Bagadiella koalae

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.


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 %)).