Diseases Caused by Fungi and Fungus-Like Organisms

First Report of *Fusarium perambucanum* Causing Fruit Rot of Muskmelon in China

X. P. Zhang,¹ J. W. Xia,^{1,†} J. K. Liu,² D. Zhao,¹ L. G. Kong,¹ and X. P. Zhu^{1,†}

¹ College of Plant Protection, Collaborative Innovation Center of Fruit & Vegetable Quality and Efficient Production in Shandong, Shandong Agricultural University, Taian, Shandong, 271018, China

² Chipping Plant Protecting Station, Liaocheng, Shandong, 252100, China

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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 muskmelons; among them, the *Fusarium* spp. is the most important pathogen, as it affects fruit yield and quality (Wang et al. 2011). In May 2017, fruit rot symptoms were observed on ripening muskmelons (cv. Jipin Zaoxue) in several fields in Liaocheng of Shandong Province, China. Symptoms appeared as brown, water-soaked lesions, irregularly circular in shape, with the lesion size ranging from a small spot (1 to 2 cm) to the decay of the entire fruit. The core and the surface of the infected fruit were covered with white to rose-reddish mycelium. Two infected muskmelons were collected from each of two fields, 10 km apart. Tissues from the inside of 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), macroconidia had a pronounced dorsiventral curvature, falcate, three to five septa, with a tapered apical cell, and a foot-shaped basal cell, measuring 19 to 36 × 4 to 6 µm. Chlamydospores were abundant and were 5.5 to 7.5 µm wide, 5.5 to 10.5 µm long, and ellipsoidal or

subglobose. No microconidia were observed. These morphological characteristics were consistent with the descriptions of *Fusarium perambucanum* (Santos et al. 2019). Because these isolates had similar morphology, one representative isolate was selected for multilocus phylogenetic analyses. DNA was extracted from the representative isolate using the CTAB method. The nucleotide sequences of the internal transcribed spacers (ITS) (White et al. 1990), translation elongation factor 1- α gene (*TEF1*), RNA polymerase II second largest subunit gene (*RPB2*), and calmodulin (*CAM*) (Xia et al. 2019) were amplified using specific primers, sequenced, and deposited in GenBank (MN822926, MN856619, MN856620, and MN865126). Based on the combined dataset of ITS, *TEF1*, *RPB2*, and *CAM*, alignments were made using MAFFT version 7, and phylogenetic analyses were processed in MEGA version 7.0 using the maximum likelihood method. The studied isolate (XP1) clustered together with *F. perambucanum* reference strain URM 7559 (99% bootstrap). To perform the pathogenicity test, 10 µl of a spore suspension (1×10^6 conidia/ml) was 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 mycelium was produced on the surface. The same fungus was 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 *F. perambucanum* causing fruit rot of 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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[†]Indicates the corresponding authors.

J. W. Xia; xiajiwen1@126.com, and X. P. Zhu; zhuxp@sda.edu.cn