Diseases Caused by Fungi and Fungus-Like Organisms

First Report of Postharvest Fruit Rot Disease of Yellow Peach Caused by *Diaporthe eres* in China

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The yellow peach (*Amygdalus persica*) is a fruit crop native to China with a golden peel and pulp that is of particular interest in fruit markets. In August 2021, yellow peaches showing fruit rot symptoms were purchased from a commercial market in Linyi City, Shandong Province, China. The symptoms included circular, tan to brown, rotten necrotic lesions and whitish mycelium masses in the center of the lesions. The infected fruit were surface disinfected with 1% NaClO for 30 s and rinsed with sterile distilled water three times. Diseased tissues from the infected fruits were cut into small segments, aseptically shifted onto potato dextrose agar (PDA) media on Petri plates, and incubated at 25°C for 5 days. Eight isolates were obtained in total from two isolation experiments. Fungal colonies were initially white, aerial, and fluffy and gradually turned brown to gray with black stromata at maturity. Alpha conidia were aseptate, hyaline, fusiform to ellipsoidal, and ranged in size from 4.16 to 7.76 × 1.95 to 3.14 µm ($n = 30$). Beta conidia were aseptate, hyaline, filiform, curved to hamate, and 15.91 to 22.55 × 0.82 to 1.66 µm ($n = 30$). The morphological characteristics were consistent with those of *Diaporthe* species (Gomes et al. 2013). For further identification, a multigene phylogenetic analysis was carried out. The internal transcribed spacer (ITS) region, translation elongation factor 1- α (TEF1- α), histone H3 (HIS), calmodulin (CAL), and β -tubulin (TUB) genes of two representative isolates were

amplified using primers ITS1/ITS4, EF1-728F/EF1-986R, CYLH3F/H3-1b, CAL228F/CAL737R, and Bt2a/Bt2b (Chaisiri et al. 2021), respectively. The sequences were deposited in GenBank (accession nos. OL375154 for ITS; OL406409 for TEF1- α ; OL406410 for HIS; OL106407 for CAL; and OL406408 for TUB). Phylogenetic analyses were conducted using the concatenation of multiple sequences (ITS, TEF1- α , HIS, CAL, and TUB) with maximum likelihood in IQtree v1.5.6 (Nguyen et al. 2015). Based on the morphological and phylogenetic characters, the isolates were identified as *Diaporthe eres*. A pathogenicity test was performed by wound inoculation on harvested fruits of *A. persica* variety Jinxiu. Mature, healthy yellow peaches purchased from Shandong, Anhui, and Hunan Provinces in China were surface sterilized with 1% NaClO solution for 1 min, rinsed with sterile water, and dried. Each fruit was wounded with a sterile scalpel creating a 2- to 3-mm incision on the peel. A 5-mm agar disc with mycelium grown on PDA at 28°C for 7 days was placed on the wound and sealed with Parafilm. Sterile PDA plugs were used as controls. Ten fruit were used for each treatment and the assays were repeated three times. The inoculated fruit were placed in sterilized transparent plastic cans containing wet, sterile paper towels. After 5 days of incubation at 25°C, the same rot symptoms were observed on fruits inoculated with mycelium, and the control remained symptomless. *D. eres* was reisolated from the lesions of inoculated fruit, and the pathogen identification was confirmed by molecular analysis, thus fulfilling Koch's postulates. Although *D. eres* was previously reported on peach trees causing shoot blight (Thomidis and Michailides 2009) and stem canker (Prencipe et al. 2017), to our knowledge, this is the first report of *D. eres* causing postharvest fruit rot of yellow peach in China. It may lead to considerable economic losses in the peach industry should post-harvest disease management practices not be implemented.

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