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Maize Stalk Rot caused by *Fusarium falciforme* (FSSC 3 + 4) in Mexico.

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Stalk rot caused by *Fusarium* spp. is one of the most destructive diseases in maize growing regions worldwide. This disease causes damage to the vascular bundles and may affect absorption and translocation of water and nutrients, thereby reducing photosynthesis and grain development, and resulting in premature plant death (Li et al. 2010). Maize plants showing necrotic regions of the internal stalk tissues were collected from a field in Culiacan, Sinaloa, Mexico in May 2018. Thirty samples were surface-disinfested in 75 % ethanol for 20 s and 0.3% NaClO for 2 min, then rinsed with sterile distilled water, and cultured on potato dextrose agar (PDA). After incubation for 5 days at 28 °C in the dark, fungal colonies with morphological characteristics of *Fusarium* spp. were observed. Monosporic isolates were obtained by transferring single spores to PDA and identified to species level based on morphological characteristics and DNA sequence analysis of translation elongation factor-1α (EF1-α) gene. White to cream-colored aerial mycelium of *Fusarium* colonies were observed on all cultures on PDA (Leslie and Summerell 2006). From 10-day-old cultures grown on carnation leaf agar medium, macroconidia were falciform, hyaline, with 4-5 septa and measured 41.6-55.7 x 6.5-8.1 µm (n = 50); microconidia were hyaline, unicellular, oblong, with zero to two septa, measured 9.6 to 14.9 × 4.0 to 6.3 µm (n = 50), and were borne in false heads that measured 7.8-16.9 x 2.1-4.8 µm (n = 50); chlamydospores were not observed. The EF1-α gene was amplified by PCR and sequenced using the primers EF-1/EF-2 (O'Donnell et al. 1998). The sequence from the isolate C4M20T was deposited in the GenBank (accession no. MK887202). Phylogenetic analysis by the Neighbor-Joining method was carried out using the EF1-α sequence (MK887202) from the C4M20T isolate and other species from the *Fusarium solani* Species Complex (FSSC). Phylogenetic analysis revealed the isolate was most closely related with *F. falciforme* (FSSC 3 + 4) (100% bootstrap). The molecular identification was confirmed via BLAST on the FUSARIUM ID

and *Fusarium* MLST databases. Pathogenicity tests with isolate C4M20T were done by individually inoculating thirty 10-leaf-stage maize plants at the second or third internode above the soil line using 20 µl of conidia suspension at a concentration of 10^6/ml as described by Zhang et al. (2016). Ten maize plants inoculated with sterilized water were used as a control. Plants were maintained for 60 days under greenhouse conditions with a 12-h photoperiod at 22 to 26°C and 70% relative humidity. After 20 days, all inoculated plants developed internal dark brown necrotic regions around the inoculated site. No symptoms were observed on the control plants after 60 days. The assay was conducted twice. The pathogen was reisolated from the necrotic tissue from inoculated plants and was identified by sequencing the partial EF1-α gene again as *F. falciforme* (FSSC 3 + 4) (O'Donnell et al. 2008). Although FSSC has been previously reported in maize causing ear rot in Estado de México, Mexico (Morales-Rodriguez et al. 2007) and Malaysia (Mohd-Zainnudin et al. 2017), to our knowledge, this is the first report of maize stalk rot caused by *Fusarium falciforme* in Mexico. Therefore, further studies should focus on the epidemiology to evaluate the impact of the disease on yield and identify the risk factors.

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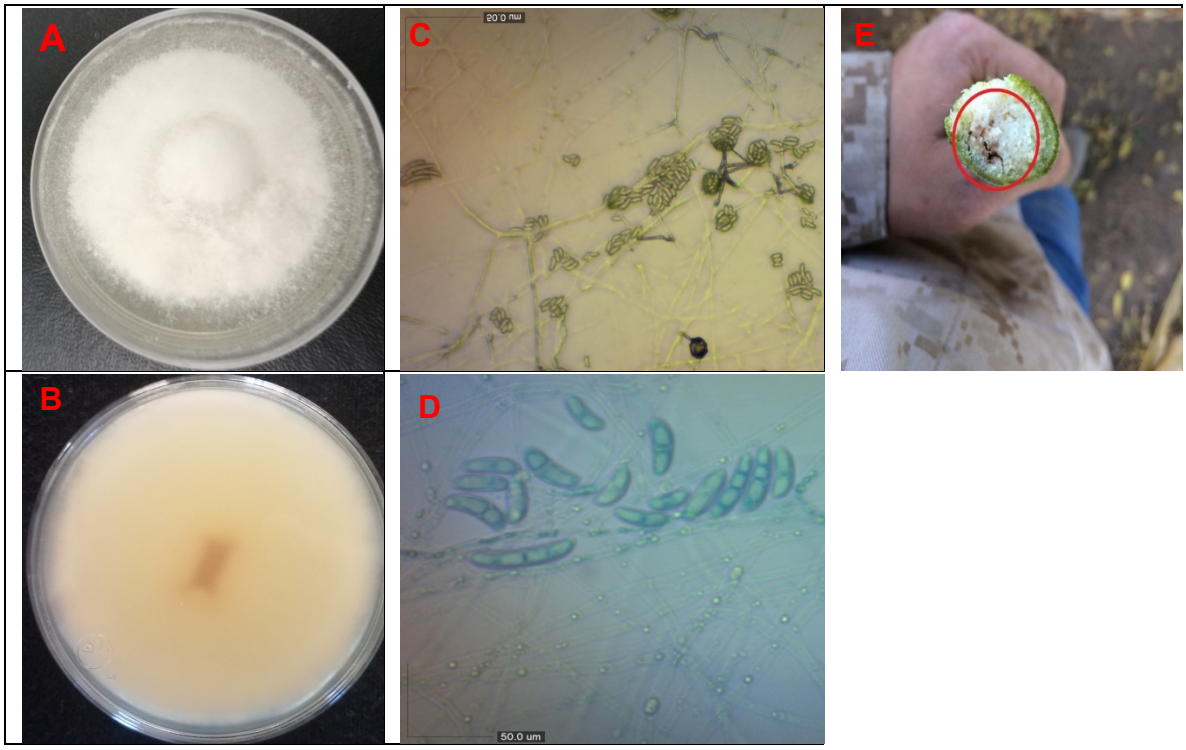

