
Bagadiella koalae

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Bagadiella koalae Crous, Pascoe, I.J. Porter & Jacq. Edwards, *sp. nov.*

Bagadiellae lunatae similis, sed conidiis majoribus, (15–)17–20 × 1.5–2 µm, discernitur.

Etymology. Named after the koala that was observed eating these *Eucalyptus globulus* leaves.

On potato-dextrose agar. Conidiophores aggregated in brown fascicles on leaves. In culture on potato-dextrose agar, sporulating on conidiophores that occur solitary on hyphae. *Mycelium* consisting of medium brown, smooth, septate, 2–2.5 µm diam hyphae. *Conidiophores* subcylindrical, brown, smooth, straight to gently curved, 1–3-septate, 15–30 × 3–4 µm. *Conidiogenous cells* terminal, integrated, pale to medium brown, smooth, 7–15 × 2–3 µm; apex with flared collarette, 1–2 × 2–3 µm. *Conidia* hyaline, smooth, curved, with bluntly rounded apex and truncate base, (15–)17–20 × 1.5–2 µm.

Culture characteristics — (in the dark, 25 °C, after 1 mo): Colonies spreading, flat, with sparse aerial mycelium, and submerged, feathery margin, reaching 35–60 mm diam; on potato-dextrose agar, surface grey olivaceous, reverse olivaceous grey; on oatmeal agar surface umber with patches of peach; on malt extract agar surface ochreous, reverse umber.

Typus. Australia, Victoria, Otway Ranges, Kennett River, Great Ocean Road, on leaves of *Eucalyptus globulus* eaten by koala, 18 Oct. 2009, *P.W. Crous*, *I.G. Pascoe, I.J. Porter & J. Edwards*, holotype CBS H-20583, cultures ex-type CPC 17682 = CBS 129523, ITS sequence GenBank JF951142 and LSU sequence GenBank JF951162, MycoBank MB560166.

Notes — Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the ITS sequence are *Bagadiella* sp. CPC 16622 (GQ303270; Identities = 706/713 (99 %), Gaps = 4/713 (1 %)) and *Bagadiella lunata* (GQ303269; Identities = 702/707 (99 %), Gaps = 1/707 (0 %)) (Cheewangkoon et al. 2009). These associations were also supported by the LSU sequence. *Bagadiella victoriae* is distinct on its ITS sequence (Identities = 705/712 (99 %), Gaps = 4/712 (1 %)) and LSU sequence (Identities = 918/922 (99 %), Gaps = 0/922 (0 %)).

Colour illustrations. Koala at Kennett River, eating leaves of *Eucalyptus globulus* from which *B. koalae* was isolated; conidiogenous cells and conidia. Scale bar = 10 µm.

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