Diseases Caused by Fungi and Fungus-Like Organisms

First Report of *Fusarium falciforme* (FSSC 3 + 4) Causing Root Rot on Chickpea in Mexico

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Chickpea (*Cicer arietinum* L.) is a legume crop of great importance worldwide. In January 2019, wilting symptoms on chickpea (stunted growth, withered leaves, root rot, and wilted plants) were observed in three fields of Culiacán, Sinaloa, Mexico, with an incidence of 3 to 5%. To identify the cause, 80 symptomatic chickpea plants were sampled. Tissue from roots was plated on potato dextrose agar (PDA) medium. Typical *Fusarium* spp. colonies were obtained from all root samples. Ten pure cultures were obtained by single-spore culturing (Ff01 to Ff10). On PDA the colonies were abundant with white aerial mycelium, hyphae were branched and septate, and light purple pigmentation was observed in the center of old cultures (Leslie and Summerell 2006). From 10-day-old cultures grown on carnation leaf agar medium, macroconidia were falciform, hyaline, with slightly curved apices, three to five septate, with well-developed foot cells and blunt apical cells, and measured 26.6 to 45.8 × 2.2 to 7.0 μm ($n = 40$). The microconidia ($n = 40$) were hyaline, one to two celled, produced in false heads that measured 7.4 to 20.1 (average 13.7) μm × 2.4 to 8.9 (average 5.3) μm ($n = 40$) at the tips of long monophialides, and were oval or reniform, with apices rounded, 8.3 to 12.1 × 1.6 to 4.7 μm; chlamydospores were not evident. These characteristics fit those of the *Fusarium solani* (Mart.) Sacc. species complex (FSSC)

(Summerell et al. 2003). The internal transcribed spacer and the translation elongation factor 1 alpha (EF1- α) genes (O'Donnell et al. 1998) were amplified by polymerase chain reaction and sequenced from the isolates Ff02 and Ff08 (GenBank accession nos. KJ501093 and MN082369). Maximum likelihood analysis was carried out using the EF1- α sequences (KJ501093 and MN082369) from the Ff02 and Ff08 isolates and other species from the FSSC. Phylogenetic analysis revealed the isolate most closely related to *Fusarium falciforme* (100% bootstrap). For pathogenicity testing, a conidial suspension (1×10^6 conidia/ml) was prepared by harvesting spores from 10-day-old cultures on PDA. Twenty 2-week-old chickpea seedlings from two cultivars (P-2245 and WR-315) were inoculated by dipping roots into the conidial suspension for 20 min. The inoculated plants were transplanted into a 50-hole plastic tray containing sterilized soil and maintained in a growth chamber at 25°C, with a relative humidity of >80% and a 12-h/12-h light/dark cycle. After 8 days, the first root rot symptoms were observed on inoculated seedlings, and the infected plants eventually died within 3 to 4 weeks after inoculation. No symptoms were observed on plants inoculated with sterilized distilled water. The fungus was reisolated from symptomatic tissues of inoculated plants and was identified by sequencing the partial EF1- α gene again and was identified as *F. falciforme* (FSSC 3 + 4) (O'Donnell et al. 2008) based on its morphological characteristics, genetic analysis, and pathogenicity test, fulfilling Koch's postulates. The molecular identification was confirmed via BLAST on the *Fusarium*-ID and *Fusarium* MLST databases. Although FSSC has been previously reported causing root rot in chickpea in the United States, Chile, Spain, Cuba, Iran, Poland, Israel, Pakistan, and Brazil, to our knowledge this is the first report of root rot in chickpea caused by *F. falciforme* in Mexico. This is important for chickpea producers and chickpea breeding programs.

References

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