Figure 1.- *Fusarium falciforme* morphological features. A-B: Culture on PDA; C: Microconidias *in situ* (50 µm bar); D: Macroconidias (50 µm bar); E: Maize plant showing necrotic regions of the internal stalk tissues.

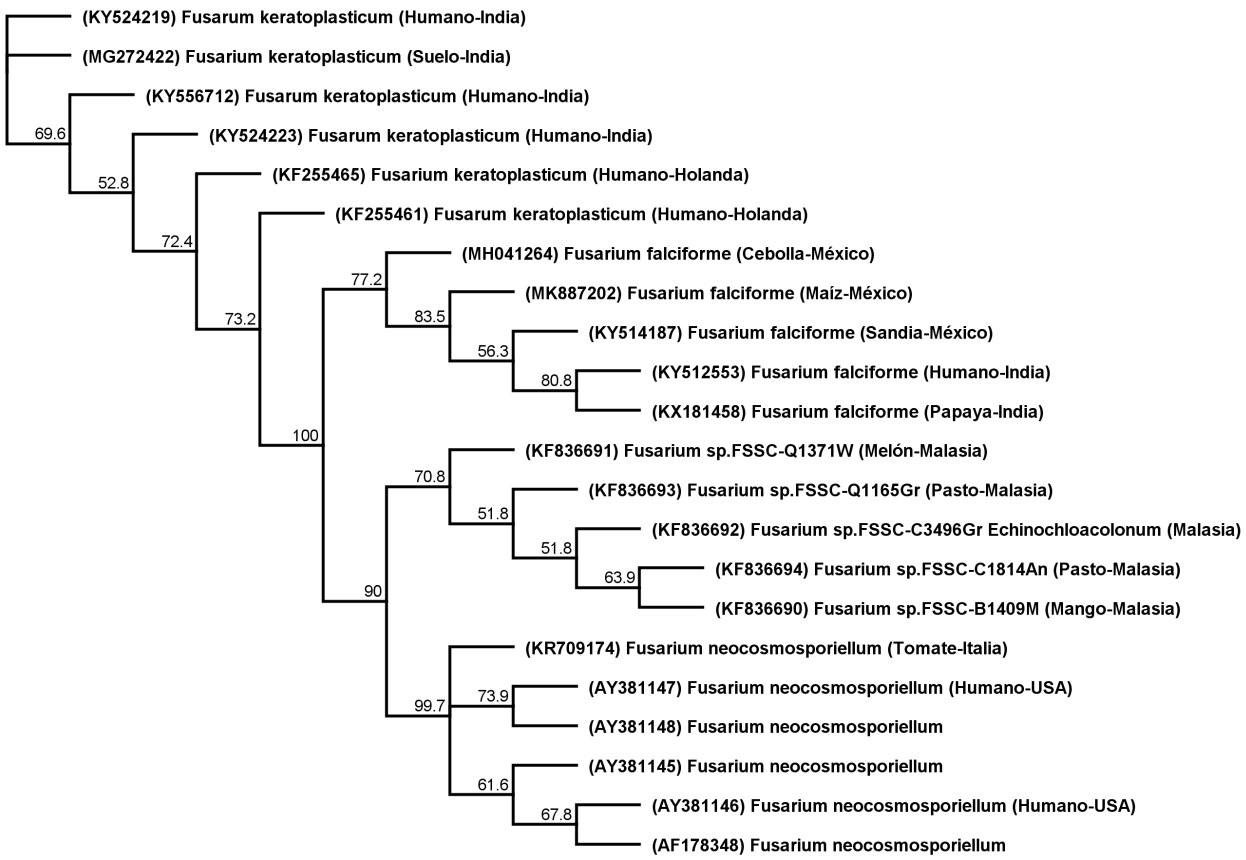

Figure 1. Phylogram of Neighbor Joining for EF-1α gene from isolates from the *Fusarium solani* Species Complex. Values at the nodes represent the percentage bootstrap scores (1000 replicates). Sequence MK887202 (isolate C4M20T) is from this study.