Disease Note

Diseases Caused by Fungi and Fungus-Like Organisms

First Report of *Colletotrichum sansevieriae* Causing Anthracnose of Snake Plant (*Dracaena trifasciata*) in Ohio and Its Draft Genome

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Dracaena trifasciata (Prain) Mabb. is a popular houseplant in the United States. In September 2021, two diseased samples from two Ohio homeowners were received by the Ornamental Pathology Laboratory at The Ohio State University. Each sample included one or two detached leaves with circular, gray, water-soaked lesions scattered throughout the lamina and blighted areas with concentric rings bearing brown to black acervuli. Lesions covered 25 to 50% of the leaf surface. Isolations were made by excising small portions of leaf tissue from lesion margins, surface disinfesting in 10% bleach for 45 s, rinsing in sterile water, and plating on potato dextrose agar (PDA). Plates were incubated at 23°C for 1 week. Two representative isolates, one per sample (FPH2021-5 and -6), were obtained by transferring hyphal tips to fresh PDA plates. Mycelia of both isolates were aerial, cottony, grayish white, producing spores in a gelatinous orange matrix, and gray to olivaceous gray on the underside. Conidia of both isolates were cylindrical, single celled, hyaline, and 12.02 to 18.11 (15.51) × 5.03 to 7.29 (6.14) µm (FPH2021-5; n = 50) and 15.58 to 20.90 (18.39) × 5.63 to 8.27 (7.05) µm (FPH2021-6; n = 50). Appressoria were globose to subglobose, single celled, dark brown to sepia, and 6.62 to 13.98 (8.97) × 5.05 to 6.58 (6.58) µm (FPH2021-5; n = 50) and 6.54 to 11.32 (8.63) × 4.54 to 8.94 (7.09) µm (FPH2021-6; n = 50). Genomic DNA (gDNA) samples were extracted from both isolates and the internal transcribed spacer (ITS) region was amplified using primers ITS1F/ITS4 (Gardes and Bruns 1993; White et al. 1990). GenBank BLAST sequence analysis resulted in 99.83% (FPH2021-5; OP410918.1) and 100% (FPH2021-6; OP410917.1) identity with 100% query coverage to the type strain of *Colletotrichum sansevieriae* Miho Nakam. & Ohzono MAFF239721 or Sa-1-2 (NR_152313.1; Nakamura et al. 2006). Whole genome sequencing was conducted for FPH2021-6 and the assembly was deposited in GenBank (JAOQIF000000000.1). The glyceraldehyde-3-phosphate dehydrogenase (*GAPDH*) and β-tubulin (*β-tub*) regions were either extracted from the genome of FPH2021-6 (OP414603.1 and OP414601.1, respectively) or amplified from FPH2021-5 gDNA using primers GDF/GDR (OP414604.1) and Bt-2b/T1 (OP414602.1), respectively (Glass and Donaldson 1995; O'Donnell and Cigelnik 1997; Templeton et al. 1992). A multilocus partitioned analysis (Chernomor et al. 2016) based on concatenated sequences of ITS, *GAPDH*, and *β-tub* using ModelFinder was performed to build a maximum likelihood tree (IQ-TREE v2.0.3), suggesting that these two isolates are phylogenetically closer to the type strain from Japan than to isolate 1047 from Florida (Palmateer et al. 2012). To fulfill Koch's postulates, two parallel leaf sections from one 10-inch *D. trifasciata* 'Laurentii' plant maintained in a 1.3-liter container were selected. Three wounds were made in each section using a sterile syringe needle. A 10-µl drop of either a 1×10^6 conidia/ml suspension of FPH2021-6 or sterile water was placed on each wound. The plant was covered with a plastic bag for 2 days postinoculation (DPI) and maintained in a greenhouse at 25°C with a 12-h photoperiod. The experiment was conducted twice. Grayish water-soaked lesions, acervuli, and leaf blight were observed on inoculated sections 3, 10, and 14 DPI, respectively; no symptoms appeared on sections treated with sterile water. *C. sansevieriae* was reisolated from the lesions and confirmed to be identical to the original isolate based on ITS sequencing and morphological examinations. To our knowledge, this is the first report of *C. sansevieriae* on *D. trifasciata* in Ohio and the first genome draft of an isolate from the United States. Whole-genome sequence data is paramount for species identification in this highly diverse fungal genus, and a powerful tool to conduct comparative genomic analyses.

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