

*Colletotrichum roseum*



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***Colletotrichum roseum* M. Zapata, M.A. Palma, M.J. Aninat & Piont., sp. nov.**

*Etymology.* The epithet refers to the rose-coloured aerial mycelia in culture.

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

*Sexual morph* not observed. *Asexual morph on synthetic nutrient poor agar* (microscopic preparations in 60 % lactic acid, with at least 50 measurements per structure). *Vegetative hyphae* 1–9.5 µm diam, hyaline, sometimes pale brown, smooth-walled, septate, branched. *Chlamydospores* not observed. *Conidiomata* acervular, consisting of conidiophores and setae formed directly on hyphae. *Setae* abundant, medium brown, smooth-walled, slightly curved or zig-zag-shaped, 0–2-septate, 35–90 µm long, base cylindrical, sometimes inflated, 3.5–6.5 µm diam at the widest part, tip rounded to acute. *Conidiophores* hyaline, smooth-walled, simple or septate and branched, up to 65 µm long. *Conidiogenous cells* hyaline, thick-walled, smooth, cylindrical, thinner towards the apex, (10–)15–28(–30) × (2–)2.5–3.5(–4), apex 0.5–1 µm diam, with periclinal thickening visible. *Conidia* hyaline, smooth-walled, aseptate, straight, cylindrical to fusiform, with one end round and one end slightly acute, cytoplasm appearing granular, (16–)18–21.5(–25) × (4–)5–5.5(–6) µm, mean ± SD = 19.5 ± 1.5 × 5.3 ± 0.3 µm, L/W ratio = 3.7. *Appressoria* single or in small groups of 2–3, medium brown to olive, smooth-walled, clavate, ovate or irregular outline, the edge entire or undulate, sometimes lobate, (6.5–)8–12.5(–16.5) × (4.5–)6–8.5(–9) µm, mean ± SD = 10.5 ± 1.8 × 6.9 ± 0.9 µm, L/W ratio = 1.6.

*Cultural characteristics* — (near UV light with a 12 h photoperiod, 20 °C after 10 d): Colonies on SNA flat with entire margin, surface hyaline to rose-violet coloured, reverse same colour, covered with appressed mycelium, reaching 30.1 ± 1.8 mm diam. Colonies on OA flat with entire margin, surface rose to grey with age, reverse reddish, covered with felty aerial mycelium, reaching 53.0 ± 1.7 mm. *Conidia in mass* salmon, more abundant in strain RGM 2616.

*Typus.* CHILE, Concepción, Cerro Caracol, on leaves of *Lapageria rosea* (*Philesiaceae*), 4 Dec. 2018, F. Franco (holotype RGM 2685, culture ex-type CBS 145754 = SAG-99199-18; ITS, LSU, *GAPDH*, *ACT* and *TUB2* sequences GenBank MK903611, MK903608, MK903603, MK903604 and MK903607, MycoBank MB830891).

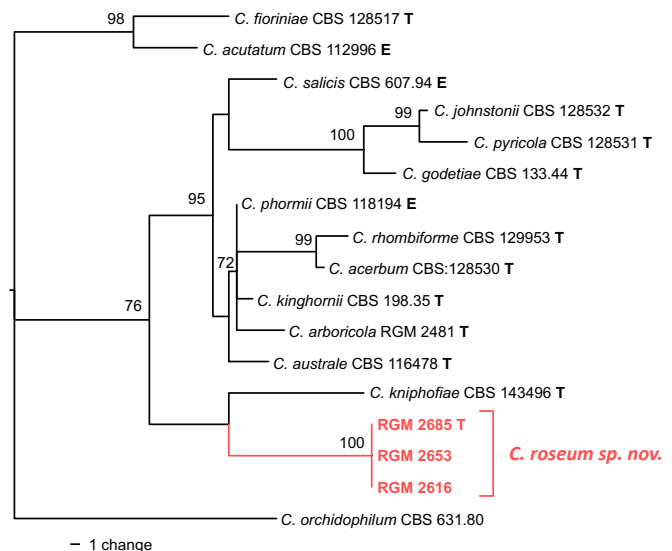
*Additional materials examined.* CHILE, Alto BioBio, on leaves of *L. rosea*, 26 Apr. 2018, J. Silva, RGM 2616 = CBS 144798 = SAG 47521-18, ITS, *GAPDH* and *TUB2* sequences GenBank MK903609, MK903601 and MK903605; Quillón, on leaves of *L. rosea*, 12 Sept. 2018, G. Atanasovici, RGM 2653 = CBS 145292 = SAG 71721-18, ITS, *GAPDH* and *TUB2* sequences GenBank MK903610, MK903602 and MK903306.

