Disease Note

Diseases Caused by Fungi and Fungus-Like Organisms

First Report of *Fusarium commune* Causing Root and Crown Rot on Maize in Italy

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Maize (*Zea mays* L.) is a cereal crop of great economic importance in Italy; production is currently of 62,587,469 t, with an area that covers 628,801 ha, concentrated in northern Italy (ISTAT 2020). *Fusarium* species are associated with root and crown rot, causing failures in crop establishment under high soil moisture. In 2019 maize seedlings collected in a farm located in San Zenone degli Ezzelini (VI, Italy) showed root and crown rot symptoms with browning of the stem tissues, wilting of the seedling, and collapsing due to the rotting tissues at the base of the stem. The incidence of diseased plants was approximately 15%. Seedlings were cleaned thoroughly from soil residues under tap water. Portions (about 3 to 5 mm) of tissue from roots and crowns of the diseased plants were cut and surface disinfected with a water solution of NaClO at 0.5% for 2 min and rinsed in sterile H_2O. The tissue fragments were plated on potato dextrose agar (PDA) amended with 50 mg/liter of streptomycin sulfate and incubated for 48 to 72 h at 25°C. Over the 80 tissue fragments plated, 5% were identified as *Fusarium verticillioides*, 60% as *Fusarium* spp., and 35% developed saprophytes. *Fusarium* spp. isolates that showed morphological characteristics not belonging to known pathogenic species on maize were selected and used for further investigation, whereas species belonging to *F. oxysporum* were discarded. Single conidia of the *Fusarium* spp. colonies were cultured on PDA and carnation leaf agar (CLA) for pathogenicity tests, morphological identification, and molecular identification. The colonies showed white to pink, abundant, densely floccose to fluffy aerial mycelium. Colony reverse showed light violet pigmentation, in rings on PDA. On CLA the isolates produced slightly curved macroconidia with three septa 28.1 to 65.5 µm long and 2.8 to 6.3 µm wide (n = 50). Microconidia were cylindrical, aseptate, 4.5 to 14.0 µm long and 1.5 to 3.9 µm wide (n = 50). Spherical chlamydospores were 8.8 ± 2.5 µm size (n = 30), produced singly or in pairs on the mycelium, according to the description by Skovgaard et al. (2003) for *Fusarium commune*. The identity of two single-conidia strains was confirmed by sequence comparison of the translation elongation factor-1α (*tef-1α*) and RNA polymerase II subunit (*rpb2*) gene fragments (O'Donnell et al. 2010). BLASTn searches of GenBank and the *Fusarium*-ID database, using the partial *tef-1α* (MW419921, MW419922) and *rpb2* (MW419923, MW419924) sequences of representative isolates DB19lug07 and DB19lug20, revealed 99% identity for *tef-1α* and for *rpb2* to *F. commune* NRRL 28387(AF246832, JX171638). Pathogenicity tests were carried out by suspending conidia from a 10-day-old culture on PDA in sterile H_2O to 5×10^4 CFU/ml. Fifty seeds were immersed in 50 ml of the conidial suspension of each isolate for 24 h and in sterile water (Koch et al. 2020). The seeds were drained, dried at room temperature, and sown in trays filled with a steamed mix of white peat and perlite, 80:20 v/v, and maintained at 25°C and relative humidity of 80 to 85% for 14 days with a 12-h photoperiod. Seedlings were extracted from the substrate, washed under tap water, and observed for the presence of root and crown rots like the symptoms observed on the seedlings collected in the field. Control seedlings were healthy, and *F. commune* was reisolated from the symptomatic ones and identified by resequencing of *tef-1α* gene. *F. commune* has been already reported on maize (Xi et al. 2019) and other plant species, such as soybean (Ellis et al. 2013), sugarcane (Wang et al. 2018), and potato (Osawa et al. 2020), indicating that some attention must be paid in crop rotation and residue management strategies. To our knowledge this is the first report of *F. commune* as a pathogen of maize in Italy.

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