Diseases Caused by Fungi and Fungus-Like Organisms

First Record of *Colletotrichum alienum* Causing Postharvest Anthracnose Disease of Mango Fruit in China

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Mango (*Mangifera indica* L.) is one of the world's most significant economic fruit crops, and China is the second-largest producer of mango (Kuhn et al. 2017). Postharvest mango anthracnose is caused by *Colletotrichum* species and reduces the shelf life of mature fruit (Wu et al. 2020). *Colletotrichum* species also cause postharvest anthracnose and fruit rot disease of apple, banana, and avocado (Khodadadi et al. 2020; Sharma et al. 2017; Vieira et al. 2017). In July 2019, mango fruits (cv. 'Jin-Hwang') were observed at different fruit markets (39°48'42.1"N, 116°20'17.0"E) of the Fengtai district, Beijing, China, exhibiting typical symptoms of anthracnose including brown to black lesions of different size (2 cm) with identified border on the mango fruit surface. Later, the lesions coalesced and extensively covered the surface of the fruit. The lesions were also initially restricted to the peel of the fruit, and the pathogen later invaded the fruit pulp. About 30% of mango fruits were affected by anthracnose disease. The margins of lesions from infected mango fruits ($n = 56$) were cut into 2 × 2-mm pieces, surface disinfected with NaClO (2% v/v) for 30 s, and rinsed thrice with distilled water for 60 s. These pieces were placed on PDA medium and incubated at 25°C for 7 days. Pure culture of fungal isolates was obtained by single-spore isolation technique. Initially, the fungal colony was off-white, and the colony extended with time, turning light gray at the center. The morphological examination revealed that conidia were hyaline, oblong, and unicellular. The conidia were measured from 10-day-old culture, and dimensions varied from 13.3 to 15.8 µm in length and 4.6 to 6.1 µm in width. For

molecular identification, a multilocus sequence analysis was performed; the internal transcribed spacer (ITS) region, partial actin (ACT) gene, glyceraldehyde-3-phosphate dehydrogenase (GAPDH) gene, and chitin synthase (CHS-1) gene were amplified by using the primer sets ITS1/4 (White et al. 1990), ACT-512F/ACT-783R (Carbone and Kohn 1999), GDF1/GDR1 (Guerber et al. 2003), and CHS1-79F/CHS-1-354R (Carbone and Kohn 1999), respectively. The partial sequences of MTY21 were deposited to GenBank accessions MT921666 (ITS), MT936119 (ACT), MT936120 (GAPDH), and MT936118 (CHS-1). All obtained sequences showed 100% similarity with reported sequences of *Colletotrichum alienum* ICMP.18691 with accession numbers JX010217 (ITS), JX009580 (ACT), JX010018 (GAPDH), and JX009754 (CHS-1), which represented the isolate MTY21 identified as *C. alienum* by constructing a maximum likelihood phylogenetic tree using Mega X (Kumar et al. 2018). For the confirmation of Koch's postulates, the pathogenicity test was conducted on 36 fresh healthy mango fruits for each treatment. Fruits were punctured with the help of a sterilized needle to create 2-mm² wounds and inoculated with 10 µl of inoculum (10⁷ spores/ml) of MTY21. Control mango fruits were inoculated with 10 µl of sterilized distilled water and incubated at 25°C with 90% relative humidity. The lesions appeared at the point of inoculation and gradually spread on the fruit surface by 7 days postinoculation. The symptoms were similar to the symptoms on the original fruit specimens. The reisolated fungus was identified as *C. alienum* based on morphological and molecular analysis. Mango anthracnose disease caused by several *Colletotrichum* species has been reported previously on mango in China (Li et al. 2019). Liu et al. (2020) reported *C. alienum* as the causal organism of anthracnose disease on *Aquilaria sinensis* in China. *C. alienum* has been previously reported causing mango anthracnose disease in Mexico (Tovar-Pedraza et al. 2020). To our knowledge, this is the first report of *C. alienum* causing postharvest anthracnose of mango in China. The prevalence of *C. alienum* was 30% on mango fruit, which reflects the importance of this pathogen as a potential problem of mango fruit in China.

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The author(s) declare no conflict of interest.

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