*Notes* — *Colletotrichum roseum* was isolated from conidiomata emerging from leaf spots on *Lapageria rosea* (Copihue). All strains examined produced infertile perithecia in culture that were immersed in the agar (after 3 mo), even though they were inoculated onto plates containing pieces of autoclaved

*Colour illustrations.* *Lapageria rosea* growing in its natural habitat in Chile (courtesy Mhyilton Jiménez-Castillo, 2019). Symptomatic leaf; colony on oatmeal at 10 d; conidiophores with seta (in lactophenol cotton-blue); conidia; setae; appressoria. Scale bars = 10 µm.

leaves of Copihue. One strain of *C. roseum* was collected on the same host and locality to that of *Physalospora lapageriae*, an older fungus described by Spegazzini (1910) which was later reclassified as *Glomerella lapageriae* (Petraik & Sydow 1934). However, it proved impossible to compare our asexual fungus with *G. lapageriae*. Type material of *G. lapageriae* is deposited at the Museo La Plata (Argentina) and is not currently available for loan to attempt DNA isolation and comparison. Under these circumstances, and considering that *C. gloeosporioides*, *C. godetiae* and *C. pyricola* have also been diagnosed on Copihue by The National Plant Protection Organization in areas close to where *C. roseum* was found, there is no certainty that *G. lapageriae* is the same species, and therefore we propose to describe the new strains as a new species.

*Colletotrichum roseum* belongs to the *Colletotrichum acutatum* species complex (Damm et al. 2012), and is phylogenetically close but clearly distinct from *C. kniphofiae*. The new species differs from *C. kniphofiae* by its shorter conidia and characteristic rose-coloured culture. *Colletotrichum roseum* can be identified with all loci studied, except LSU, with *GAPDH* and *ACT* performing best as a diagnostic sequence. Based on a megablast search of NCBI's GenBank nucleotide database restricted to ex-type strains, the closest hit using the *GAPDH* sequences were *C. phormii* (GenBank JQ948777, Identities = 238/252 (94.4 %), 3 gaps), *C. acerbum* (GenBank JQ948790; Identities = 235/252 (93.3 %), 3 gaps) and *C. johnstonii* (GenBank JQ948775; Identities = 234/252 (92.9 %), 3 gaps). Closest hits using the *ACT* sequence were *C. phormii* (GenBank JQ949767, Identities = 239/247 (96.8 %), no gaps), *C. arboricola* (GenBank MH817956; Identities = 242/252 (96.0 %), no gaps) and *C. salicis* (GenBank JQ949781; Identities = 237/247 (96.0 %), no gaps).



One of the six equally most parsimonious trees (212 steps, CI = 0.670, HI = 0.330, RI = 0.741) obtained from the multi-locus phylogenetic analysis (ITS-*GAPDH*-*ACT*-*TUB2*) for selected *Colletotrichum* species. The analysis was conducted with PAUP v. 4.0b10 (Swofford 2003). DNA sequences were aligned using MAFFT v. 7.0 employing the E-INS-i strategy. Bootstrap support values ≥ 70 % are shown above nodes (1000 replicates). The tree was rooted with *Colletotrichum orchidophilum*. T = ex-type, E = ex-epitype.

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