Diseases Caused by Fungi and Fungus-Like Organisms

First Report of *Fusarium oxysporum* Causing Fruit Rot on Apricot (*Prunus armeniaca*) in China

F. Wu,¹ S. C. Li,¹ Q. L. Ma,¹ Y. B. Wang,¹ W. W. Peng,¹ M. Chen,¹ J. Y. Chen,^{1,2} and M. L. Xiang^{1,†}

¹ College of Agronomy, Jiangxi Agricultural University, Collaborative Innovation Center of Postharvest Key Technology and Quality Safety of Fruits and Vegetables in Jiangxi Province, Jiangxi Key Laboratory for Postharvest Technology and Non-destructive Testing of Fruits & Vegetables, Nanchang, Jiangxi 330045, China

² Pingxiang University, Pingxiang, Jiangxi 337055, China

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Apricot (*Prunus armeniaca*) is one of the most economically important fruit species in China, and it is highly prized for its excellent quality and high nutritional value. In June 2020, fruit rot was observed on 10 to 15% of apricot fruit at the full fruit stage in an orchard in Yiyang County (34.54° N, 112.28° E), Luoyang City, Henan Province, China. Initially, the symptoms appeared as brown lesions. With aggravation of the disease, the lesions enlarged, and white hyphae appeared on the fruit surface, which eventually turned soft and rotted brown. To identify the pathogen, the surface of symptomatic fruit was sterilized with 2% sodium hypochlorite for 2 min, followed by 70% ethanol for 30 s, and rinsed three times with sterilized water. Tissues (5 × 5 mm) from the margin of the necrotic lesion were cut and cultured on potato dextrose agar (PDA) and incubated for 7 days at 28 ± 1°C for morphological identification. Five pure isolates were obtained from single spores. Initially, the isolates had abundant white aerial mycelia that turned light violet on the third day. Macroconidia were falciform, two to five septate, straight or slightly curved, and 15.27 to 37.18 × 1.97 to 3.99 μm (*n* = 50). Microconidia predominated and were elliptical or oval, hyaline, zero to one septate, and 5.08 to 14.42 × 1.65 to 4.10 μm (*n* = 50). Chlamydospores were spherical and intercalary or terminal. According to these morphological characteristics,

the fungus was initially identified as *Fusarium* species (Leslie and Summerell 2006). To confirm the identification, the *ITS*, *cal*, *RPB2*, *EF*, and *ACT* genes were amplified and sequenced with the primers *ITS1/ITS4* (White et al. 1990), *CLIC/CL2C* (O'Donnell et al. 2000), *fRPB2-5F/fRPB2-7cR* (Liu et al. 1999), *EF-1Ha/EF-2Tb*, and *ACT-512F/ACT-783R* (Carbone and Kohn 1999), respectively. Compared with the sequence in GenBank, it showed 99 to 100% homology to *Fusarium oxysporum* (GenBank accessions nos. MT560381, LS423442, AB986568, MN417202, and MK001023), and the results of sequences were deposited into GenBank with accession nos. MW812394, MW849863, OK067318, MW792498, and MW849864. A maximum likelihood phylogenetic analysis based on the *ITS*, *EF*, and *RPB2* sequences using MEGA7.0. (Mao et al. 2021) revealed that the isolates were placed in the *F. oxysporum* species complex. To confirm pathogenicity, a spore suspension was prepared from the cultures grown on PDA for 7 days at 28 ± 1°C. Twenty healthy *P. armeniaca* fruit were disinfected with 75% ethanol. Half of the disinfected fruit were wounded using a sterile needle, and the other half remained nonwounded. These wounded and nonwounded fruit were inoculated with spore suspension (1.0 × 10⁶ conidia/ml). Fruit inoculated with sterilized water served as the controls. After 5 days of incubation at 28 ± 1°C and 90% relative humidity (12 h light/dark), all the inoculated fruit developed typical symptoms similar to the original diseased fruit, whereas the control fruit remained healthy. The pathogenicity test was repeated two times, and *F. oxysporum* was reisolated from the inoculated fruit, fulfilling Koch's postulates. Although the pathogenicity of *F. oxysporum* has been previously studied in apricot fruit in vivo (Seyed and Raeisi 2018), this is the first report of *F. oxysporum* causing fruit rot on *P. armeniaca* in nature. This finding will help develop effective disease management strategies.

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[†]Indicates the corresponding author.
M. L. Xiang; mlxiang@jxau.edu.cn