Diseases Caused by Fungi and Fungus-Like Organisms

First Report of Passion Fruit Anthracnose Caused by *Colletotrichum constrictum*

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Passion fruit (*Passiflora edulis*) is widely cultivated in tropic and subtropic regions. Because of its unique and intense flavor and high acidity, passion fruit juice concentrate is used in making delectable sauces, desserts, candy, ice cream, sherbet, or blending with other fruit juices. Anthracnose of passion fruit is favored by frequent rainfall and average temperatures above 27°C. In August 2018, anthracnose on passion fruit was observed in commercial plantings in Lincang, Yunnan, China (23.88°N, 100.08°E). Symptoms included lesions of oval to irregular shapes with brown to dark brown borders. Infection covered most of the fruit surface with pink-to-dark sporulation as reported by Tarnowski and Ploetz (2010). A conidial mass from an individual sorus observed on an infected fruit was isolated and cultured on potato dextrose agar supplemented with 50 µg/ml of streptomycin. From a single microscopic field, two monospore isolates were dissected using a sterile needle, subcultured, and referred to as BXG-1 and BXG-2. Morphological characters including conidia color, size, and shape were similar between the two isolates. Conidia were aseptate and cylindrical with apex and rounded base. Conidial length ranged from 12.3 to 16.1 µm (average 13.5 µm), and width ranged from 5.5 to 6.2 µm (average 5.7 µm). Morphologic data were consistent with *Colletotrichum constrictum* (Damm et al. 2012). To further confirm the fungal species, the ribosomal internal transcribed spacer (ITS), partial sequences of actin (ACT), chitin synthase (CHS-1), glyceraldehyde-3-phosphate dehydrogenase (GAPDH), and β-tubulin 2 (TUB2) were amplified and

sequenced. Primers and PCR amplification were as described by Damm et al. (2012). The sequences were compared with type sequences in GenBank. The results showed the ITS (GenBank accessions MW828148 and MW828149), ACT (MW855882 and MW855883), CHS-1 (MW855884 and MW855885), GAPDH (MW855886 and MW855887), and TUB2 (MW855888 and MW855889) sequences of the isolates BXG-1 and BXG-2 were 98% identical with sequence data from strain CBS:128504 of *C. constrictum*. A maximum likelihood tree was constructed using MEGA-X version 10.1.6 (Kumar et al. 2018) based on a combined dataset of the ITS, ACT, CHS-1, GAPDH, and TUB2 sequences of BXG-1 and BXG-2 along with those of 18 *Colletotrichum* spp. previously deposited in GenBank (Damm et al. 2012). The phylogenetic analysis showed that BXG-1 and BXG-2 belong to the *C. constrictum* clade. Based on morphology and DNA sequencing, BXG-1 and BXG-2 were identified as *C. constrictum*. To verify pathogenicity, passion fruits were sprayed with a suspension of 1×10^5 conidia/ml. Control fruits were sprayed with sterilized water. After inoculation, fruits were incubated in an artificial climate box at 27°C and 80% relative humidity. Necrotic symptoms appeared 8 days after inoculation and were similar to those observed on fruit from the field. The pathogen was reisolated from lesions, thus fulfilling Koch's postulates. *C. constrictum* has been reported to cause anthracnose of citrus from Australia (Wang et al. 2021) and mango from Italy (Ismail et al. 2015). To our knowledge, this is the first report of *C. constrictum* causing anthracnose on passion fruit worldwide, and these data will provide useful information for developing effective control strategies.

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