DISEASE NOTES

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First Report of *Fusarium hostae* Causing Crown Rot on Wheat in Azerbaijan

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In June 2017, 76 fields were surveyed in the main bread wheat (*Triticum aestivum* L.) and durum wheat (*Triticum durum* Desf.) growing regions of Azerbaijan to identify the fungi causing crown and root rot. Diseased plants were collected at just prior to maturity, at maturity, and/or after harvest. About 20 to 30 tillers of wheat were randomly sampled from each field (about 5 ha), put in paper bags, and transported to the laboratory. The crown, root, and stem base tissues of each plant were rinsed with tap water to remove soil particles and examined for lesions. Sections (3 cm) of symptomatic tissues were surface disinfested with 1% NaOCl for 1 min, rinsed with sterile distilled water, and air dried on sterilized filter paper in a laminar flow. Dried sections were cut into 1-cm lengths and placed on 1/5

strength potato dextrose agar (PDA) amended with streptomycin (0.1 g/liter) and chloramphenicol (0.05 g/liter). Following 5 days of incubation in the dark at 20°C, *Fusarium*-like colonies were purified using the single spore isolation method and then transferred onto PDA and Spezieller-Nährstoffarmer agar and then incubated at 20°C for 10 days to evaluate for conidia and chlamydospores (**Leslie and Summerell 2006**). The EF1/EF2 primers described by **O'Donnell et al. (1998)** were used to amplify the translation elongation factor 1-alpha (EF1-α) locus of putative *Fusarium* spp. isolates. Amplified DNA was subjected to bidirectional sequencing (Macrogen, Seoul, Korea). Morphological and molecular assays revealed that out of the 439 *Fusarium* spp. isolates, 11 isolates from six fields in Ismailli and Oguz locations were identified as *Fusarium hostae*. Nucleotide BLAST similarity analysis of the sequences of two reference isolates showed 99 to 100% homology with the EF1-α sequence of *F. hostae* strain NRRL 29889 (AY329034), and they were deposited in GenBank (accession nos. MK577923 and MK590116). Isolates were white to purplish with aerial mycelial growth on PDA. Microconidia (n = 50) were hyaline, oval to kidney shaped, usually aseptate and rarely with one transverse septum, and measured 2.1 to 3.9 × 4.7 to 10.6 µm, and macroconidia (n = 50) were abundant, hyaline, fusiform, with a foot-shaped basal cell, with two to four septa (generally three), and measured 2.9 to 4.8 × 24.2 to 46.2 µm. To test for pathogenicity of *F. hostae* on wheat, five pregerminated seeds of cultivar Seri 82 were placed onto a sterile mixture substrate of peat, vermiculite, and soil (1:1:1, v/v/v) in 9-cm-diameter plastic pots (17 cm long). The inoculation was performed by placing the actively growing mycelial plugs (1-cm diameter) removed from cultures of the reference isolates and covering with the mixture substrate. Sterile agar plugs were used for controls. Inoculated pots were placed in a growth chamber with a 12-h photoperiod at 24°C. The pathogenicity test was repeated two times for each isolate. Six weeks postinoculation, crown browning and necrosis occurred in the inoculated plants, whereas no symptoms were observed in the control plants. The pathogen was reisolated from the crowns of diseased plants and identified by the method described above to fulfill Koch's postulates. To our knowledge, this is the first report of *F. hostae* causing crown rot on wheat in Azerbaijan. Although *F. hostae* may still be considered a minor pathogen in Azerbaijan, it is important to include it in the *Fusarium* species complex that causes crown rot in wheat. This pathogen was isolated from all regions surveyed in Turkey (**Shikur Gebremariam et al. 2016**), which indicates that it has the potential to spread to noncontaminated wheat cultivation areas. Further studies are needed to better understand the role of the pathogen in the disease-causing complex.

The author(s) declare no conflict of interest.

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