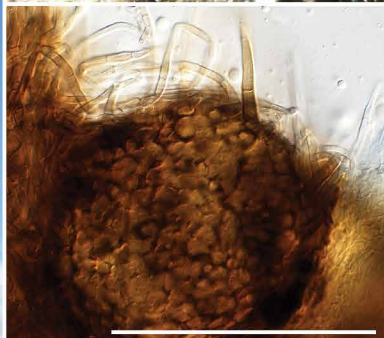
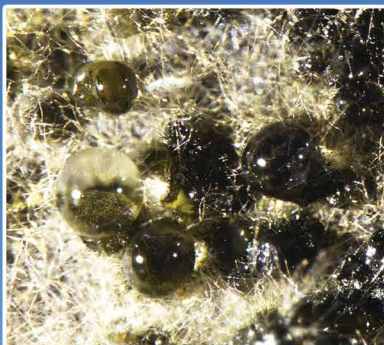


*Neoconiothyrium viticola*



Fungal Planet 971 – 18 December 2019

## *Neoconiothyrium viticola* Crous, *sp. nov.*

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

*Classification* — *Coniothyriaceae*, *Pleosporales*, *Dothideomycetes*.

*Conidiomata* immersed to erumpent, solitary, brown, globose, 100–200 µm diam, with central ostiole; wall of 3–6 layers of brown *textura angularis*; wall covered in brown setae, flexuous, thick-walled, unbranched, smooth, apex obtuse, septate, up to 100 µm long, 4–5 µm wide. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* lining inner cavity, hyaline, smooth, ampulliform to doliiform, 4–6 × 5–6 µm; phialidic with periclinal thickening or percurrent proliferation at apex. *Conidia* solitary, aseptate, globose or broadly ellipsoid, becoming golden brown, smooth to finely roughened, (4–)5–6(–6.5) × (3–)4 µm.

*Culture characteristics* — Colonies flat, spreading, with sparse to moderate aerial mycelium and smooth, lobate margin, reaching 45 mm diam after 2 wk at 25 °C. On MEA surface pale olivaceous grey, reverse olivaceous grey. On PDA surface fawn to diffuse vinaceous pigment, reverse sepia. On OA surface iron-grey.

*Typus.* NEW ZEALAND, North Island, Hastings, 2091 Maraekakaho Road, on stems of *Vitis vinifera* (*Vitaceae*), 4 Nov. 2010, *M. Romney* (holotype CBS H-24246, culture ex-type T10\_04730 = CPC 36397 = CBS 146049, ITS, LSU and *rpb2* sequences GenBank MN562123.1, MN567631.1 and MN556804.1, MycoBank MB832881).

*Notes* — *Neoconiothyrium* is characterised by species that can have conidiomata covered in setae, phialidic conidiogenous cells, and hyaline to medium brown, smooth to finely verruculose, ellipsoid to subclavate or subcylindrical, 0–1-septate conidia (Crous et al. 2017a). Although the taxonomy of the coniothyrium-like genera is still far from settled, the present collection is tentatively named in *Neoconiothyrium*, being closely related to *N. hakeae*.

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Querciphoma carteri* (strain CBS 101633, GenBank JF740180.1; Identities = 452/472 (96 %), 2 gaps (0 %)), *Coniothyrium hakeae* (strain CPC 27620, GenBank NR\_154839.1; Identities = 553/581 (95 %), 14 gaps (2 %)), and *Coniothyrium multiporum* (strain SRMC-MYCO6, GenBank KY806410.1; Identities = 460/484 (95 %), 2 gaps (0 %)). Closest hits using the **LSU** sequence are *Ochrocladosporium frigidarii* (strain CBS 103.81, GenBank NG\_064123.1; Identities = 879/891 (99 %), no gaps), *Coniothyrium telephii* (strain UTHSC DI16-189, GenBank LN907332.1; Identities = 880/893 (99 %), no gaps), and *Wojnowicia rosicola* (strain MFLUCC 15-0128, GenBank MG829091.1; Identities = 865/878 (99 %), 4 gaps (0 %)). Closest hits using the **rpb2** sequence had highest similarity to *Coniothyrium hakeae* (strain CPC 29612, GenBank KY173584.1; Identities = 877/909 (96 %), no gaps), *Pyrenophora dictyoides* (strain DAOM 75616, GenBank JN993617.1; Identities = 624/756 (83 %), 9 gaps (1 %)), and *Drechslera phlei* (strain DAOM 226243, GenBank JN993628.1; Identities = 616/756 (81 %), 8 gaps (1 %)).

*Colour illustrations.* *Vitis vinifera* in New Zealand. Colony on potato dextrose agar; conidioma; conidiomatal setae; conidiogenous cells; conidia. Scale bars = 150 µm (conidioma), 10 µm (all others).

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