Diseases Caused by Fungi and Fungus-Like Organisms

First Report of *Colletotrichum siamense* Causing Anthracnose of Guava (*Psidium guajava*) in Mexico

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Guava (*Psidium guajava* L.) is a small tree belonging to the Myrtaceae family and it is distributed worldwide in the tropical and subtropical areas. During the summer of 2019, symptoms of fruit anthracnose were observed on approx. 90% of 250 guava trees located in backyards in Juan Jose Rios, Sinaloa, Mexico. Lesions on guava fruit were irregular, necrotic, and sunken. On advanced infections, acervuli containing salmon-pink masses of spores were observed on the lesions. Twenty fruits were collected from 10 trees (two fruits per tree). *Colletotrichum*-like colonies were consistently isolated on potato dextrose agar (PDA) medium and 20 monoconidial isolates were obtained. Four isolates were selected as representatives for morphological characterization, multilocus phylogenetic analysis, and pathogenicity tests. The isolates were deposited in the Culture Collection of Phytopathogenic Fungi of the Faculty of Agriculture of El Fuerte Valley at the Sinaloa Autonomous University (accession nos. FAVF205–FAVF208). Colonies on PDA medium were flat with an entire margin, with abundant felty and white aerial mycelium, and pink conidial masses. Conidia ($n = 100$) were cylindrical, hyaline, aseptate, with ends rounded, and

measuring 14.8 to 18.1×4.4 to $5.3 \mu\text{m}$. Based on morphological features, the isolates were tentatively allocated in the *Colletotrichum gloeosporioides* species complex (Weir et al. 2012). For molecular identification, genomic DNA was extracted, and the internal transcribed spacer (ITS) region (White et al. 1990), as well as partial sequences of actin (ACT), glyceraldehyde-3-phosphate dehydrogenase (GAPDH), β -tubulin (TUB2), chitin synthase (CHS-1), and glutamine synthetase (GS) genes were amplified by PCR (Weir et al. 2012) and sequenced. A phylogenetic tree based on Bayesian inference and including published ITS, GAPDH, TUB2, ACT, CHS-1, and GS data for *Colletotrichum* species was constructed. The multilocus phylogenetic analysis clearly distinguished the four isolates FAVF205–FAVF208 as *C. siamense*, separating it from all other species within the *C. gloeosporioides* species complex. The sequences were deposited in GenBank (accessions nos. ITS: MW598512–MW598515; GAPDH: MW595216–MW595219; TUB2: MW618012–MW618015; ACT: MW595208–MW595211; CHS-1: MW595212–MW595215; and GS: MW618008–MW618011). Pathogenicity of the four isolates was verified on 40 healthy guava fruits. Twenty fruits were wounded with a sterile toothpick (2 mm in depth) and a mycelial plug (6 mm diameter) was placed on each wound. Ten fruits inoculated with a PDA plug without mycelial growth served as controls. The fruit was kept in a moist plastic chamber at 25°C for 7 days. Pathogenicity of each isolate was tested with both nonwound and wound inoculation methods. The experiments were repeated twice with similar results. All inoculated fruits developed sunken necrotic lesions 4 days after inoculation, whereas no symptoms were observed on the control fruits. The fungi were consistently reisolated only from the diseased fruits, fulfilling Koch's postulates. *C. siamense* has been previously reported on guava fruit in India (Sharma et al. 2015). However, to our best knowledge, this is the first report of *C. siamense* causing fruit anthracnose on guava in Mexico. Therefore, it is necessary to explore the diversity of *Colletotrichum* species on guava in detail through subsequent phylogenetic studies as well as to monitor the distribution of this pathogen into other Mexican regions.

References:

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