



Fungal Planet 782 – 13 July 2018

***Elsinoë banksiigena* Crous, sp. nov.**

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

Classification — *Elsinoaceae*, *Myriangiales*, *Dothideomycetes*.

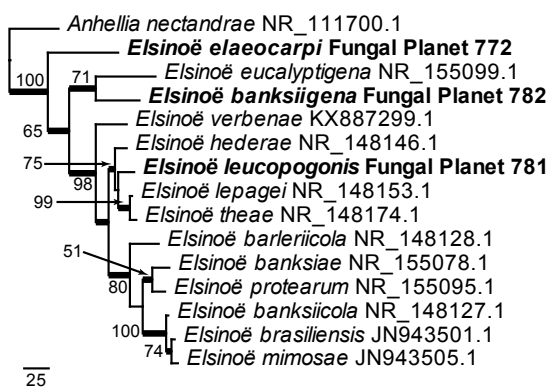
Leaf spots epiphyllous, subcircular to irregular, medium brown, somewhat raised, 1–5 µm diam, surrounded by a diffuse chlorotic border. *Conidiomata* acervular, brown, 30–50 µm diam, prominently breaking through epidermis on leaf surface. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* hyaline, smooth, ampulliform to doliiiform, 3–5 × 3–4 µm. *Conidia* hyaline, smooth, aseptate, guttulate, subcylindrical with obtuse ends, 2–4 × 1.5–2 µm *in vitro* and *in vivo*.

Culture characteristics — Colonies erumpent, with sparse aerial mycelium, surface folded, with even, lobed margin, reaching 5 mm diam after 2 wk at 25 °C. On MEA and PDA surface saffron, reverse ochreous. On OA surface saffron.

Typus. AUSTRALIA, New South Wales, Seven Mile Beach, on leaves of *Banksia marginata* (*Proteaceae*), 26 Nov. 2016, P.W. Crous (holotype CBS H-23563, culture ex-type CPC 32402 = CBS 144440, ITS, LSU, *rpb2* and *tef1* sequences GenBank MH327823.1, MH327859.1, MH327875.1 and MH327886.1, MycoBank MB825438).

Notes — Two species of *Elsinoë* are known from *Banksia*, namely *E. banksiae* (on *B. serrata*) and *E. banksicola* (on *B. prionotes*). A key to the species occurring on *Proteaceae* was provided by Fan et al. (2017). Phylogenetically, *E. banksiigena* is distinct from all taxa known from *Proteaceae*, being allied to *E. eliocarpiae* (see ITS phylogeny). Although it has been assumed that there was one dominant species of *Elsinoë* infecting various species of *Banksia*, the present study suggests that many more distinct *Elsinoë* spp. could await description.

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the ITS sequence had highest similarity to *Elsinoë eucalyptigena* (GenBank NR_155099.1; Identities = 503/591 (85 %), 29 gaps (4 %)), *Elsinoë fawcettii* (GenBank FJ010362.1; Identities = 441/527 (84 %), 30 gaps (5 %)) and *Sphaceloma bidentis* (GenBank KF421115.1; Identities = 516/615 (84 %), 43 gaps (6 %)). Closest hits using the LSU sequence are *Elsinoë quercus-ilicis* (GenBank KX887040.1; Identities = 720/740 (97 %), 4 gaps (0 %)), *Elsinoë eucalyptorum* (GenBank DQ923530.1; Identities = 859/885 (97 %), 4 gaps (0 %)) and *Sphaceloma erythrinae* (GenBank JN940392.1; Identities = 833/861 (97 %), 3 gaps (0 %)). Closest hits using the *rpb2* sequence had highest similarity to *Zalaria obscura* (GenBank KX579108.1; Identities = 492/661 (74 %), 5 gaps (0 %)), *Sarcinomyces crustaceus* (GenBank GU250948.1; Identities = 489/664 (74 %), 3 gaps (0 %)) and *Elsinoë pitangae* (GenBank KX887150.1; Identities = 541/746 (73 %), 11 gaps (1 %)). No significant hits were obtained when the *tef1* sequence was used in BLASTn and megablast searches.



The first of two equally most parsimonious trees obtained from the ITS alignment using PAUP v. 4.0b10 (Swofford 2003; 15 sequences including the ingroup, 522 included characters of which 141 were parsimony-informative). The tree was rooted with *Anhellia nectandrae* (GenBank NR_111700.1). Novel *Elsinoë* species described here are indicated in **bold italic** text and their corresponding Fungal Planet numbers are indicated. The scale bar represents the number of changes and parsimony bootstrap support values > 50 % from 1000 replicates are indicated at the nodes (thickened lines are present in the strict consensus tree).

Colour illustrations. *Banksia marginata* at Seven Mile Beach; leaf spots, colony on MEA, conidioma (*in vivo*) (scale bar = 50 µm), conidiogenous cells and conidia (scale bars = 10 µm).

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