Diseases Caused by Fungi and Fungus-Like Organisms

First Report of *Diaporthe terebinthifolii* Causing Leaf Spot on *Pleoroma fotherghillae* in Brazil

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Pleoroma fotherghillae, also known as “princess flower”, is an ornamental species native to Brazil and naturalized in several countries (Faravani and Bakar 2007). *P. fotherghillae* has a high economic value, with an ornamental and landscape application (Nienow et al. 2010). In September 2018, leaf spots were observed in approximately 80% of the 50 *P. fotherghillae* plants grown in a nursery in the municipality of Curitiba-Paraná, Brazil. The spots were round shaped, with a necrotic brown center and a reddish-brown halo, ranging from 1 to 4 mm in diameter. High leaf fall was observed among plants presenting a higher severity. Symptomatic leaf fragments were collected and disinfected as described by Pereira et al. (2019). The fragments were transferred to a potato dextrose agar medium supplemented with streptomycin sulfate and incubated at $24 \pm 1^\circ\text{C}$ with a photoperiod of 12 h for 7 days. Four monosporic cultures were obtained from colonies isolated. The isolates had a grayish-white cottony aerial mycelium and reverse olive-yellow with black dots. The colonies reached approximately 60 mm in diameter, forming globular and conical pycnidia, brown to black in color with white or cream globular conidial mass. Beta conidia were hyaline, smooth, curved to the size of 19 to 25×1 to $1.5 \mu\text{m}$ ($n = 50$). No alpha nor gamma conidia were observed. The characteristics are similar to the description of *Diaporthe*

terebinthifolii (Gomes et al. 2013). The total genomic DNA of a representative isolate, LEMIDPRPf-19-02, was extracted for amplification and sequencing of the internal transcribed spacer (ITS) region and partial of the tubby (TUB) and thymotroph embryonic factor (TEF) genes. The sequences of the ITS (no. MN415990.1), TUB (no. MW505549), and TEF (no. MW505550) genes were deposited in GenBank. BLAST analysis showed similarity above 99% with *D. terebinthifolii* sequences (KC343219.1, KC344187.1, and KC343945.1). The multigene phylogenetic analysis, based on Bayesian inference, grouped the isolate in a clade with other sequences of *D. terebinthifolii*. Four healthy plants of *P. fotherghillae* about 5 months old were used for pathogenicity testing. A suspension containing 10^5 conidia/ml was sprayed on the surface of the leaves of four plants to the point of runoff. The plants were covered with a transparent plastic bag for 24 h. The leaves of four other plants received sterile distilled water and served as the control treatment. The plants were kept in a greenhouse at $20 \pm 5^\circ\text{C}$. Necrotic lesions appeared 10 to 15 days after inoculation. No symptoms were observed in the control plants. The pathogen was reisolated from symptomatic leaves and had the same characteristics as the isolate LEMIDPRPf-19-02. A representative sample (MBM 331603) was deposited at the Museu do Jardim Botânico (Botanical Garden Museum), Curitiba, Brazil. *D. terebinthifolii* was previously reported as endophytic in Brazil and Uruguay, isolated from *Schinus terebinthifolius* and *Pyrus communis*, respectively (Gomes et al. 2013; Sessa et al. 2017). To our knowledge, this is the first report of *D. terebinthifolii* causing leaf spot on *P. fotherghillae* in Brazil and worldwide.

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