Diseases Caused by Fungi and Fungus-Like Organisms

First Report of Anthracnose on *Passiflora edulis* Caused by *Colletotrichum siamense* in Guangdong Province in China

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Passion fruit (*Passiflora edulis* Sims) is an important tropical and subtropical species with high commercial value due to its wide use in juice production and fresh fruit consumption. A disease affecting the leaves was observed on passion fruit vines in the South Subtropical Botanical Garden in Zhanjiang City in April and September 2020 with an incidence of 30 to 60%. Affected leaves usually developed small circular reddish-brown spots, which enlarged to oval spots and large irregular spots. The spots were brown and surrounded by a yellow halo with sunken cavities, which are typical symptoms of anthracnose. Diseased leaves of cultivar Huangjin were collected in Zhanjiang City (21.2°N, 110.3°E), Suixi City (21.4°N, 110.2°E), and Leizhou City (20.9°N, 110.1°E) in Guangdong Province. Leaf samples were disinfested with 1% NaOCl for 5 min and cultured on potato dextrose agar (PDA) at 28°C for 1 week. Eight single-spore isolates were recovered from PDA medium. Colonies developing on PDA were grayish white with a regular border. Conidia were straight, hyaline with rounded ends, and 5.3 to 6.8 × 15.2 to 21.3 μm ($n = 50$ conidia of each isolate). Fungal mycelia were hyaline, septate, and branched. Conidia were born on a long conidiogenous cell, and appressoria were dark, smooth-walled, oval, and 15.5 to 21.3 × 4.0 to 5.8 μm ($n = 50$). The isolates were morphologically identified as *Colletotrichum* sp. (Weir et al. 2012). Tests of pathogenicity were performed according to Koch's postulates using three isolates. Five plants with two to three vines were inoculated with each isolate separately, and three to four leaves of each plant were inoculated. Fresh wounds were made with a sterile needle on the healthy surface of leaves of *P. edulis* 'Huangjin', and each leaf was covered

with a piece of cotton drenched with 200 μl of conidial suspension (10^6 conidia/ml) from each isolate. Control seedlings were inoculated identically, except sterile water was used to drench the cotton. Inoculated plants were placed in a moisturizing light incubator at 25°C and 80% humidity under a 12-h light/dark cycle for 14 days and examined daily to monitor disease symptom development. Small round brown spots were observed at the inoculation sites 3 days after the inoculation and eventually became large brown lesions. There were no symptoms observed in the water-inoculated plants. A *Colletotrichum* sp. strain based on morphology was consistently reisolated from leaf lesions, fulfilling Koch's postulates. For molecular identification, the internal transcribed spacer (ITS) region of ribosomal DNA, calmodulin (Cal), tubulin (Tub), and ApMAT loci of three isolates were amplified using primer pairs of ITS4/ITS5, CL1C/CL2C, T1/T2, and AM-F/AM-R (Sharma et al. 2015). A phylogenetic tree derived from a neighbor-joining analysis of a concatenated alignment of ITS, CAL, Tub, and ApMAT sequences was created. The accession numbers of the three isolates (BXGZJ 1-1, BXGSX 2-2, and BXGLZ 3-2) used in this study were MZ605383 to MZ605385 for ITS, MZ605389 to MZ605391 for CAL, MZ605392 to MZ605394 for Tub, and MZ605386 to MZ605388 for ApMAT. The sequences of the three isolates were aligned with related species of *Colletotrichum* (Sharma et al. 2015). Analyses based on concatenated data sets of four genes showed that the sequences of the three isolates had the highest identity of 99% to those of the type strain *C. siamense* ICMP18578. According to both morphological and sequence analyses, the *P. edulis* pathogen was identified as *C. siamense*. There is a report of foliar diseases on *P. edulis* caused by *C. brevisporum* in Hainan Province in China (Qiu et al. 2021). To our knowledge, this is the first report of anthracnose on *P. edulis* caused by *C. siamense* in China. Identification of pathogens could provide valuable information for disease diagnosis and effective chemicals to control the disease, which could reduce yield loss and improve fruit quality.

References:

- Qiu, F., et al. 2021. Australas. Plant Pathol. 50:229.
- Sharma, G., et al. 2015. Fungal Divers. 71:247.
- Weir, B. S., et al. 2012. Stud. Mycol. 73:115.

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