Diseases Caused by Fungi and Fungus-Like Organisms

First Report of Fruit Rot Caused by *Fusarium luffae* in Muskmelon in China

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Funding: This study was funded by Shandong Provincial Agricultural Major Applied Technology Innovation Project (grant no. SD2019ZZ004), Key Research and Development Program of Shandong Province (2019JZZY010707), and Weifang Science and Technology Development (2020GX062). Plant Dis. 106:1763, 2022; published online as <https://doi.org/10.1094/PDIS-12-21-2666-PDN>. Accepted for publication 30 December 2021.

Muskmelon (*Cucumis melo* L.) is one of the most widely cultivated and economically important fruit crops in the world. However, many pathogens can cause decay of muskmelon fruit, including *Fusarium* spp. *Fusarium* spp. are the most important pathogen, affecting muskmelon fruit yield and quality (Wang et al. 2011). In August 2020, fruit rot symptoms were observed on ripening muskmelons (cv. Tianbao) in several fields in Jiyang District, Jinan City of Shandong Province, China. The incidences of infected muskmelon ranged from 15 to 30% and caused an average 20% yield loss. Symptoms appeared as pale brown, water-soaked lesions that were irregular in shape, with the lesion sizes ranging from a small spot (1 to 2 cm) to decay of the entire fruit. The core and surface of infected fruit were colonized and covered with white mycelia. Two infected muskmelons were collected from two fields, 3.5 km apart. Tissues removed from inside the infected fruit were surface disinfected with 75% ethanol for 30 s, and cultured on potato dextrose agar (PDA) at 25°C in the dark for 5 days. Four purified cultures were obtained using the single spore method. On carnation leaf agar (CLA), 3 to 5

septate, falcate, with a pronounced dorsiventral curvature macroconidia with tapered apical cell, and foot-shaped basal cell, measuring 20 to 40 × 3.5 to 4.5 µm. Microconidia and chlamydospores were not observed. These morphological characteristics were consistent with the description of *F. luffae* (Wang et al. 2019). Because these isolates had similar morphology, two representative isolates (XP11 and XP12) were selected for multilocus phylogenetic analyses. DNA was extracted from the representative isolates using a CTAB method. Nucleotide sequences of the internal transcribed spacers (ITS) (White et al. 1990), calmodulin (*CAM*), RNA polymerase II second largest subunit (*RPB2*), and translation elongation factor 1- α gene (*TEF1*) (Xia et al. 2019) were amplified using specific primers, sequenced, and deposited in GenBank (ITS: MW391509 and MW391510, *CAM*: MW392789 and MW392790, *RPB2*: MW392797 and MW392798, *TEF1*: MW392793 and MW392794). Alignments of a combined dataset of ITS, *CAM*, *RPB2*, and *TEF1* were made using MAFFT v. 7, and phylogenetic analyses were conducted in MEGA v. 7.0 using the maximum likelihood method. The muskmelon isolates (XP11 and XP12) clustered together with the *F. luffae* reference strain LC12167 (99% bootstrap). To perform a pathogenicity test, 10 µl of conidial suspensions (1×10^6 conidia/ml) were injected into each muskmelon fruit using a syringe, and the control fruit was inoculated with 10 µl of sterile distilled water. There were 10 replicated fruits for each treatment. The test was repeated three times. After 7 days at 25°C, the interior of the inoculated muskmelons began to rot, and the rot lesion expanded from the core toward the surface of the fruit, then white mycelia were produced on the surface. Ten isolations were reisolated from the infected tissues and confirmed to fulfill Koch's postulates. No symptoms were observed on the control muskmelons. To our knowledge, this is the first report of fruit rot caused by *F. luffae* in muskmelon in China. Considering the economic value of the muskmelon crop, correct identification can help farmers select appropriate field management measures for control of this disease.

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The author(s) declare no conflict of interest.

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Keywords: fruit rot, *Fusarium luffae*, muskmelon

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