Diseases Caused by Fungi and Fungus-Like Organisms

First Report of *Colletotrichum siamense* Causing Anthracnose of Chili Pepper Fruit in Korea

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In October 2015, typical anthracnose symptoms were observed on approximately 15 to 20% of the chili fruits (cv. Manita) growing in Goesan County, Chungcheong Province, South Korea. Infection of fruits was characterized by the presence of circular, sunken lesions with concentric rings of orange conical acervuli. Fresh samples were collected from the infected fruits, and lesions from seven symptomatic fruits were cut into small pieces (5 mm²) and surface sterilized by soaking them in 1% sodium hypochlorite for 3 min, followed by rinsing thrice using sterilized water, and drying on sterilized filter paper. The tissue pieces were then placed on potato dextrose agar (PDA) and incubated at 25 ± 2°C with a 12-h photoperiod. After 2 to 3 days, single hyphal tips were transferred to fresh PDA, and a total of seven isolates were selected from typical single hyphae. The upper surfaces of the colonies formed on PDA were white to gray in color with cottony mycelia, in which salmon-colored acervuli were clearly visible. Thirty conidia were examined; all were hyaline, smooth-walled, aseptate, straight, mainly cylindrical with round ends, 12 to 17 µm long, and 3 to 4.5 µm wide. Appressoria were oval to irregular in shape, dark brown in color, and ranged from 9.5 to 11.5 × 6.5 to 7.5 µm in size. Morphological characteristics of the seven isolates were identical and resembled those of *Colletotrichum siamense* (Weir et al. 2012). To confirm the identification of the fungal isolates, DNA from seven isolates was extracted (Cenis et al. 1992), and the genes encoding glyceraldehyde-3-

phosphate dehydrogenase (GAPDH), internal transcribed spacer (ITS) rDNA regions, and β-tubulin-2 (TUB2) were partially amplified and sequenced. Sequences from all seven isolates were identical to each other. Nucleotide sequences of ITS, GAPDH, and TUB2 from representative isolates CNU180002 and CNU180012 were deposited in GenBank under accession numbers MH085103, MH085105, and MH085107 for CNU180002 and MK033503, MK033504, and MK033505 for CNU180012, respectively. The sequences for all three genes exhibited 99 to 100% identity with *C. siamense*, GenBank accession numbers FJ972613 (ITS), FJ972575 (GAPDH), and FJ907438 (TUB2) for both isolates. A multilocus phylogenetic tree with closely related reference sequences downloaded from the GenBank database demonstrated that these two isolates were aligned with *C. siamense*. Pathogenicity of isolates CNU180002 and CNU180012 was confirmed on healthy fruits (cv. Manita) by using a pin-pricked wound/drop (1 mm depth) and non-wound/drop inoculation method (Oo et al. 2017), and control fruits were mock inoculated with sterilized distilled water. Three fruits were inoculated for each isolate, and the pathogenicity test was repeated thrice. After inoculation, the fruits were placed on a sterilized paper tissue in moistened clean boxes with a relative humidity of approximately 90% and incubated for 7 days at 25°C in the dark. Disease symptoms were appeared 5 to 7 days after inoculation on wounded fruits, whereas on nonwounded fruits they were observed after 10 days. The two isolates showed identical symptoms, and control fruits remained symptomless. Both isolates were reisolated from infected fruits and were identical to the original isolates in morphological characteristics as well as in molecular sequences of ITS, GAPDH, and TUB2 genes. To our knowledge, this is the first report of anthracnose caused by *C. siamense* on chili pepper fruit in Korea.

References:

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The author(s) declare no conflict of interest.

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