

*Elsinoë othonnae*





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***Elsinoë othonnae* Crous & A.R. Wood, sp. nov.**

*Etymology.* Name reflects the host genus *Othonna*, from which the species was isolated.

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

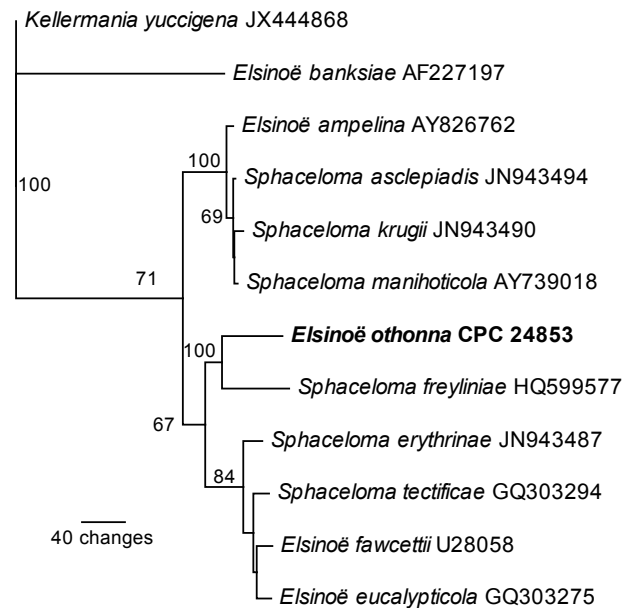
*Caulicolous.* Lesions circular to subcircular, pale grey-brown with dark red-brown border, 1–10 mm diam. *Conidiomata* sporodochial to acervular on stems, medium brown, wall composed of medium brown *textura angularis*. On SNA and PDA sporodochial, erumpent, hyaline, up to 400 µm diam. *Conidiophores* hyaline, smooth, subcylindrical to doliiform, 0–1-septate, branched below, 15–30 × 4–6 µm. *Conidiogenous cells* enteroblastic, polyphialidic, hyaline, smooth, subcylindrical to doliiform, 7–17 × 3–4 µm; loci indistinct, 0.5 µm diam. *Conidia* (on SNA) hyaline, guttulate, smooth, aseptate, ellipsoidal to subcylindrical, apex obtuse, base bluntly rounded to truncate, (5–)6–7 × (2.5–)3(–4) µm in vitro.

*Culture characteristics* — Colonies erumpent, spreading, surface folded, margins smooth, lobed, with sparse aerial mycelium, reaching 15 mm diam after 1 mo at 25 °C. On PDA surface and reverse blood. On OA surface apricot. On MEA surface vinaceous, reverse brick.

*Typus.* SOUTH AFRICA, Western Cape province, Brackenfell, Bracken Nature Reserve, on stems of *Othonna quinqueidentata* (*Asteraceae*), 10 May 2014, A.R. Wood (holotype CBS H-22239, culture ex-type CPC 24853 = CBS 139910; ITS sequence GenBank KR476726, LSU sequence GenBank KR476761, MycoBank MB812454); CPC 24954.

*Notes* — Species of *Elsinoë* are commonly associated with scab diseases of diverse hosts, but are especially severe on legumes (Mchau et al. 1998), as well as cut flowers and citrus (Swart et al. 2001). No species of *Elsinoë* (asexual morph: *Sphaceloma*) are known from *Othonna* in South Africa (Crous et al. 2000), and *Elsinoë othonnae* appears to represent a new stem pathogen of this host.

*Colour illustrations.* *Othonna quinqueidentata* growing in Bracken Nature Reserve; close-up of stem lesions; colonies on SNA; conidiogenous cells and conidia. Scale bars = 10 µm.



First of two equally most parsimonious trees obtained from the ITS alignment based on a heuristic analysis with 100 random taxon additions and tree-bisection-reconnection algorithm using PAUP v. 4.0b10 (Swofford 2003; TL = 438, CI = 0.826, RI = 0.702, RC = 0.580). GenBank accession numbers are indicated behind the species names. Bootstrap support values > 50 % from 1 000 replicates are shown at the node and the scale bar indicates the number of changes. The tree was rooted to *Kellermania yuccigena* (GenBank JX444868) and the novel species described in this study is indicated in **bold face**. The alignment and tree were deposited in TreeBASE (Submission ID 17580).