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First report of basal rot of onion caused by *Fusarium brachygibbosum* in Sinaloa, Mexico.

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Onion (*Allium cepa*) is an important food crop in Mexico, with an estimated production of 1.635 million metric tons in 2016. In August 2016, two-month old commercial onion plants (cv. Carta Blanca) within municipality of Sinaloa de Leyva (Sinaloa, Mexico) showed symptoms of wilting without leaf yellowing and stunting of plants. Diseased plants exhibited severe necrosis that advanced through the main root causing a visible bulb rot, causing death of onion plants. Twenty symptomatic onion plants were sampled. Diseased tissue from roots and bulbs were plated on potato dextrose agar (PDA) media. One pure culture was obtained by single-spore culturing (FB20). White colonies with abundant aerial mycelium produced red pigmentation on PDA. From 10-day-old culture grown on CLA media, macroconidia were slightly curved, mostly five marked septa, wide central cells, slightly sharp apexes, basal cells with foot-like shape, and measuring 20.3 ± 4.4 µm × 3.3 ± 0.4 µm (n = 50). Microconidia were rarely observed on either PDA or CLA. Spherical chlamydospores with 6.8 ± 0.4 µm × 5.5 ± 0.7 µm (n = 50) were produced from mycelium in all isolates. These structures were intercalary or terminal, single, and in chains. Morphological characteristics of the isolates were similar to the features of *Fusarium brachygibbosum* previously described by Padwick (1945). Molecular identification was performed by partial sequences of *EF1-α* gene (EF1 and EF2 primers) (O'Donnell et al. 2010) and rDNA-ITS (ITS1 and ITS4 primers) (White et al. 1990). Blast search in the Fusarium ID showed that *EF1-α* were 96 % similar to the corresponding gene sequence of Fusarium *brachygibbosum* strain NRRL34033 (accession no. GQ505418) and 100 % similar with the ITS sequence with this same strain. Also, the GenBank blast showed that *EF1-α* were 96 % similar to the corresponding gene sequence of the isolate HN-1 (KX984345). And the ITS sequence was 100 % similar to the corresponding gene sequence of *F. brachygibbosum* strain FbDAG47 (KX583250) (Renteria-Martinez et al. 2015). Pathogenicity tests were performed on onion plants (cv. Carta Blanca) grown on autoclaved vermiculite. 40-day-old onion plants (n = 20) (cv. Carta Blanca) were inoculated by drenching with 20 ml of a conidial suspension (1×10^5 conidia/ml) 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 plants inoculated with sterilized water served as controls. Plants were maintained for 60 days under greenhouse conditions with a 12-h photoperiod at 22 to 26 ^{o}C and 70 % relative humidity. The assay was conducted twice. Bulb rot and necrosis similar to the one observed on the infected plants in the field was observed on the bulbs. The pathogen was reisolated from the necrotic tissue from all inoculated plants and was identified by sequencing partial *EF1-α* gene again. No symptoms were observed on noninoculated controls after 60 days. To our knowledge, this is the first report of basal rot in onion caused by *Fusarium brachygibbosum* in the world. This is very important for onion producers and *Fusarium* worldwide community. 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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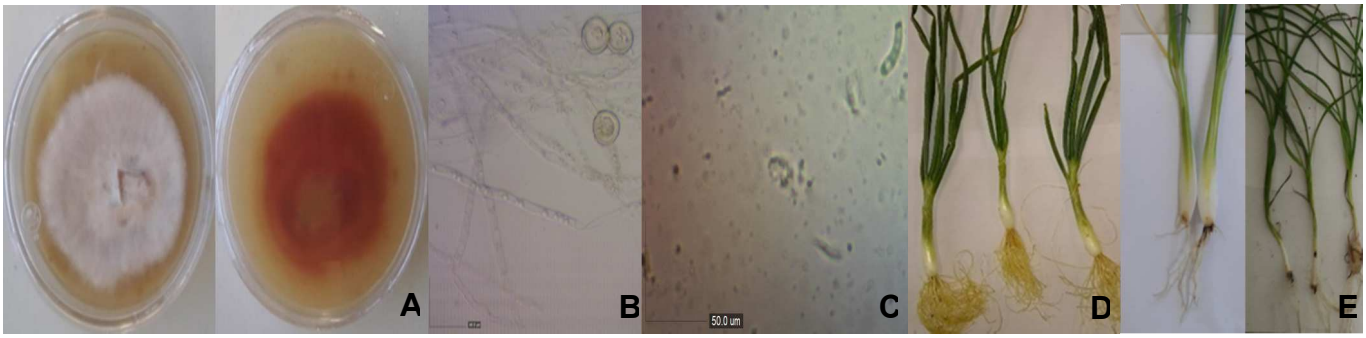

Fig. 1. The morphological characteristics and symptoms on onion bulbs associated with *Fusarium brachygibbosum*. (A) Colony morphology on potato dextrose agar (PDA) (front and reverse). (B) Spherical chlamydosphores. (C) Macroconidia. (D) Healthy onion bulbs (control). (E) Necrosis in the basal part of bulbs and decrease in roots caused by *Fusarium brachygibbosum*.