Elsinoë elaeocarpi
**Elsinoë elaeocarpi** Crous, sp. nov.

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

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

**Leaf spots** primarily epiphyllous, irregular in outline, 1–3 mm diam, grey with feathery, dark brown border, containing brown to black ascomata. *Ascomata* round to ellipsoid, 150–250 µm diam. *Asci* obovoid, hyaline, smooth, bitunicate, 30–55 x 20–25 µm, 8-spored, with well-defined apical chamber, 4–5 µm diam. *Ascospores* hyaline, smooth, fusoid-ellipsoid, constricted at median septum, widest just above septum with 5–7 transverse and 3–4 vertical septa, (22–)25–28 x (6–)7(–8) µm.

**Culture characteristics —** Colonies erumpent, spreading, with sparse aerial mycelium and smooth, lobate margin, reaching 5–7 mm diam after 2 wk at 25 °C. On MEA, PDA and OA surface and reverse iron-grey.

**Typus.** *Australia*, Victoria, close to Eden, on leaves of *Elaeocarpus* sp. (*Elaeocarpaceae*), 29 Nov. 2016, P.W. Crous (holotype CBS H-23572, culture ex-type CPC 32853 = CBS 144431, ITS, LSU and *rpb2* sequences GenBank MH327812.1, MH327848.1 and MH327870.1, MycoBank MB825425).

**Notes —** The genus *Elsinoë* was recently treated by Fan et al. (2017), providing an overview phylogeny for the majority of the species presently known from culture. *Elsinoë elaeocarpi* is phylogenetically allied to *E. banksiigena* (see Fungal Planet 782) and *E. eucalyptigena* (both only known from Australia), and represents a phylogenetically distinct taxon on *Elaeocarpus*.

Based on a megablast search of NCBI’s GenBank nucleotide database, the closest hits using the ITS sequence had highest similarity to *Elsinoë verbenae* (GenBank KX887299.1; Identities = 439/532 (83 %), 37 gaps (6 %)), *Elsinoë fawcettii* (GenBank KF010881.1; Identities = 439/533 (82 %), 43 gaps (8 %)) and *Elsinoë tiliae* (GenBank KX887296.1; Identities = 435/530 (82 %), 35 gaps (6 %)). Closest hits using the LSU sequence are *Elsinoë fawcettii* (GenBank JN940382.1; Identities = 686/731 (94 %), 2 gaps (0 %)), *Sphaceloma erythrinae* (GenBank JN940392.1; Identities = 686/731 (94 %), 3 gaps (0 %)) and *Elsinoë eucalypticola* (GenBank GQ303306.1; Identities = 685/730 (94 %), 2 gaps (0 %)). Closest hits using the *rpb2* sequence had highest similarity to *Myriangium hispanicum* (GenBank GU371744.1; Identities = 771/1045 (74 %), 4 gaps (0 %)), *Mendogia macrostroma* (GenBank KU940162.1; Identities = 767/1047 (73 %), 4 gaps (0 %)) and *Strangospora pinicola* (GenBank AY641080.1; Identities = 761/1046 (73 %), 6 gaps (0 %)).

Colour illustrations. Forest in Victoria, close to Eden; foliar lesion on *Elaeocarpus* sp., asci with ascospores (*in vivo*). Scale bars = 10 µm.