Diseases Caused by Fungi and Fungus-Like Organisms

First Report of *Colletotrichum jiangxiense* Causing Avocado Anthracnose in Mexico

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Mexico is the largest avocado (*Persea americana*) producer and exporter in the world. In January of 2019, typical symptoms of fruit anthracnose were observed on approximately 90% of avocado trees in backyards localized in Leonardo Bravo municipality in Guerrero, Mexico. Lesions on avocado fruits were circular, necrotic, and sunken, and the mesocarp showed a soft rot with dark brown discoloration. To perform fungal isolation, small pieces from adjacent tissue to lesions of five symptomatic fruits were surface disinfested by immersion in a 1% sodium hypochlorite solution for 2 min, rinsed in sterile distilled water, and placed in a Petri dish containing potato dextrose agar (PDA). Plates were incubated at 25°C for 5 days in darkness. *Colletotrichum*-like colonies were consistently isolated, and seven monoconidial isolates were obtained. An isolate was selected as a representative for morphological characterization, molecular analysis, and pathogenicity tests. The isolate was deposited in the Culture Collection of Phytopathogenic Fungi at the Colegio Superior Agropecuario del Estado de Guerrero (accession no. CSAEG-CJ19). After 8 days on PDA, the colonies were gray on the upper surface and with orange conidial masses. Conidia ($n = 100$) were cylindrical, hyaline, aseptate, with rounded ends, 14.4 to 18.5×4.5 to 6.2 μm . Based on morphological features, the isolate was tentatively identified in the *Colletotrichum gloeosporioides* species complex (Weir et al. 2012). For molecular identification, genomic DNA was extracted, and the internal transcribed spacer (ITS) region of rDNA and

partial sequences of actin (ACT), β -tubulin (TUB2), and glyceraldehyde-3-phosphate dehydrogenase (GAPDH) genes were amplified by PCR, and they were sequenced with primers ITS5/ITS4 (White et al. 1990), ACT-512F/ACT-783R (Carbone and Kohn 1999), Bt2A/Bt2B (Glass and Donaldson 1995), and GDF/GDR (Templeton et al. 1992), respectively. BLAST analysis of the obtained sequences of the ITS, ACT, TUB2, and GAPDH genes revealed 100, 99.63, 99.77, and 100% identity with those of isolate LF687 of *Colletotrichum jiangxiense* in GenBank (accession nos. KJ955201, KJ954471, KJ955348, and KJ954902). A phylogenetic tree based on Bayesian inference and including published ITS, ACT, TUB2, and GAPDH data for *Colletotrichum* species was constructed. The multilocus phylogenetic analysis clearly distinguished isolate CSAEG-CJ19 as *C. jiangxiense*, separating it from all other species within the *C. gloeosporioides* species complex. The sequences were deposited in GenBank (accession nos.: ITS, MT011397; ACT, MN968784; TUB2, MN968786; and GAPDH, MN968785). To conduct Koch's postulates, 20 healthy avocado fruits (cv. Hass) were wounded with a sterile toothpick (2 mm in depth), and a drop of 15 μl of conidial suspension (1×10^5 spores/ml) was placed on each wound. Ten control fruits were wounded and treated with sterilized water. All the fruits were kept in a moist plastic chamber at 25°C for 8 days. All inoculated fruits developed circular and necrotic lesions (12 to 18 mm in diameter) 5 days after inoculation, whereas control fruits remained healthy. The fungus was consistently reisolated from the inoculated fruits. Previously, *C. jiangxiense* has been reported as a pathogen on *Camellia sinensis* and *Citrus sinensis* in China (Farr and Rossman 2020). To our knowledge, this is the first report of *C. jiangxiense* causing anthracnose on avocado worldwide. This study showed another species in the *C. gloeosporioides* complex associated with avocado diseases in Mexico. Therefore, it is necessary to explore the diversity of *Colletotrichum* species in detail through subsequent phylogenetic studies as well as to monitor the distribution of this pathogen into other Mexican regions.

References:

- Carbone, I., and Kohn, L. M. 1999. Mycologia 91:553.
- Farr, D. F., and Rossman, A. Y. 2020. Fungal Databases, Syst. Mycol. Microbiol. Lab., ARS, USDA. Retrieved February 15, 2020, from <https://nt.ars-grin.gov/fungaldbatabases/>.
- Glass, N. L., and Donaldson, G. 1995. Appl. Environ. Microbiol. 61:1323.
- Templeton, M. D., et al. 1992. Gene 122:225.
- Weir, B. S., et al. 2012. Stud. Mycol. 73:115.
- White, T. J., et al. 1990. Page 315 in: PCR Protocols: A Guide to Methods and Applications. Academic Press, San Diego, CA.

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