

*Eucasphaeria proteae*



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***Eucasphaeria proteae* Crous, sp. nov.**

*Etymology.* Name refers to the host genus *Protea* from which it was isolated.

*Classification* — *Niessliaceae*, *Hypocreales*, *Sordariomycetes*.

*Mycelium* consisting of hyaline, smooth, branched, septate, 1.5–2.5 µm diam hyphae. *Conidiomata* sporodochial, 100–300 µm diam, becoming aggregated, forming large orange, mucoid colonies on agar; basal stroma of hyaline *textura angularis*, giving rise to hyaline, smooth, branched, 3–10-septate conidiophores, subcylindrical, 20–70 × 2–3 µm. *Conidiogenous cells* integrated, terminal and intercalary, subcylindrical, flexuous, phialidic, hyaline, smooth, 8–20 × 2.5–3 µm. *Conidia* solitary, hyaline, smooth, guttulate, subcylindrical, straight to slightly curved, apex obtuse, base truncate, 1.5–2 µm diam, 0(–3)-septate, (8–)15–17(–20) × (2–)2.5(–3) µm; 3-septate conidia can become up to 65 µm in length, and frequently undergo microcyclic conidiation.

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

*Typus.* SOUTH AFRICA, Western Cape Province, Clanwilliam, on leaves of *Protea neriifolia* (*Proteaceae*), 2018, P.W. Crous, HPC 3030 (holotype CBS H-24433, culture ex-type CPC 38661 = CBS 146815, ITS, LSU, *rpb2* and *tef1* (second part) sequences GenBank MW175357.1, MW175397.1, MW173116.1 and MW173129.1, MycoBank MB837848).

*Notes* — Culture CPC 38661 was originally derived from hyaline, aseptate microconidia found on the surface of leaves of *Protea neriifolia*. In culture, sporodochia with an *Eucasphaeria* asexual morph developed (Crous et al. 2007b). Based on LSU the present fungus proved to be closely related to *Rosasphaeria moravica*, which was described as forming densely aggregated orange pycnidial conidiomata in culture (Jaklitsch & Voglmayr 2012). Based on the sporodochia, and conidial morphology, the present collection is best accommodated in *Eucasphaeria*, although the relationship with *Rosasphaeria* deserves further study.

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Rosasphaeria moravica* (strain CBS 124270, GenBank NR\_138377.1; Identities = 489/572 (85 %), 26 gaps (4 %)), *Neoeucasphaeria eucalypti* (strain CBS 145075, GenBank NR\_161136.1; Identities = 489/573 (85 %), 35 gaps (6 %)), and *Eucasphaeria rustici* (strain CPC 28946, GenBank NR\_154028.1; Identities = 488/573 (85 %), 31 gaps (5 %)). Closest hits using the **LSU** sequence are *Rosasphaeria moravica* (strain LMM, GenBank JF440985.1; Identities = 836/851 (98 %), two gaps (0 %)), *Eucasphaeria capensis* (strain CBS 120027, GenBank EF110619.1; Identities = 855/874 (98 %), two gaps (0 %)), and *Niesslia pulchriseta* (strain CBS 839.96, GenBank MG826846.1; Identities = 854/877 (97 %), five gaps (0 %)). Closest hits using the **rpb2** sequence had highest similarity to *Rosasphaeria moravica* (strain LMM, GenBank JF440986.1; Identities = 586/683 (86 %), two gaps (0 %)), *Ophiocordyceps mosingtoensis* (strain BCC 30904, GenBank MK214100.1; Identities = 545/679 (80 %), six gaps (0 %)), and *Ophiocordyceps coccidiicola* (strain NBRC 100682, GenBank AB968545.1; Identities = 542/678 (80 %), two gaps (0 %)). Closest hits using the **tef1** (second part) sequence had highest similarity to *Tolypocladium tropicale* (strain MX338, GenBank KF747113.1; Identities = 793/864 (92 %), two gaps (0 %)), *Isaria takamizusanensis* (strain F896, GenBank GU979994.1; Identities = 831/911 (91 %), two gaps (0 %)), and *Nectria haematococca* (strain GJS89-70, GenBank AY489624.1; Identities = 831/912 (91 %), four gaps (0 %)).

*Colour illustrations.* Flowers and leaves of *Protea neriifolia*. Sporodochia on OA; conidiogenous cells giving rise to conidia; conidia. Scale bars = 10 µm.