Diseases Caused by Fungi and Fungus-Like Organisms

First Report of *Colletotrichum siamense* Causing Anthracnose of *Monstera deliciosa* in Zhanjiang, China

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Monstera deliciosa Liebm. is an ornamental foliage plant (Peng et al. 2020). In July of 2019, anthracnose lesions were observed on leaves of *M. deliciosa* cv. Duokong with 20% disease incidence of 100 plants at the Guangdong Ocean University campus (21.17N, 110.18E), Guangdong Province, China. Initially, affected leaves showed chlorotic spots, which coalesced into larger irregular or circular lesions. The centers of spots were gray with a brown border surrounded by a yellow halo. Twenty diseased leaves were collected for pathogen isolation. Margins of diseased tissue were cut into 2 × 2-mm pieces, surface disinfected with 75% ethanol for 30 s and 2% sodium hypochlorite (NaOCl) for 60 s, and rinsed three times with sterile water before isolation. Potato dextrose agar (PDA) was used to culture pathogens at 28°C in the dark. Successively, pure cultures were obtained by transferring hyphal tips to new PDA plates. Fourteen isolates were obtained from 20 leaves. Three single-spore isolates (PSC-1, PSC-2, and PSC-3) were obtained, which were identical in morphology and molecular analysis (ITS). Therefore, the representative isolate PSC-1 was used for further study. The culture of isolate PSC-1 on PDA was initially white and later became cottony and light gray in 4 days at 28°C. Conidia were single celled, hyaline, cylindrical, clavate, and measured 13.2 to 18.3 × 3.3 to 6.5 µm (*n* = 30). Appressoria were elliptical or subglobose, dark brown, and were 6.3 to 9.5 × 5.7 to 6.5 µm (*n* = 30). Morphological characteristics of isolate PSC-1 were consistent with the description of *Colletotrichum siamense* (Prihastuti et al. 2009; Sharma et al. 2013). DNA

of the isolate PSC-1 was extracted for PCR sequencing using primers for the rDNA ITS (ITS1/ITS4), *GAPDH* (GDF1/GDR1), *ACT* (ACT-512F/ACT-783R), *CAL* (CL1C/CL2C), and *TUB2* (βT2a/βT2b) (Weir et al. 2012). Analysis of the ITS (accession no. MN243535), *GAPDH* (MN243538), *ACT* (MN512640), *CAL* (MT163731), and *TUB2* (MN512643) sequences revealed a 97 to 100% identity with the corresponding ITS (JX010161), *GAPDH* (JX010002), *ACT* (FJ907423), *CAL* (JX009714), and *TUB2* (KP703502) sequences of *C. siamense* in GenBank. A phylogenetic tree was generated based on the concatenated sequences of ITS, *GAPDH*, *ACT*, *CAL*, and *TUB2*, which clustered the isolate PSC-1 with *C. siamense* type strain ICMP 18578. Based on morphological characteristics and phylogenetic analysis, the isolate PSC-1 associated with anthracnose of *M. deliciosa* was identified as *C. siamense*. Pathogenicity testing was performed in a greenhouse at 24 to 30°C with 80% relative humidity. Ten healthy plants of cultivar Duokong (3 months old) were grown in pots with one plant in each pot. Five plants were inoculated by spraying a spore suspension (10⁵ spores/ml) of isolate PSC-1 onto leaves until runoff, and five plants were sprayed with sterile water as controls. The test was conducted three times. Anthracnose lesions as earlier were observed on the leaves after 2 weeks, whereas control plants remained symptomless. The pathogen reisolated from all inoculated leaves was identical to the isolate PSC-1 by morphology and ITS analysis, but not from control plants. *C. gloeosporioides* has been reported to cause anthracnose of *M. deliciosa* (Katakam et al. 2017). To the best of our knowledge, this is the first report of *C. siamense* causing anthracnose on *M. deliciosa* in China, which provides a basis for focusing on the management of the disease in future.

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