Diseases Caused by Fungi and Fungus-Like Organisms

First Report of *Fusarium lacertarum* Causing Fusarium Head Blight on Sorghum in North Carolina

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In August 2018, sorghum plants (*Sorghum bicolor* [L.] Moench) from research field plots in Wake County, North Carolina, were observed with head blight symptoms including panicles with red lesions, visible mycelium, and necrosis. At the time of collection, all plants in research plots displayed symptoms of Fusarium head blight, and panicles averaged 33% area affected by symptoms and signs. From these affected plants, samples ($n = 5$) were collected for further identification. Symptomatic grains were surface sterilized for 1 min in 0.825% sodium hypochlorite solution and rinsed for 1 min in sterile deionized water. After drying on sterile paper towels, grains were plated onto water agar. Resulting fungal hyphal tips were then transferred to antibiotic-amended potato dextrose agar and incubated at 25°C. Cultures were incubated for 3 to 5 days. Isolates had abundant white hyphae accompanied with peach-colored pigment production. Macroconidia with five to six septations were 23.47 ± 7.74 μm long and 3.47 ± 0.66 μm wide with foot-shaped basal cells, tapering to hooked apical cells. Chlamydospores were present in chains, but microconidia were not present. Morphological species recognition criteria tentatively identified the isolate as *Fusarium lacertarum* Subrahm., in the *Fusarium incarnatum-equiseti* species complex (FIESC) using characteristics described by Leslie and Summerell (2006). Molecular characterization using translation elongation factor 1 α (TEF-1 α , primers EF1 and EF2 from O'Donnell et al. 1998), β -tubulin (TUB2, primers T1 and T22 from O'Donnell and Cigelnik 1997), and ribosomal protein subunit II (RPB2, primers 5F2 and 11AR from Cerón-Bustamante et al. 2018) was conducted to confirm morphological identification. DNA from the hyphae of pure cultures was extracted using the DNeasy PowerSoil DNA extraction kit according to the manufacturer's guidelines. DNA amplification conditions followed the protocols for each primer set (Cerón-Bustamante et al. 2018;

O'Donnell et al. 1998; O'Donnell and Cigelnik 1997). BLASTn analysis of TEF-1 α (isolate accession MT149915, 573 bp) alignment had 99.8% identity to *F. lacertarum* (NCBI accession JF740828), TUB2 (isolate accession MT149914, 1,183 bp) alignment had 99.3% identity to *F. equiseti* (NCBI accession KJ396338), and RPB2 (isolate accession MT184173, 1,538 bp) concatenated sequences had 95.3% identity to *F. lacertarum* (NCBI accession MH582185). The TUB2 region most closely aligns to *F. equiseti*, which is likely due to an absence of TUB2 sequences labeled for *F. lacertarum* in the NCBI database. Pathogenicity was confirmed by spray-inoculating Southern Harvest 80G4 sorghum panicles ($n = 9$) at anthesis with 4 ml of conidial suspension (3.3×10^4 conidia/ml). Control plants ($n = 9$) were sprayed with sterile water. Plastic bags were placed around panicles for 24 h to ensure moist conditions during the infection period. Plants were maintained in a greenhouse under a 12-h light cycle and fertilized biweekly with 20-20-20 fertilizer. Symptoms were observed on inoculated panicles after 14 days, and the *F. lacertarum* isolate was recovered from inoculated plants and confirmed using methods described above. *Fusarium* spp. were not reisolated from noninoculated control plants. Members of FIESC are known to contribute to the Fusarium head blight disease complex and may be capable of producing mycotoxins associated with infections (Lincy et al. 2011; Marín et al. 2012; Moretti et al. 2017); however, mycotoxin characterization in *F. lacertarum* has not been characterized. To our knowledge, this is the first report of *F. lacertarum* causing disease to sorghum in North Carolina and the United States. *F. lacertarum* may cause impactful losses to sorghum producers due to direct yield and quality losses by the pathogen as well as the potential for mycotoxins to impact trade.

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