Disease Notes

Diseases Caused by Fungi and Fungus-Like Organisms

First Report of *Fusarium poae* Causing Fusarium Head Blight of Wheat in Georgia, U.S.A.

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Fusarium head blight (FHB) is one of the most troublesome fungal diseases challenging U.S. wheat (*Triticum aestivum* L.) production (Savary et al. 2019). Harmful mycotoxin contamination, primarily due to deoxynivalenol (DON) in the *Fusarium*-damaged kernels (FDK), can negatively impact human and livestock health (McMullen et al. 1997). Although *Fusarium graminearum* is the primary causal agent of FHB, several other species including *Fusarium poae* could pose a risk by producing dangerous mycotoxins such as nivalenol, DON, HT-2, and T-2 (Stenglein 2009). Severe FHB epidemics on wheat have occurred in recent years, along with increased corn acreage across the southeast United States, specifically in Georgia (Ghimire et al. 2020). Five symptomatic wheat heads displaying bleaching symptoms were randomly collected from 19 different fields across 13 counties of Georgia in late spring of 2018. Infected kernels were dipped in 6% sodium hypochlorite for 10 min and rinsed three times with sterilized water. Blot-dried kernels were placed on potato dextrose agar (PDA) and incubated for 7 days at 25°C under a 12-h photoperiod. Three isolates (GA18W-2.1.6, GA18W-6.1.4, and GA18W-10.2.3) from Terrell, Peach, and Sumter counties exhibited dense, whitish mycelium colony typical of *F. poae* (Leslie and Summerell 2006). When grown in carboxymethylcellulose broth, isolates produced globose to piriform microconidia (5.1 to 12.4 by 4.4 to 11.2 µm) that were aseptate or had a single septation. The morphological identification was further confirmed by DNA sequencing. Single hyphal tip isolates were grown on cellophane overlain on PDA for 10 days. Fungal DNA was extracted using a Qiagen DNeasy Plant Mini Kit. Genomic DNA was sequenced using TEF1 and TEF2 primer pairs that target the translation elongation factor 1-α locus (O'Donnell et al. 1998). A BLASTn query identified the obtained sequences of GA18W-2.1.6 (accession no. MT856907) and GA18W-10.2.3 (accession no. MT856909) as *F. poae* with a 99% sequence homology with GenBank reference accession MK629641, while GA18W-6.1.4 (accession no. MT856908) displayed 100% similarity with *F. poae* accession KJ947343. Koch's postulates were performed under greenhouse conditions. Three seeds of the FHB-susceptible wheat cultivar 'SS8641' were planted in individual Cone-tainers with three replications (two Cone-tainers per replicate). Wheat plants were vernalized for 6 weeks and then moved back to the greenhouse. Each *F. poae* isolate was spray inoculated (50,000 spores/ml) at the flowering stage onto 18 to 24 wheat heads. A field isolate of *F. graminearum* was included as a positive control, whereas heads mock-inoculated with water were used as a negative control. Inoculated wheat heads were incubated in black plastic bags for 48 h. Disease severity and FDK were recorded 3 weeks postinoculation. Disease severities were 6.7% (GA18W-2.1.6), 8.3% (GA18W-10.2.3), and 15.2% (GA18W-6.1.4) compared with 90.0% in the positive control, similar to Arrúa et al. (2019). No symptoms were observed in the negative control. FDK was 18% (GA18W-2.1.6), 28% (GA18W-10.2.3), and 44% (GA18W-6.1.4). *F. poae* was reisolated from the infected heads and found to be morphologically identical to the isolates used for inoculation. To our knowledge, this is the first report of *F. poae* associated with FHB of wheat in the state of Georgia, U.S.A. *F. poae* isolates from Georgia might produce mycotoxins in addition to reducing grain yield, which needs further study.

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