Diseases Caused by Fungi and Fungus-Like Organisms

First Report of *Pyrus pyrifolia* ‘Cuiguan’ Fruit Rot Caused by *Monilinia fructicola* in Southern China

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The early-ripening pear (i.e., Asian pear; *Pyrus pyrifolia* [Burm. f.] Nak.) cv. Cuiguan is an important fruit crop in southern China. In July 2020, an unknown fruit rot was observed on pear during storage in postharvest lab of Jiangxi Agricultural University, which were harvested from an orchard in Xiajiang County of Jiangxi Province (27.62° N, 115.33° E). The incidence of this disease was 15% of 1,000 postharvest pear fruit after 10 days in a storage room (20°C, 90% relative humidity). Initial symptoms were small, brown, nearly circular (10 to 20 mm diameter) lesions with water-soaked edges on the fruit surface. The lesions expanded as concentric circles, and a gray-white mold developed in the center of the lesions. Ten fruits with typical symptoms were collected and surface-sterilized with 75% ethanol for 30 s. Small fragments (5 × 5 mm) at the junction of diseased and healthy tissues were disinfected with 1% sodium hypochlorite for 2 min, washed with sterile water three times, transferred to potato dextrose agar (PDA), and incubated at 28 ± 1°C for 3 days. Five fungal colonies that looked similar were single-spored. The resultant fungal colonies produced irregular concentric rings with abundant gray-white aerial mycelia and gradually turned gray-brown. Conidia were unicellular, hyaline, lemon-shaped, 11.1 to 24.8 × 10.3 to 17.4 μm ($n = 50$) in size and were produced in branched moniloid chains. These morphological characteristics were consistent with *Monilinia fructicola* (G. Winter

Honey (Hilber-Bodmer et al. 2010; Peter et al. 2015). To further confirm species identification, genomic DNA of a representative isolate was obtained using an extraction kit (Biocolor, Shanghai, China), and primers ITS1/ITS4 (Munda et al. 2010), IMf F/IMf R (Ma et al. 2003), MO368-5 F/MO368-10 R (Côté et al. 2004), Mon-TubF1/Mon-TubR1, and Mon-G3pdhF/Mon-G3pdhR (Hu et al. 2011) were used to amplify the internal transcribed spacer (ITS), microsatellite, and polymorphic regions, as well as the glyceraldehyde-3-phosphate dehydrogenase (g3pdh) and beta-tubulin (tub2) genes, respectively. A BLAST search with obtained DNA sequences (GenBank accession nos. MW740236, MW788382, MW788383, MZ243141, and MZ243142, respectively) indicated 100% identity with *M. fructicola* (accession nos. LC312668.1 [513/513 bp], AY237426.1 [438/438 bp], FM994904.1 [490/500 bp], MN709392.1 [744/744 bp], and HQ908768.1 [1,534/1,534 bp], respectively). To confirm pathogenicity, 20 μl of a spore suspension (1.0×10^6 spores/ml) prepared from 7-day-old PDA colonies of each of the five isolates was applied to the surface of 10 needle-wounded and 10 nonwounded, surface-disinfected ‘Cuiguan’ pear fruit. Ten wounded and nonwounded pears were inoculated with sterile water as controls. The experiment was repeated three times. All fruit were incubated at 25°C, 90% relative humidity. After 5 days, all wounded and nonwounded pears inoculated with *M. fructicola* showed symptoms similar to those observed in the storage room. Symptoms of nonwounded pears were milder than the wounded inoculated pears, while the control fruit remained healthy. A fungus with similar morphology to *M. fructicola* was reisolated from the inoculated fruits, and thus, Koch’s postulates were fulfilled. To our knowledge, *M. fructicola* has been reported to cause brown rot of pear fruit in northern China (Zhu et al. 2016), but this is the first report of *M. fructicola* causing rot on *P. pyrifolia* in southern China. As an emerging rot disease in this region, and based on its economic importance in other pear growing regions, its presence is of concern to the ‘Cuiguan’ pear fruit industry.

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