Diseases Caused by Fungi and Fungus-Like Organisms

First Report of Anthracnose on *Ctenanthe oppenheimiana* Caused by *Colletotrichum siamense* in China

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Ctenanthe oppenheimiana (E. Morren) K. Schum. (*Maranta oppenheimiana*) is a shade-loving, monocotyledonous ornamental plant in the family Marantaceae. It has attractive foliage and is used in parks and around office buildings. Six million seedlings were produced in China in 2017 (China Flower Association 2018). Plants were seriously infected with a year-round foliar disease. The disease occurred in all planting areas; ~53.1 and 48.3% of the plants in Guangdong and Fujian provinces in China in March 2017 were infected, and it caused economic loss to control plant diseases with chemicals. The initial symptoms were observed 1 month after planting and included small brown lesions that expanded to form large irregular yellow lesions at the tips or margins of the leaves in the campus of Guangdong Ocean University. Diseased plants were collected in Zhanjiang city (110°30' E, 21°20' N) and Gaozhou city (117.42E, 25.3N) in Guangdong province and in Zhangping city (117°42' E, 25°30' N) in Fujian province. Seven single-spore cultures were recovered from symptomatic samples after they were disinfested with 1% NaOCl and plated on potato sucrose agar (PSA) at 28°C for 1 week. Three isolates were used for the pathogenicity test; 200 µl of conidial suspension (10⁶ conidia/ml) was dropped on the leaf sites with a sterile needle-prick wound at five- to eight-leaf stage. There were three replicates for each treatment, and the experiment was repeated three times. Plants were placed in an incubator at 25°C, with 80% humidity and a 12-h light/dark cycle. Control seedlings were treated identically, except sterile water was placed on the wounds. Round brown necrotic lesions in the middle of the leaves grew in the inoculated wounded leaves 5 days after inoculation, and brown necrotic lesions developed into brown lesions of 2.2 to 3.6 cm 10 days after inoculation; there were no symptoms in the negative controls. *Colletotrichum* was reisolated from the lesions in inoculated leaves, fulfilling

Koch's postulates. Colonies on PSA were grayish white with a regular border and a felty aerial mycelium that contained masses of orange conidia. No setae were observed in the PSA culture. Conidia were straight and hyaline with rounded ends measuring 10.0 to 15.0 × 5.0 to 6.0 µm (avg. = 14.2 × 5.3 µm, *n* = 50). Conidiophores hyaline, septate. Conidiogenous cells were hyaline, cylindric, and 13.2 to 22.5 × 4.5 to 5.5 µm (avg. = 19.5 × 4.6 µm, *n* = 50). Appressoria were cylindrical, 5.2 to 10.5 × 4.0 to 6.8 µm (avg. = 7.5 × 5.2 µm, *n* = 50). For molecular identification, the colony PCR method with MightyAmp DNA Polymerase (Takara-Bio, Dalian, China) (Lu et al. 2012) was used to amplify the ITS of ribosomal DNA, glutamine synthetase (GS), calmodulin (CAL), and ApMat loci of three isolates using primer pairs ITS4/ITS5, GSF1/GSR1, CL1C/CL2C, and AM-F/AM-R (Liu et al. 2015). A phylogenetic tree was derived from a neighbor-joining analysis of a concatenated alignment of ITS, GS, CAL, and ApMat sequences. The accession numbers of three isolates (ZJCG, GZCG, and FJCG) used in this study were KP635210, MN133235, and MN133236 for ITS; MT594433, MT594434, and MT594435 for CAL; MT594436, MT594437, and MT594438 for GS; and MN133228, MN133229, and MN133230 for ApMat. The sequences were aligned with those of the related species in *C. gloeosporioides* complex (Liu et al. 2015). Analyses based on concatenated data sets of four genes showed that the sequences had high levels of identity to those of the *Colletotrichum siamense* strains. According to both morphological and sequence analyses, the *C. oppenheimiana* pathogen was identified as *C. siamense*. There are two reports of foliar pathogens on *C. oppenheimiana*, *Rhizoctonia solani* and *Pyricularia oryzae* (Baiswar et al. 2010; Pappas and Vloutoglou 1996). This is the first report of anthracnose on *C. oppenheimiana* caused by *C. siamense* in China. Identification of the pathogen of this disease is essential for the development of effective and economical management practices.

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