptate, sickle-shaped, apex subobtuse, base truncate, (13–)15–17(–20) × 1.5 µm.

Culture characteristics — Colonies erumpent, spreading, surface folded, with sparse aerial mycelium and smooth, lobate margins, reaching 10 mm diam after 2 wk at 25 °C. On MEA, PDA and OA surface dirty white, reverse luteous.


Notes — The genus Paraphysalospora is related to Clypeophysalospora and Neophysalospora (Xylariales), both occurring on Eucalyptus (Crous et al. 2014b, Giraldo et al. 2017). Based on the ascospore shape, mucoid appendages and sporodochial asexual morph, Paraphysalospora clearly represents yet another genus in this complex. There were only a few ascomata on the leaf tissue, and hence the ascomatal anatomy remains to be elucidated pending further collections.

Based on a megablast search using the ITS sequence, the closest matches in NCBI’s GenBank nucleotide database were Castanediella hyalopenicillata (GenBank KX306751; Identities 397/427 (93 %), 3 gaps (0 %)), Bagadiella lunata (GenBank NR_132832; Identities 567/610 (93 %), 20 gaps (3 %)) and B. koalae (GenBank JF951142; Identities 565/611 (92 %), 21 gaps (3 %)). The highest similarities using the LSU sequence were Neophysalospora eucalypti (GenBank KP004490; Identities 821/839 (98 %), 2 gaps (0 %)), Clypeophysalospora latitans (GenBank KX820265; Identities 772/792 (97 %), 1 gap (0 %)) and Plectosphaera eucalypti (GenBank DQ923538; Identities 828/853 (97 %), 4 gaps (0 %)).