Diseases Caused by Fungi and Fungus-Like Organisms

First Report of Anthracnose Caused by *Colletotrichum fruticola* on Hybrid Pear Fruit in Korea

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In August 2020, anthracnose-like symptoms were observed on pear fruit (*Pyrus pyrifolia* × *P. communis*) cultivated on 0.2 ha by the National Institute of Horticultural and Herbal Science Pear Research Institute at the Rural Development Administration (Naju, Jeonnam Province in Korea). Symptoms were observed only on fruit (112 days after full bloom [DAFB]), and disease incidence was at least 90%. Initial black specks developed into larger brown or black lesions on fruit after 3 days. Later, sunken lesions with orange conidial masses were observed. Finally, infected fruit dropped prematurely. To isolate and identify the pathogen, small pieces (5 × 5 mm) from the margin of lesions on fruit were surface sterilized by immersing in 70% ethanol for 1 min, washed three times with sterile water, dried, placed on water agar amended with 100 ppm of streptomycin, and then incubated in the dark at 25°C. Hyphae emerging from the three independent tissues were subcultured on potato dextrose agar (PDA), resulting in three independent isolates (CP-1, CP-2, CP-3) after single-spore isolation. Colonies were pale gray on PDA, but the colony edges were white. Conidia were transparent, cylindrical with rounded ends, and 13.8 to 20.1 × 4.8 to 6.2 µm (avg. 18.3 × 5.4 µm, *n* = 100). Appressoria were dark brown, globose or subcylindrical, and 6.3 to 9.5 × 5.2 to 6.9 µm (8.1 × 6.1 µm, *n* = 100). The morphological characteristics were similar to the descriptions of *Colletotrichum gloeosporioides* species complex (Weir et al. 2012). Sequences of ITS (MT921589 to 91), GAPDH

(MT921987 to 89), CAL (MT921990 to 92), ACT (MT921993 to 95), CHS-1 (MT921996 to 98), TUB2 (921999 to 2001), and ApMAT (MT922002 to 04) sequences from CP-1, CP-2, and CP-3 matched with *Colletotrichum fruticola* strains BRIP 62871 (100%; MK298285), HXQT-2 (100%; MN52588), HXQT-2 (100%; MN52839), HXQT-2 (99.65; MN525801), ICKP18B4 (99.34%; LC494275), HB5 (100%; MH985245), and GQHZJ23 (100%; MN338294), respectively. Concatenated gene sequences were used for a phylogenetic analysis based on the maximum likelihood method. The reference gene accessions and other information are presented in Weir et al. (2012). The analysis placed the isolates within a clade comprising *C. fruticola*. Pathogenicity of CP-1 was tested using 120 healthy pear fruits. The fruit surfaces were sterilized with 70% ethyl alcohol for 2 min and washed twice with sterilized water. Three 120 DAFB fruits were inoculated with 10 µl of a conidial suspension (1 × 10⁶ conidia/ml) with and without wounding. Another three control fruits were inoculated with sterile distilled water with and without wounding. The inoculated fruits were placed in a plastic box to maintain high humidity and incubated in the dark at 25°C. Symptoms were observed on wounded fruits after 3 days postinoculation (dpi) and on the unwounded fruits after 5 dpi. No symptoms were observed in the control on both the wounded fruits. Pathogenicity tests were performed in duplicate. The pathogen was reisolated from symptomatic tissues (100%) on treatments on both the wounded and unwounded fruits, but not the control. The identity of the reisolated pathogen from both the wounded and unwounded fruits was confirmed via analysis of seven genes and morphological characteristics, thus fulfilling Koch's postulates. Although *C. fruticola* has been reported on apples and peaches in Korea (Kim et al. 2018; Lee et al. 2020), this is the first report of anthracnose caused by *C. fruticola* on pear fruit in Korea, highlighting the need for systematically investigating the diversity and incidence of pear anthracnose in Korea. This study will contribute to the development of control strategies for anthracnose disease on pear fruit in Korea.

References:

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