Diseases Caused by Fungi and Fungus-Like Organisms

First Report of Anthracnose Caused by *Colletotrichum brasiliense* on Violet Passion Fruit in China

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Violet passion fruit (*Passiflora edulis* Sims) is an important tropical and subtropical perennial evergreen vine with large-scale cultivation in Guangxi, China. Between May and September 2020, anthracnose symptoms occurred on passion fruit (cultivar Tainong No. 1) in Xingye county (22.7713°N, 110.0780°E) in Guangxi Province, China. The disease incidence varied from 25 to 60% in different orchards. Initial symptoms on young fruits appeared as multiple tiny water-soaked, oval to irregular pale greenish spots. As the disease progressed, the lesions became medium brown, with sunken cavities. Under humid conditions, acervuli containing masses of conidia and dark setae were found on the lesions. The affected fruits became shriveled. Tissue pieces (5 × 5 mm) were cut out from infected fruits, surface sterilized in 75% ethanol for 15 s and 0.1% HgCl₂ for 2 min, washed three times with sterile water, placed onto potato dextrose agar (PDA), and incubated at 28°C for 3 days. Of the 29 *Colletotrichum* isolates obtained, the isolate B13 was selected for morphological characterization. B13 was purified by single spore isolation and incubated on PDA at 25°C under continuous fluorescent light, producing white to pale yellow colonies with dense aerial mycelia. The reverse side of the colony was pale yellowish to olive. Conidia were hyaline, unicellular, straight, cylindrical, with both ends slightly round or one end round and the other slightly pointed, measuring 10.5 to 18.8 (avg. 16.4) × 5.4 to 7.2 (avg. 6.3) μm (*n* = 50). Appressoria were light brown to dark black,

smooth-walled, lobed, often with a roundish outline, sometimes also triangular, 7.2 to 10.9 (avg. 9.1) × 6.8 to 9.2 (avg. 8.2) μm (*n* = 50). Morphological characteristics of the isolate matched those of *Colletotrichum brasiliense* (Damm et al. 2012). The internal transcribed spacers (ITS), actin (ACT), glyceraldehyde-3-phosphate dehydrogenase (GAPDH), and beta-tubulin (TUB2) genes of strain B13 were sequenced using the method and primers of Damm et al. (2012). Sequences of the amplified DNA regions were submitted to GenBank (ITS: MW198820; ACT: MW266083; GAPDH: MW266084; and TUB2: MW266085). A concatenated maximum likelihood phylogenetic tree was built using MEGA 7.0.21 in which B13 clustered with *C. brasiliense* and clearly separated from other *Colletotrichum* spp. Pathogenicity of B13 was assayed using 1-year-old plants of violet passion fruit cultivar Tainong No. 1. Conidial suspensions were prepared from 7-day-old cultures grown on PDA at 28°C. Sterile distilled water was used to dislodge conidia from the culture dish and the conidial concentration was adjusted to 1 × 10⁶ spores ml⁻¹ using a hemocytometer. Fruits were rinsed with sterilized water and wounded with a sterile needle at three locations. Three fruits were inoculated by spraying with 20 ml of the conidial suspension. Control fruits were sprayed with distilled water. Fruits were then covered with plastic bags to maintain high relative humidity. After 9 days, all inoculated fruits developed brown spots with sunken cavities, resembling symptoms observed in the field, and controls remained symptomless. Fungal cultures with phenotypic features similar to *C. brasiliense* were reisolated from the symptomatic fruits, verifying *C. brasiliense* as the causal agent of the disease based on Koch's postulates. *C. boninense*, *C. gloeosporioides*, *C. queenslandicum*, *C. brevisporum*, and *C. karstii* were reported as causal agents of anthracnose on passion fruit (Du et al. 2017; James et al. 2014; Júnior et al. 2010; Power et al. 1984; Ran et al. 2019). To our knowledge, this is the first report of *C. brasiliense* causing anthracnose on passion fruit in China.

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