

Greeneria kielmeyerae



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Greeneria kielmeyerae C.P. Nicolli, F.S. Carmo, C.A. Inácio, P.A.S. Marbach, J.T. De Souza, *sp. nov.*

Etymology. *kielmeyerae*, named after the host genus, *Kielmeyera coriacea* (Calophyllaceae).

Classification — *Melanconiellaceae*, *Diaporthales*, *Diaporthomycetidae*, *Sordariomycetes*.

Pathogenic on leaves of *Kielmeyera coriacea*. *Leaf spots* up to 3 cm diam, rather irregular, sometimes confluent and covering almost the whole blade, often at the margins, amphigenous, showing small dark points of conidiomata at the upper side of the leaves. *Conidiomata* acervular at maturity, 175–300 µm diam, with brownish wall layers of *textura angularis*, subcuticular to intraepidermal, scattered. *Conidiophores* hyaline to pale brown, 5–10-septate, 11–25 × 2.5–5 µm, branched, smooth. *Vegetative hyphae* internal, hyaline to pale brown, smooth, intermingled with the host cells, branched, 1–3 µm diam. *Conidiogenous cells* hyaline, phialidic with a conspicuous collarette, 6–15 × 1–1.5 µm, percurrent proliferation with a serrate collarette. *Conidia* hyaline to pale brown, variable, sometimes elongate-fusoid, fusoid to ellipsoidal, aseptate, smooth and thick-walled, attenuate and papillate at the apex, truncate at the base, guttulate, 15–21 × 6–9 µm, 2–3 µm. Conidial cirrhi arising from conidiomata on the surface of infected leaves.

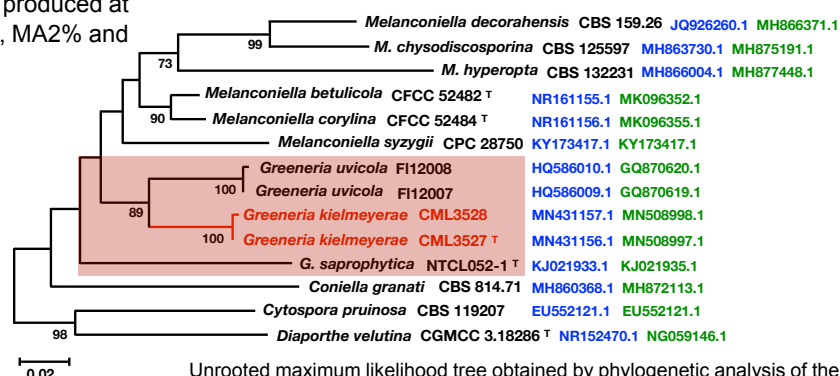
Culture characteristics — Colonies on potato dextrose agar (PDA), malt agar (MA2%) and oatmeal agar (OA) (near-UV light, 12 h photoperiod) with a pale brown centre surrounded by a greyish olivaceous ring containing dark spore masses, followed by a pale brown area with aerial feltose mycelium and irregular margins. A reddish to vinaceous pigment is produced in all media (either side of the plates), more intensely in PDA. Slow growth on all media, no growth at 10, 15, and 35 °C on PDA and MA2% and at 10, 15, 20 and 35 °C on OA. Growth / d at 20 °C on PDA was 0.9 and 0.5 mm (for isolates CML3527 and CML3528, respectively) while on MA2% it was 2.9 and 2.1 mm. Growth at 25 °C on PDA (1 and 1.6 mm), on MA2% (3.9 and 4.9 mm), on OA (4.5 and 5.2 mm). Growth at 30 °C on PDA was 0.7 mm for both isolates, on MA2% was 0.1 and 0.2 mm and on OA 0.3 and 0.1 mm. Conidia were produced at approximately 8, 10 and 14 d, respectively on OA, MA2% and PDA at 25 °C.

Colour illustrations. *Kielmeyera coriacea* with leaves showing symptoms of *Greeneria kielmeyerae* at the Bocaina hills in Lavras, Minas Gerais, Brazil. Fourteen-d-old colonies growing at 25 °C on PDA, both sides of a plate showing the reddish to vinaceous pigment produced by the fungus, immature conidioma, conidiophores showing the collarette and irregular percurrent proliferation, conidia. Scale bars = 1 cm (culture), 50 µm (conidioma) and 10 µm (other structures).

Typus. BRAZIL, DF, Brasilia, UNB campus, S15°53' W47°51', on leaf spots of *Kielmeyera coriacea* (Calophyllaceae), 20 May 2015, J.T. De Souza (holotype HURB 24682, dried culture on PDA, culture ex-type CML3527 = COAD2237; ITS, LSU and SSU sequences GenBank MN431156.1, MN508997.1 and MN508390.1, MycoBank MB834842).

Additional material examined. BRAZIL, Minas Gerais, Itutinga, from a leaf spot on *K. coriacea*, S21°18' W44°39', 20 Apr. 2016, J.T. De Souza, CML3528 = COAD2238; ITS, LSU and SSU sequences GenBank MN431157.1, MN508998.1 and MN508391.1.

Notes — *Greeneria kielmeyerae* is related to the other species of the genus, *G. uvicola* (Farr et al. 2001) and *G. saprophytica* (Tangthirasunun et al. 2014), but differs from these species in the production of a reddish to vinaceous pigment on plates, for having larger conidia (18 × 7.5 in *G. kielmeyerae*, 9.5 × 4.25 in *G. uvicola* and 12 × 5.5 in *G. saprophytica*) and a larger length to width ratio of the conidia (2.4 in *G. kielmeyerae*, 2.23 in *G. uvicola* and 2.18 in *G. saprophytica*). The closest phylogenetic relative of *G. kielmeyerae* CML3527^T (accession MN431156.1) with ITS sequences was *Melanconiella spodiocarpa* SPOD1 (GenBank JQ926301.1; 81.82 % identity), it had 80.1 % identity with the ITS sequence of *G. uvicola* FI12007 (GenBank HQ586009.1) and 77.93 % identity with the ITS of *G. saprophytica* NTCL052-1 (GenBank KJ021933.1). With LSU sequences the closest relative of *G. kielmeyerae* CML3527^T (GenBank MN508997.1) was *G. uvicola* USvitis (GenBank JN547723.1; 98.42 %) and it was 97.04 % identical to the LSU sequence of *G. saprophytica* NTCL052-1 (GenBank KJ021935.1). With SSU sequences, the closest relative of *G. kielmeyerae* CML3527^T (GenBank MN508390.1) was *Coryneum heveanum* MFLUCC17-0369 (GenBank NG_065764.1; 99.56 % identity), and had 99.33 % identity with the SSU sequence of *G. saprophytica* NTCL052-1 (GenBank KJ021934.1). The phylogenetic relationships of the genus *Greeneria* and closely-related genera are not well defined as observed by Tangthirasunun et al. (2014).



Unrooted maximum likelihood tree obtained by phylogenetic analysis of the combined ITS and LSU sequences from *Greeneria kielmeyerae* and phylogenetically related species performed in the software MEGA v. 6.06 (Tamura et al. 2013) employing the GTR+G model with 1 000 bootstrap re-samplings. Bootstrap support values > 70 % are presented. The new species is shown in red text (^T = ex-type) and the genus *Greeneria* is delimited in a pale red box. GenBank accession numbers are given after each strain (ITS = blue, LSU = green).

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