**Elsinoe salignae** Crous & Carnegie, *sp. nov.*

**Etymology.** Name refers to *Eucalyptus saligna*, the host species from which this fungus was isolated.

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

Conidiomata erumpent, sporodochial, 50–150 mm diam, based on a pale brown stroma giving rise to densely aggregated conidiophores. Conidiophores unbranched, hyaline to pale brown, smooth-walled, subcylindrical, 1–2-septate, 15–25 × 3–5 mm. Conidiogenous cells integrated, subcylindrical, hyaline, smooth-walled, monon- to polyphialidic, 8–12 × 3–4 mm. Conidia solitary, aggregating in mucoid mass, aseptate, hyaline, smooth-walled, guttulate, subcylindrical to ellipsoid, apex obtuse, base truncate, (4.5–)5–6(–6.5) × (2–)2.5 mm.

Culture characteristics. — Colonies erumpent, surface folded, with sparse aerial mycelium and smooth, lobate margin, reaching 7 mm diam after 2 wk at 25 °C. On MEA surface sienna, reverse ochreous. On PDA surface ochreous to umber, reverse luteous with diffuse luteous pigment. On OA surface ochreous.

**Typus.** AUSTRALIA, New South Wales, Bulladelah State Forest, on leaves of *Eucalyptus saligna* (Myrtaceae), 16 Apr. 2016, A.J. Carnegie, HPC 2415 (holotype CBS H-23948, culture ex-type CPC 35713 = CBS 145552, ITS, LSU and rpb2 sequences GenBank MK876389.1, MK876430.1 and MK876485.1, MycoBank MB830837).

Notes. — The genus *Elsinoe* was recently revised by Fan et al. (2017), who also provided a key to the species occurring on *Eucalyptus*. *Elsinoe salignae* is phylogenetically related to, but distinct from *E. leucopogonis* (on *Leucopogon* sp., Australia) (Crous et al. 2018c).

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the ITS sequence had highest similarity to *Elsinoe leucopogonis* (GenBank NR_159836.1; Identities = 567/580 (98 %), 3 gaps (0 %)), *Elsinoe hederae* (GenBank NR_148146.1; Identities = 502/521 (96 %), 12 gaps (2 %)) and *Elsinoe lepagei* (GenBank MH856598.1; Identities = 519/549 (95 %), 14 gaps (2 %)). Closest hits using the LSU sequence are *Elsinoe hederae* (GenBank KX886994.1; Identities = 733/736 (99 %), no gaps), *Elsinoe lepagei* (GenBank KX887004.1; Identities = 732/736 (99 %), no gaps) and *Elsinoe fagarae* (GenBank KX886981.1; Identities = 732/736 (99 %), no gaps). Closest hits using the rpb2 sequence had highest similarity to *Elsinoe leucopogonis* (GenBank MH327874.1; Identities = 848/872 (97 %), no gaps), *Elsinoe hederae* (GenBank KX887113.1; Identities = 634/744 (85 %), no gaps) and *Elsinoe lepagei* (GenBank KX887122.1; Identities = 617/741 (83 %), 2 gaps (0 %)).

**Colour illustrations.** *Eucalyptus saligna* plantation. Colony on malt extract agar; conidiogenous cells; conidia. Scale bars = 10 µm.

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