Diseases Caused by Fungi and Fungus-Like Organisms

First Report of Fruit Rot of Melon Caused by *Fusarium asiaticum* in China

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Melon (*Cucumis melo* L.) is a member of the Cucurbitaceae family, an important economic and horticultural crop, which is widely grown in China. In May 2020, fruit rot disease with water-soaked lesions and pink mold on cantaloupe melons was observed in several greenhouses with 50% disease incidence in Ningbo, Zhejiang Province in China. In order to know the causal agent, diseased fruits were cut into pieces, surface sterilized for 1 min with 1% sodium hypochlorite (NaClO) followed by 2 min with 75% ethyl alcohol, rinsed in sterile distilled water three times (Zhou et al. 2019), and then placed on potato dextrose agar (PDA) medium amended with streptomycin sulfate (100 µg/ml) plates at 25°C for 4 days. The growing hyphae were transferred to new PDA plates using the hyphal tip method, and putative *Fusarium* colonies were purified by single-sporing. Twenty-five fungal isolates were obtained and formed red colonies with white aerial mycelia at 25°C for 7 days, which were identified as *Fusarium* isolates based on the morphological characteristics and microscopic examination. The average radial mycelial growth rate of *Fusarium* isolate Fa-25 was 11.44 mm/day at 25°C in the dark on PDA. Macroconidia were stout with curved apical and basal cells, usually with four to six septa, and 29.5 to

44.2 × 3.7 to 5.2 µm on Spezieller Nährstoffarmer agar (SNA) medium at 25°C for 10 days (Leslie and Summerell 2006). To identify the species, the internal transcribed spacer (ITS) region and translational elongation factor 1- α (TEF1- α) gene of the isolates were amplified and cloned. ITS and TEF1- α were amplified using primers ITS1/ITS4 and EF1/EF2 (O'Donnell et al. 1998), respectively. Sequences of ITS (545 bp, GenBank accession MT811812) and TEF1- α (707 bp, GenBank accession MT856659) for isolate Fa-25 were 100 and 99.72% identical to those of *Fusarium asiaticum* strains MSBL-4 (ITS, GenBank accession MT322117.1) and Daya350-3 (TEF1- α , GenBank accession KT380124.1), respectively. A phylogenetic tree was established based on the TEF1- α sequences of Fa-25 and other *Fusarium* spp., and Fa-25 was clustered with *F. asiaticum*. Thus, both morphological and molecular characterizations supported the isolate as *F. asiaticum*. To confirm the pathogenicity, mycelium agar plugs (6 mm in diameter) removed from the colony margin of a 2-day-old culture of strain Fa-25 were used to inoculate melon fruits. Before inoculation, healthy melon fruits were selected, soaked in 2% NaClO solution for 2 min, and washed in sterile water. After wounding the melon fruits with a sterile needle, the fruits were inoculated by placing mycelium agar plugs on the wounds, and mock inoculation with mycelium-free PDA plugs was used as a control. Five fruits were used in each treatment. The inoculated and mock-inoculated fruits were incubated at 25°C with high relative humidity. Symptoms were observed on all inoculated melon fruits 10 days postinoculation, which were similar to those in naturally infected fruits, whereas the mock-inoculated fruits remained symptomless. The fungus reisolated from the diseased fruits resembled the colony morphology of the original isolate. The experiment was conducted three times and produced the same results. To our knowledge, this is the first report of fruit rot of melon caused by *F. asiaticum* in China.

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