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DISEASE NOTES

First Report of Onion Basal Rot Caused by *Fusarium falciforme* in Mexico

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Basal rot is one of the most destructive diseases in onion (*Allium cepa*) growing regions worldwide. This disease can reduce crop yields by interfering with the absorption and translocation of water and nutrients, causing premature plant death ([Delgado-Ortíz et al. 2016](#)). In August 2016, unusual disease symptoms were observed in commercial onion crops (cv. Carta Blanca) within municipality of Angostura (Sinaloa, Mexico). These included yellowish and chlorotic leaves from the tip, progressively developing downward, dwarfing in the plants, soft consistency in bulbs, necrosis in the basal part of the bulb, and decrease in roots. Forty symptomatic onion plants were sampled. Tissue from roots and bulbs was plated on potato dextrose agar (PDA) medium. Typical *Fusarium* spp. colonies were obtained from all root and bulb samples. Three pure cultures were obtained by single-spore culturing (Fs05 to Fs07). On PDA the colonies were abundant white aerial mycelium, 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, three to five septate, with well-developed foot cells and blunt apical cells, and measured 27.3 to 46.3×2.1 to $7.1 \mu\text{m}$ ($n = 40$). The microconidia ($n = 40$)

were hyaline, one to two celled, oval or reniform, 8.2 to 12.3×1.6 to $4.8 \mu\text{m}$, and borne in false heads that measured 7.5 to 20 (average 13.75) $\mu\text{m} \times 2.3$ to 9.0 (average 5.3) μm ($n = 40$); chlamydospores were not evident. 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 isolate Fs05 (GenBank accession nos. MH038177 and MH041264). Maximum likelihood analysis was carried out using the EF1- α sequence (MH041264) from the Fs05 isolate and other species from the *Fusarium solani* species complex (FSSC). Phylogenetic analysis revealed the isolate most closely related with *F. falciforme* (100% bootstrap). Pathogenicity tests were performed on onion plants (cv. Carta Blanca) grown on autoclaved vermiculite. Ten plants per isolate ($n = 3$) were inoculated by drenching with 20 ml of a conidial suspension (1×10^5 CFU/ml) of each isolate per plant. The suspension was obtained by collecting the spores of each isolate grown on PDA, with 10 ml of an isotonic saline solution. Ten noninoculated plants served as controls. Plants were maintained for 60 days under greenhouse conditions. The assay was conducted twice. Bulb rot and necrosis similar to those observed on the infected plants in the field were observed on the bulbs. The pathogen was reisolated from the necrotic tissue from all 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 FusariumID and *Fusarium* MLST databases. No symptoms were observed on noninoculated controls after 60 days. Although FSSC has been previously reported causing bulb rot in onion in Tukey, Japan, and Iran, to our knowledge this is the first report of basal rot in onion caused by *F. falciforme* in Mexico. This is important for onion producers and the *Fusarium* worldwide community. Also, *Fusarium* mycotoxin contamination of onion bulb could pose a public health risk.

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Section:

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