Diseases Caused by Fungi and Fungus-Like Organisms

Leaf Blight of *Magnolia coco* Caused by *Nothophoma quercina* in China

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Magnolia coco (Lour.) DC. is an ornamental shrub and widely cultivated in southern China (Kato et al. 2017). In April 2020, leaf blight symptoms were observed on the leaves of *M. coco* in the Chengdu campus of Sichuan Agricultural University, and roughly 70% of leaves per plant were diseased. The initial symptoms presented on the leaf apex, which was manifested as dark brown spots surrounded with an obvious yellowish halo. As the disease progressed, spots gradually enlarged and coalesced, covering the leaf, and severe infection finally caused leaf necrosis and plant decline. Four specimens from different diseased plants were used for pathogen isolation and morphological observation. Four fungal isolates were obtained from four specimens, following the method of Chomnunti et al. (2014). Colonies on potato dextrose agar (PDA) medium were initially white and then light brown to dark brown. Pycnidia measured 284 to 427 × 326 to 554 μm ($\bar{x}$ = 372.8 × 476.1 μm, n = 20) and were brownish-black to black, broadly globose to irregular. The pycnidial wall measured 16 to 27 μm wide (n = 20) and was composed of hyaline to brown cells of textura angularis. Conidiophores were absent, and the conidiogenous cells were pear-shaped, colorless, and smooth. Conidia measured 5 to 8 × 4 to 6 μm ($\bar{x}$ = 6.5 × 4.6 μm, n = 50) and were elliptical or subglobose, thick-walled, aseptate, hyaline, smooth, and brown. These asexual structures were similar to *Nothophoma quercina*

(Syd. & P. Syd.) Qian Chen & L. Cai described by Chen et al. (2017). The genomic DNA of representative isolate SICAUCC 21-0011 was extracted, and the internal transcribed spacers (ITS), 28S large subunit rDNA (LSU), RNA polymerase II large subunit 2 (RPB2), and beta-tubulin (TUB2) regions were amplified using the primer pairs ITS5/ITS4, LR0R/LR5, FRPB2-5F/FRPB2-7cR, and T1/BT4R, respectively. The accession numbers deposited in GenBank were MW541930 (ITS), MW541934 (LSU), MW883395 (RPB2), and MW883394 (TUB2). Nucleotide BLAST showed high homology with the sequences of *N. quercina*: GU237900 (ITS, 485/486, 99.79%), EU754127 (LSU, 862/862, 100%), KT389657 (RPB2, 593/596, 99.49%), and GU237609 (TUB2, 333/335, 99.40%). Phylogenetic analyses based on a combined dataset showed 100% bootstrap support values in a clade with *N. quercina* complexes. Four healthy potted plants (2 years old) with 15 to 20 leaves per plant were sprayed with conidial suspension (10⁵ conidia/ml) prepared from 4-week-old cultures of SICAUCC 21-0011, which were incubated on PDA at 25°C, onto the wounded sites via pin-prick inoculation as described by Desai et al. (2019). Another four plants were sprayed with sterile distilled water as controls. Inoculated plants were cultured in a growth chamber (25°C, 95% relative humidity, and 12-h photoperiod). About 30 days later, brown spots were found on the inoculated leaves, which were similar to those observed in the field. There were no symptoms on the control plants, and the pathogen was reisolated from the diseased leaves and characterized morphologically. *N. quercina* has been reported on *Photinia × fraseri* Dress, *Aucuba japonica*, *Malus micromalus*, and *Chaenomeles sinensis* (Lv et al. 2020; Triki et al. 2019; Zou et al. 2021). To our knowledge, this is the first report of leaf blight on *M. coco* caused by *N. quercina*. *M. coco* is one of the important ornamentals in courtyards, streets, and parks in China; the risk of this pathogen needs further exploration, and effective control measures should be made.

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