Gnomoniopsis rosae
**Gnomoniopsis rosae** Crous, *sp. nov.*

**Etymology.** Name refers to Rosa, the host genus from which this fungus was isolated.

**Classification.** *Glomerellaceae, Glomerellales, Sordariomycetes.*

*Conidiomata* erumpent, globose, brown, 200–400 µm diam, acervular, opening by irregular rupture, exuding a creamy conidial mass; wall of 6–8 layers of brown *textura angularis*. *Conidiophores* lining the inner cavity, hyaline, smooth, 0–2-septate, subcylindrical, branched at base or not, 10–20 × 3–4 µm. *Conidiogenous cells* integrated, terminal and intercalary, hyaline, smooth, subcylindrical with apical taper, 6–13 × 2.5–3.5 µm; phialidic with prominent periclinal thickening. *Conidia* solitary, aseptate, fusoid, straight, hyaline, smooth-walled, guttulate, apex subobtuse, base truncate, 1 µm diam, (9–)10–12(–13) × (3–)3.5(–4) µm.

**Culture characteristics.** Colonies flat, spreading, with moderate aerial mycelium and feathery, lobate margin, covering dish after 2 wk at 25 °C. On MEA and PDA surface greyish sepia, reverse umber. On OA surface ochreous centre, greyish sepia in outer region.


Notes — *Gnomoniopsis* represents a genus of mostly host-specific fungi (Sogonov et al. 2008, Walker et al. 2010). *Gnomoniopsis rosae* is phylogenetically distinct from the species presently known from DNA. Unfortunately, only the asexual morph was found, making comparisons with older literature difficult. Based on a megablast search of NCBI’s GenBank nucleotide database, the closest hits using the ITS sequence had highest similarity to *Cryptosporella umbrina* (GenBank MH855393.1; Identities = 618/620 (99 %), no gaps), *Discula quercina* (GenBank GQ452285.1; Identities = 574/623 (92 %), 30 gaps (4 %)) and *Gnomoniopsis smithogilvyi* (GenBank KY930638.1; Identities = 572/623 (92 %), 32 gaps (5 %)). Closest hits using the LSU sequence are *Gnomoniopsis smithogilvyi* (GenBank MH877030.1; Identities = 898/898 (100 %), no gaps), *Cryptosporella umbrina* (GenBank MH866843.1; Identities = 895/896 (99 %), 1 gap (0 %)) and *Gnomoniopsis idaeicola* (GenBank MH875092.1; Identities = 893/895 (99 %), no gaps). Closest hits using the *rpb2* sequence are *Gnomoniopsis paraclavulata* (GenBank EU219248.1; Identities = 692/758 (91 %), no gaps), *Discula campestris* (GenBank EU199143.1; Identities = 692/758 (91 %), no gaps) and *Gnomoniopsis clavulata* (GenBank EU219251.1; Identities = 689/758 (91 %), no gaps).

**Colour illustrations.** Rosa sp. growing in New Zealand; colony sporulating on oatmeal agar, conidiophores, conidiogenous cells and conidia. Scale bars = 10 µm.

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