Diseases Caused by Fungi and Fungus-Like Organisms

First Report of Anthracnose on Pecan (*Carya illinoensis*) Caused by *Colletotrichum siamense* in Korea

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In 2020, severely infected fruits of pecan, *Carya illinoensis*, showing distinct anthracnose symptoms were observed from pecan orchards in Uiseong (36°21'31.5"N, 128°27'15.9"E) and Miryang (35°22'54.9"N, 128°48'06.5"E) in South Korea. Visible symptoms occurred on fruit of the tree between June and July, which included being covered with dark, depressed, and irregularly shaped lesions. As the disease progressed, the lesions expanded and merged over time, leading to abscission of the fruit, which resulted in severe yield loss of pecan fruit. Of pecan varieties including Caddo, Giles, and Perique that were cultivated in each pecan orchard, Perique appeared to be most susceptible to the disease. Estimated losses were approximately 30 and 70% for the Uiseong and Miryang pecan orchard, respectively. For pathogen isolation, 10 symptomatic fruits of pecan were randomly collected and brought to the laboratory. The fruits were surface disinfested for 30 s with 70% ethanol and 1% sodium hypochlorite. These were then rinsed with sterile distilled water twice, placed in a humid chamber, and incubated at 25 ± 1°C with a photoperiod of 12 h. Acervuli filled with salmon-colored conidial masses were produced abundantly on the fruit a day after the incubation. Conidia were single celled, hyaline, cylindrical having rounded ends, smooth walls, guttulate, 15.5 to 17.7 µm long, and 3.4 to 4.8 µm wide ($n = 20$). Monoconidial isolates were made on 2% malt extract agar and incubated at 25°C for 2 weeks in the dark condition. Of those that were successfully retained, two representative isolates from each orchard were deposited in the culture collection (CDH) of the National Institute of Forest Science, Korea (accession nos. CDH2020-17 to 18). To ensure the identity of the pathogen, molecular identification was

made based on three gene regions, the internal transcribed spacer (ITS) region of rDNA, beta-tubulin (TUB2) gene, and a partial sequence of the actin (ACT), which were amplified with ITS1F/ITS4, T1/Bt2b, and ACT-512F/ACT-783R, respectively (Weir et al. 2012). These were then submitted to GenBank with accession numbers of MW380423 to 24 for ITS, MW387129 to 30 for TUB2, and MW387127 to 28 for ACT. A BLAST search in GenBank revealed that the sequences showed high similarity to those of *Colletotrichum siamense*, which were identical to MT434615 and MT274214 for ITS and ACT, respectively, and 99.7% to MK967337 for TUB2. Phylogenetic analysis based on the maximum likelihood method further showed that the isolates recovered in this study clustered with *C. siamense*, confirming its identity. Pathogenicity was confirmed by inoculating living pecan trees. Healthy fruits from five trees were surface cleaned with cotton soaked in sterile water and air dried. To inoculate the pathogen, three to five fruits per tree were wounded with a sterilized needle, and an aliquot of 10 µl of spore suspension (1.0×10^5 conidia/ml) of *C. siamense* (CDH2020-18) was dropped on each wound. To keep moisture, each treated fruit was enveloped by a plastic bag in which cotton soaked in sterile water had been placed. Controls were treated with sterile distilled water drops. The symptoms with dark, depressed, and irregularly shaped lesions developed from all inoculated treatments 6 weeks after the inoculations, which were identical to those observed in the field. However, no symptoms were observed on the control. *C. siamense* was successfully reisolated, fulfilling Koch's postulates. Taken together, it was confirmed that *C. siamense* is the causal agent of anthracnose on pecan. In Korea, *C. siamense* was reported causing anthracnose on apple, persimmon, and plum (Farr and Rossman 2020). However, to our knowledge, this is the first report of anthracnose on pecan caused by *C. siamense* in Korea. To control the disease effectively, more attention should be paid to other regions of the country where the disease caused by the pathogen might occur.

References:

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