Myrtapenidiella balenae
Myrtapenidiella balenae Crous, sp. nov.

Etymology. The name is derived from the Latin word Balena for whale, and refers to the fact that whales were present close to the shoreline at the time that this fungus was collected at Point Ann in Western Australia.

Classification — Teratosphaeriaceae, Capnodiales, Dothideomycetes.

Conidiophores erect, flexuous, unbranched, solitary (not fasciculate), subcylindrical, thick-walled, finely roughened, medium brown, multisepitate, 70–200 × 4–5 μm. Conidiogenous cells integrated, terminal, subcylindrical, medium brown, finely verruculose, 15–25 × 3–4 μm; scars thickened, darkened, 1.5–2 μm diam, proliferating sympodially. Primary ramoconidia medium brown, verruculose, 0–1-septate, guttulate, 20–40 × 4–5 μm, frequently with mucoid sheath; hila thickened, darkened, 2.5–3 μm diam. Secondary ramoconidia subcylindrical, 0–1-septate, medium brown, verruculose with mucoid sheath, proliferating sympodially, 17–20 × 4–5 μm. Conidia in branched chains of up to 7, medium brown, verruculose with mucoid sheath, proliferating sympodially, (13–)15–17(–18) × (3–)4 μm; hila thickened and darkened, 1.5–2 μm diam.

Culture characteristics — Colonies flat, spreading, with moderate aerial mycelium and smooth, lobate margins, reaching 20 mm diam after 2 wk at 25 °C. On MEA surface and reverse olivaceous grey. On PDA surface olivaceous grey with patches of pale olivaceous grey, reverse olivaceous grey. On OA surface olivaceous grey.

Typus. AUSTRALIA, Western Australia, Albany, Fitzgerald River National Park, Point Ann, on leaves of Eucalyptus sp. (Myrtaceae), at Phytophthora site, 22 Sept. 2015. P.W. Crous (holotype CBS H-23090, culture ex-type CPC 29235 = CBS 142527, ITS, LSU, tef1, and tub2 sequences GenBank KY979761, KY979816, KY979899, and KY979927, MycoBank MB 820954).

Notes — Myrtapenidiella balenae is phylogenetically closely related to M. tenuiramis (on E. tenuiramis, Tasmania; conidia (6–)8–10(–12) × 3–4 μm; Crous et al. 2009a), but morphologically distinct in having larger conidia, (13–)15–17(–18) × (3–)4 μm. Based on a megablast search using the ITS sequence, the best match was M. tenuiramis (GenBank NR_145118; Identities = 474/482 (98 %), 2 gaps (0 %)), followed by M. corymbia (GenBank NR_145115; Identities = 472/482 (98 %), 2 gaps (0 %)). Based on a megablast search using the tub2 sequence, the best match was M. corymbia (GenBank KF442481; Identities = 328/349 (94 %), 2 gaps (0 %)).