

Phaeomoniella niveniae



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***Phaeomoniella niveniae* Crous, sp. nov.**

Phaeomoniellae prunicolae similis, sed conidiis majoribus, 3–4(–5) × 1.5(–2) µm, discernitur.

Etymology. Named after the host genus from which it was collected, *Nivenia*.

Leaf spots subcircular, brown, amphigenous, up to 6 mm diam, or associated with leaf tip blight. On pine needle agar. *Mycelium* thick-walled, hyaline, covered in mucoid sheath, septate, branched, 2–4 µm diam. *Conidiomata* pycnidial, up to 250 µm diam, green-brown, aggregated, opening by irregular rupture, wall of 2–3 layers of *textura angularis*. *Conidiophores* hyaline, smooth, subcylindrical, consisting of dense clusters of conidigenous cells, 1–5-septate, 5–20 × 3–4 µm. *Conidigenous cells* hyaline, smooth, subcylindrical to ampulliform, terminal and lateral, 4–7 × 2.5–3 µm, monophialidic, opening 1–1.5 µm diam with minute collarette. *Conidia* hyaline, smooth, bacilliform to ellipsoid, with rounded ends, 3–4(–5) × 1.5(–2) µm. *Chlamydospores* not seen.

Culture characteristics — (in the dark, 25 °C, after 2 wk): Colonies erumpent, spreading, with folded surface and feathery, lobed margins, reaching 15 mm diam after 2 wk. On potato-dextrose agar primrose with patches of dark herbage green due to sporulation, reverse primrose. On malt extract agar surface honey with patches of isabelline due to sporulation, reverse honey. On oatmeal agar concolorous with medium, with isabelline patches due to sporulation; colonies with sweet fruity odour.

Typus. SOUTH AFRICA, Western Cape Province, Betties Bay, Harold Porter Botanical Garden, on leaves of *Nivenia stokoei*, 4 May 2010, P.W. Crous, holotype CBS H-20773, cultures ex-type CPC 18231 = CBS 131316, ITS sequence GenBank JQ044435 and LSU sequence GenBank JQ044454, MycoBank MB560707.

Notes — The genus *Phaeomoniella* was established for *P. chlamydospora*, a species commonly associated with Petri disease of grapevines (Crous & Gams 2000, Mostert et al. 2006). Subsequent to this, additional species have been recorded from hosts such as *Encephalartos* (Crous et al. 2008), pines (Lee et al. 2006), and fruit trees (Damm et al. 2010). *Phaeomoniella niveniae* can be distinguished from the taxa presently recognised based on its conidial dimensions, culture characteristics, and distinct DNA phylogeny. A megablast search of the NCBI's GenBank nucleotide sequence database using the ITS sequence of *P. niveniae* retrieves as closest hits *Phaeomoniella zymoides* (GenBank GQ154600; Identities = 537/552 (97 %), Gaps = 5/552 (1 %)), *Phaeomoniella capensis* (GenBank FJ372391; Identities = 573/652 (88 %), Gaps = 47/652 (7 %)) and numerous other sequences identified as *Phaeomoniella* sp. A megablast search of the NCBI's GenBank nucleotide sequence database using the LSU sequence of *P. niveniae* retrieves as closest hits *Xenocylindrosporium kirstenboschense* (GenBank GU229891; Identities = 811/874 (93 %), Gaps = 17/874 (2 %)), *Phaeomoniella capensis* (GenBank FJ372408; Identities = 802/875 (92 %), Gaps = 17/875 (2 %)) and *Capronia villosa* (GenBank AF050261; Identities = 836/918 (91 %), Gaps = 26/918 (3 %)), amongst others.

Colour illustrations. *Nivenia stokoei* growing at the Harold Porter Botanical Garden, Betties Bay, South Africa; colonies sporulating on potato-dextrose agar and oatmeal agar; conidiophores; conidia. Scale bars = 10 µm.