Diseases Caused by Fungi and Fungus-Like Organisms

First Report of Fruit Blotch on Plum Caused by *Fusarium fujikuroi* in China

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Plum is commercially cultivated worldwide for the rich nutrients in its fruit. In May 2019, plums with symptoms of fruit rot were collected from fields located in Liuma town, Guizhou Province, China. The incidence of the disease varied from 10 to 20%, which was observed in 15 plum orchards (18 ha) surveyed. Estimated yield loss was ~5 to 10% for each field. Diseased fruits showed deformity, wilting, and sunken lesions, and they subsequently became melanized and rotted. Diseased tissues were surface disinfected with 70% ethanol for 45 s and rinsed with sterile distilled water three times. Four morphologically similar colonies with white fluffy aerial mycelium and a reddish pigment were obtained after 3 days of incubation on potato dextrose agar (PDA) at 25°C. Four single-spore isolates produced conidia with one to two septa that were sickle-shaped, thin-walled, with a tapering and curved apical cell, measuring 15.6 to 29.6 × 4.8 to 8.7 µm (average 19.5 × 5.9 µm, n = 50). Based on the cultural and conidial morphology, the isolates were identified as *Fusarium* (Leslie and Summerell 2006; Mun et al. 2012). DNA of two isolates was extracted using the Ezup Column Fungal Genomic DNA Extraction Kit (Sangon Bioengineering Shanghai, Ltd.). To confirm the morphological diagnosis, DNA sequence data from three loci were obtained. PCR amplification was carried out with universal primers ITS1/ITS4 (White et al. 1990), translation elongation factor (EF-1α), EF1-H (5′-ATGGGTAAGGAAGACAAGAC-3′) and EF2-T (5′-GGAAGTACCAG TGATCATGTT-3′) (O'Donnell et al. 1998), and the second largest subunit of RNA polymerase II (*RPB2*), 5F2 (5′-GGGGWGAYCAGAAGAAGGC-3′) and 7cR (5′-CCCATRGCTTGYTTRCCCAT-3′) (O'Donnell et al. 2007). Primers ITS1 and ITS4 produced a 559-bp amplicon (GenBank accession MW085028). BLAST analysis showed 100% sequence identity to sequences of several species deposited in GenBank, including *Fusarium fujikuroi*. The EF-1α sequence (MW086868) was 100% identical to that of *F. fujikuroi* (MN193860.1). The *RPB2* primers amplified a fragment (MW086869) that was 99.9% identical to that of *F. fujikuroi* (MN193888.1). The BLASTn results based on the partial EF-1α and *RPB2* sequences suggest isolate HJGF1 is *F. fujikuroi*. A pathogenicity assay was conducted using an agar disk inoculation method on plum. Fruits were stab inoculated with HJGF1 by piercing 1 mm at three points using a sterile needle, and fruits were mock inoculated with sterile PDA; each fruit was inoculated with three disks. The treated fruits were maintained in a growth chamber with 90% relative humidity at 25°C and a daily 12-h photoperiod. After 5 days, the artificially inoculated fruits showed blotches with sunken lesions similar to those observed in the orchards, whereas no symptoms were observed on the control fruits. The experiment was repeated twice with similar results. *F. fujikuroi* was reisolated from infected tissues and confirmed by sequence analysis. To our knowledge, this is the first report of *F. fujikuroi* causing fruit blotch of plum in China. Considering the economic importance of plum in China and throughout the world, *F. fujikuroi* may be an emerging problem for plum cultivation. Thus, further study of fruit blotch of plum is warranted.

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