

Aspergillus banksianus



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***Aspergillus banksianus* Pitt, sp. nov.**

Etymology. Named for the Australian endemic tree *Banksia integrifolia*, from the rhizosphere of which this species was isolated.

Classification — *Aspergillaceae*, *Eurotiales*, *Eurotiomycetes*.

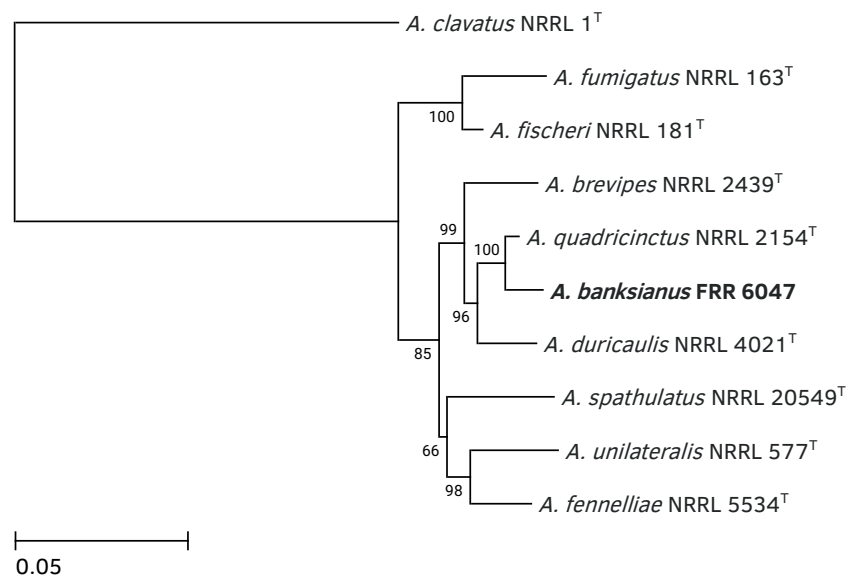
Culture characteristics — Czapek yeast extract agar (CYA), 25 °C, 7 d: Colonies 25–30 mm diam, low and dense, plane or irregularly wrinkled, with narrow margins of white mycelium; conidiogenesis moderate to heavy, dark grey to dark grey blue (M. 24–25D–E2–3); exudate absent, soluble pigment brown; reverse Deep Green (M. 29F3–4). MEA, 25 °C, 7 d: Colonies 40–45 mm diam, low and plane, with wide uncoloured margins, light to heavily sporing, coloured as on CYA or slightly greener (M. 26D3); exudate and soluble pigment absent; reverse centrally Dark Green (M. 27F5), paler towards the margins. 25 % Glycerol nitrate agar (G25N), 25 °C, 7 d: Colonies up to 5 mm diam, of white mycelium. 37 °C, CYA, 7 d: Colonies 40–45 mm diam, heavily sporing, dull green to grey green; reverse dark green, greyish green or black.

Conidiophores borne from aerial hyphae, sometimes unbranched, and then (5–)50–120 × 2.5–3 µm, sometimes bearing a short lateral stipe 10–40 µm long as well; broadening slowly to spathulate vesicles, 5–15 µm diam, fertile area characteristically hemispherical but sometimes asymmetrical to give a ‘nodding’ appearance. *Phialides* short and stout, 3.5–6 × 2.5–3 µm, with narrow bases and very short narrow necks, sometimes almost ellipsoidal. *Conidia* 2.5–3 µm diam, smooth to finely roughened, borne in short disordered chains, separating in wet mounts.

Media formulations are from Pitt & Hocking (2009); (M.) colours are from Kornerup & Wanscher (1978).

Typus. AUSTRALIA, New South Wales, Collaroy, from rhizosphere soil beneath a specimen tree of the endemic species *Banksia integrifolia* (*Proteaceae*), 2004, A.-L. Markovina (holotype DAR 85042, cultures ex-type FRR 6047 = MST FP2248; ITS, *BenA*, *CaM* and *RPB2* sequences GenBank MH280013, MT184780, MT184786, MT184792, MycoBank MB835223).

Notes — *Aspergillus banksianus* clusters in *Aspergillus* subgenus *Fumigati*, in a small clade that includes *A. brevipes* and *A. duricaulis*, with which it shares slow growth at 25 °C, green conidial colouration and intermittent production of asymmetrical fruiting structures. Colonies of *A. banksianus* on CYA have a deep green reverse colour, in contrast with *A. duricaulis*, ‘colorless to pinkish drab’ or *A. brevipes* ‘becoming purple-red’ (Raper & Fennell 1965). Molecularly, *A. banksianus* is particularly close to *A. quadricinctus*, from which the most obvious difference is lack of the *Neosartorya* sexual morph. *Aspergillus banksianus* when grown on agar, liquid media or grain, displays a unique chemotaxonomic profile comprising banksialactones A-I, and banksiamarins A and B, which are not present in the closely related species *A. quadricinctus* and *A. duricaulis* (Chaudhary et al. 2018). *Aspergillus banksianus* also produces known metabolites clearanol and dothideomynone A, together with the pigments endocrocin and questin previously reported from other *Aspergillus* species.



Colour illustrations. A specimen tree of the endemic species *Banksia integrifolia*, planted on a street in Collaroy, NSW, from under which a soil sample included *A. banksianus*. Colonies grown on CYA (upper) and malt extract agar (MEA) (lower) for 7 d at 25 °C; fruiting structures and conidia. Scale bars = 10 µm (fruiting structures) and 5 µm (conidia).

A maximum likelihood tree inferred from the combined ITS, *BenA*, *CaM* and *RPB2* sequences of taxa within *Aspergillus* sect. *Fumigati*. The combined sequence alignment was partitioned by marker; substitution models for each partition were chosen according to the Bayesian Information Criteria using ModelTest-NG v. 0.1.6 (Darriba et al. 2020). The TrN+I model was used for ITS sequences, K80+G4 for *BenA*, TrNef+G4 for *CaM* and TIM2ef+I+G4 for *RPB2*. The tree was constructed using RAxML-NG v. 0.9.0 (Kozlov et al. 2019). Bootstrap support values are derived from 1 000 bootstrap replicates. Alignment available in TreeBASE (study S25912).

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