Diseases Caused by Fungi and Fungus-Like Organisms

First Report of Anthracnose of Papaya (*Carica papaya*) Caused by *Colletotrichum siamense* in China

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Funding: The research was supported by Guangxi Natural Science Foundation (2017GXNSFBA198218, 2018GXNSFBA281077). Plant Dis. 105:2252, 2021; published online as <https://doi.org/10.1094/PDIS-10-20-2154-PDN>. Accepted for publication 14 February 2021.

Papaya (*Carica papaya* L.) is a rosaceous plant widely grown in China that is economically important. Anthracnose caused by *Colletotrichum* sp. is an important postharvest disease, which severely affects the quality of papaya fruits (Liu et al. 2019). During April 2020, some mature papaya fruits with typical anthracnose symptoms were observed in Fusui, Nanning, Guangxi, China, with an average of 30% disease incidence (DI) and over 60% DI in some orchards. Initial symptoms of these papayas appeared as watery lesions, which turned dark brown, sunken, with a conidial mass appearing on the lesions under humid and warm conditions. The disease severity varied among fruits, with some showing tiny light brown spots, and some ripe fruits presenting brownish, rounded, necrotic, and depressed lesions over part of their surface. Samples from two papaya plantations (107.54°E, 22.38°N) were collected and brought to the laboratory. Symptomatic diseased tissues were cut into 5 × 5-mm pieces, surface sterilized with 2% (v/v) sodium hypochlorite for 1 min, and rinsed three times with sterilized water. The pieces were then placed on potato dextrose agar (PDA). After incubation at 25°C in the dark for 1 week, colonies with uniform morphology were obtained. The aerial mycelium on PDA was white on the top side with concentric rings of salmon acervuli on the underside. A gelatinous layer of spores was observed on part of PDA plates after 7 days at 28°C. The conidia were elliptical, aseptate, and hyaline (Zhang et al. 2020). The length and width

of 60 conidia were measured for each of the two representative isolates, MG2-1 and MG3-1, and these averaged 13.10 × 5.11 μm and 14.45 × 5.95 μm. DNA was extracted from mycelia of these two isolates with the DNAsure Plant Kit (Tiangen Biotech, China). The internal transcribed spacer (ITS), partial actin (ACT), calmodulin (CAL), chitin synthase (CHS), β-tubulin 2 (TUB2), and glyceraldehyde 3-phosphate dehydrogenase (GAPDH) regions were amplified by PCR and sequenced. The sequences were deposited into GenBank with accessions MT904003, MT904004, and MT898650 to MT898659. BLASTN analyses against the GenBank database showed that they all had over 99% identity to the type strain of *Colletotrichum siamense* isolate ICMP 18642 (GenBank accession nos. JX010278, GQ856775, JX009709, GQ856730, JX010410, and JX010019) (Weir et al. 2012). A phylogenetic tree based on the combined ITS, ACT, CAL, CHS, TUB2, and GAPDH sequences using the neighbor-joining algorithm also showed that the isolates were *C. siamense*. Pathogenicity tests were conducted on 24 mature, healthy, and surface-sterilized papaya fruits. On 12 papaya fruits, three well-separated wounded sites were made for inoculation, and for each wounded site, six adjacent pinhole wounds were made in a 5-mm-diameter circular area using a sterilized needle. A 10-μl aliquot of 1 × 10⁶ conidia/ml suspension of each of the isolates (MG2-1 and MG3-1) was inoculated into each wound. For each isolate, there were six replicate fruits. The control fruits were inoculated with sterile distilled water. The same inoculation was applied to 12 nonwounded papaya fruits. Fruits were then placed in boxes, which were first washed with 75% alcohol and lined with autoclaved filter paper moistened with sterilized distilled water to maintain high humidity. The boxes were then sealed and incubated at 28°C. After 10 days, all the inoculated fruits showed symptoms, whereas the fruits that were mock inoculated were without symptoms. Koch's postulates were fulfilled by reisolation of *C. siamense* from diseased fruits. To our knowledge, this is the first report of *C. siamense* causing anthracnose of papaya in China. This finding will enable better control of anthracnose disease caused by *C. siamense* on papaya.

References:

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The author(s) declare no conflict of interest.

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Keywords: anthracnose, papaya, *Colletotrichum siamense*

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