Diseases Caused by Fungi and Fungus-Like Organisms

First Report of Anthracnose on *Cinnamomum burmannii* Caused by *Colletotrichum scovillei* in China

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The mei pian tree belongs to a new physiological type of *Cinnamomum burmannii* discovered in the eastern part of the Guangdong province in China in 1987 (Chen et al. 2011). Although the external morphology of the mei pian tree is similar to *C. burmannii*, the leaves of the mei pian tree, known as an important traditional Chinese medicine, are rich in natural d-borneol, which protects the heart, brain, and other organs, regulates the central nervous system and promotes the absorption of other drugs (Fu et al. 2020; Yang et al. 2020). In April 2020, we found that the yield and quality of mei pian tree leaves were seriously threatened by anthracnose. Approximately 40 to 60% of trees were infected in Pingyuan County, Meizhou City, Guangdong Province (N24°28'31.13", E115°50'50.02"). Small circular black spots were initially observed on infected leaves, and spots continued to grow and developed chlorotic margins and concentric rings with sunken areas. As the disease progressed, multiple spots were observed on almost all leaves. Four symptomatic leaves were collected and used for pathogen isolation. The areas of symptomatic and healthy-appearing leaf tissues at the margin of spots were surface sterilized with 0.5% NaClO for 2 min and 70% alcohol for 30 s. The sterilized leaves were washed three times with sterile water, air dried, plated on potato dextrose agar (PDA) medium, and incubated at 28°C for 4 days in the dark. A total of six single-spored isolates were obtained and named from MPS-1 to MPS-6, respectively. Among those isolates, MPS-2, MPS-5, and MPS-6 were identical when cultured on a PDA plate. The colonies were white to pale gray with dense aerial mycelia, and the reverse side of the colonies was light reddish brown. Conidia were cylindrical and measured 9.0 to 14.0 µm in length and 3.0 to 4.5 µm in width ($n = 35$). For molecular

identification, the primers ITS1/ITS4, GDF/GDR, CHS-79F/CHS-345R, ACT-512F/ACT-783R, and T1/Bt2b were used to amplify the partial regions of rDNA-ITS, glyceraldehyde-3-phosphate dehydrogenase (GAPDH), chitin synthase (CHS1), actin (ACT), and β -tubulin (TUB2), respectively, from the genomic DNA extracted from fresh mycelia of MPS-2 (Damm et al. 2012). The resulting sequences were deposited in GenBank with accession numbers MW091490, MW125584, MW125585, MW125586, and MW125587, respectively. The phylogenetic tree was generated by the maximum likelihood method of the MEGA 7 software using a concatenated alignment of ITS, GAPDH, CHS1, ACT, and TUB2 sequences. According to both morphological and sequence analyses, MPS-2 was identified as *Colletotrichum scovillei* (Damm et al. 2012, 2020). Pathogenicity tests were performed by inoculating healthy mei pian tree leaves with 5-mm PDA plugs containing actively growing mycelium of MPS-2 and wound inoculated by spraying MPS-2 conidial suspension (10^6 conidia ml⁻¹). Controls were inoculated only with sterile PDA plugs and ddH₂O. All inoculated plants were maintained in a moist chamber (RH > 90%) at 25°C, with an 8-h photoperiod under T5 LED lights. All inoculated leaves developed symptoms similar to those on naturally infected leaves after 5 days, but leaves on control plants remained asymptomatic. The fungus on the inoculated plants was identical in morphology to that found on the original sample collected in the field, thus fulfilling Koch's postulates. In previous studies, *C. scovillei* also caused anthracnose on banana (*Musa* spp. AAA group), pepper (*Capsicum annuum*), and mango (*Mangifera indica* L.) in China (Qin et al. 2019; Zhao et al. 2016; Zhou et al. 2017). To our knowledge, this is the first report of *C. scovillei* causing anthracnose on *C. burmannii* in China and worldwide. The identification of *C. scovillei* as the causal agent of the observed anthracnose on *C. burmannii* is critical to the prevention and control of this disease in the future.

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