Diseases Caused by Fungi and Fungus-Like Organisms

First Report of Wilt on Lentil (*Lens culinaris*) Caused by *Fusarium redolens* in Tunisia

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Lentil (*Lens culinaris* Medik.) is widely grown in arid and semiarid regions of Tunisia. Low yields are often attributed to it being grown on marginal agricultural land. Since 2016, symptoms of wilt including yellowing and discoloration of the stem and root tissues were observed in lentils in several region of Tunisia. The annual mean incidence of infected plants ranged from 10 to 15%. In the 2019 to 2020 growing seasons, symptomatic adult plants were randomly sampled from two fields in south Tunisia (33°37'N; 11°4'E and 33°33'N; 11°2'E), and one field in northwest Tunisia (36°7'N; 8°43'E). Pieces were cut from roots and stem, surface sterilized, and plated on 1/4-strength potato dextrose agar (PDA) + 100 mg liter⁻¹ streptomycin sulfate (Burgess et al. 1994). Cultures were incubated for 5 to 6 days. Nine colonies with floccose mycelia, sparse or abundant, white to violet in color, and morphologically similar to *Fusarium redolens* according to Leslie and Summerell (2006) were isolated from both roots and stems. They were single-spored (Burgess et al. 1994). Microconidia were formed in false heads on short monophialides. They were oval to elliptical or reniform and were 0 to 1 septate. Three-septate macroconidia with short apical cells were also observed. The strains were deposited in the microbial ITEM Collection of the Institute of Sciences of Food Production. Extraction of genomic DNA of *Fusarium* sp. strains was carried out according to Wizard Magnetic DNA Purification System (Promega, Fitchburg, WI, U.S.A.). Molecular identification

was carried out based on translation elongation factor (TEF) gene sequencing, as described in Fallahi et al. (2019). The TEF sequences were searched on GenBank database using the Basic Local Alignment Search Tool (BLAST). The sequences of four strains (Z2P6, Z2P7, Z3P2, and Z3P5) from a total of nine recovered from lentil roots from the two fields of south Tunisia showed 100% homology with TEF sequences of the epitype culture of *F. redolens* NRRL25600 (accession no. MT409453) (Balmas et al. 2010; Gargouri et al. 2020). Sequences of the strains were submitted to GenBank with accession numbers MW393853, MW393854, MW393856, and MW393857. Pathogenicity of the four strains of *F. redolens* was evaluated on the 'Kef' lentil variety (Kharrat et al. 2007). Inoculum was produced on sterilized oats colonized with each strain. The colonized grains were air-dried on filter paper, ground in a laboratory mill, mixed at 10% to soil (10 g of each isolate inoculum for 100 g of disinfected soil substrate) and potted. Three germinated lentil seeds were placed in each pot and irrigated periodically. The test was replicated four times. After 21 days, 60% (33 to 100%) of the plants inoculated with the four *F. redolens* strains showed symptoms of wilting, yellowing, and rotting of roots and 17% died when inoculated by the Z2P6 and Z2P7 strains. Noninoculated plants showed no symptoms. *F. redolens* was isolated from 100% of the inoculated plants' roots. This is the first report of *F. redolens* as a pathogen on lentil in Tunisia. This species has also been associated with lentil wilting in other regions of the world, including Italy (Riccioni et al. 2008), Canada (Taheri et al. 2011), and Pakistan (Rafique et al. 2020). *F. redolens* was previously reported from wilted chickpea crops in Tunisia (Bouhadida et al. 2017). These findings are important for the Tunisian national legumes program and call for larger surveys to better understand the biology and ecology of this species and to prevent the disease from spreading.

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