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## DISEASE NOTES



## ***Fusarium falciforme* (FSSC 3 + 4) Causing Root and Stem Rot in Papaya (*Carica papaya*) in Mexico**

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Mexico is the third largest producer of papaya in the world with an estimated production of 961,768 metric tons per year ([FAOSTAT 2017](#)). In July 2018, in the center zone of Sinaloa State (Mexico) (24°36'38"N; 107°15'04" W), papaya trees in the production stage were observed with an incidence (10%) of root and stem rot with reddish-dark coloration and necrotic tissue. Symptomatic tissues were collected from 10 papaya plants, which were cut into small pieces and surface sterilized sequentially with 70% alcohol for 20 s and 1% sodium hypochlorite for 2 min, dried, placed on potato dextrose agar (PDA), and incubated at 26°C in darkness for 5 days. Ten monosporic cultures were morphologically characterized on PDA and carnation leaf agar (CLA) media. On PDA, aerial mycelium was abundant white to cream colored, and light pink pigmentation was observed in the center of old cultures. From 10-day-old cultures grown on CLA medium, macroconidia were falciform with three septa, hyaline, with well-developed foot cells and blunt apical cells, and measured 23.7 to 51.2 × 2.8 to 6.9 µm ( $n = 40$ ). The microconidia ( $n = 40$ ) were hyaline, with zero to two septa, oval or reniform, 4.8 to 11.2 × 2.4 to

4.4  $\mu\text{m}$ , and borne in false heads that measured  $7.3$  to  $19.2 \times 3.5$  to  $6.0 \mu\text{m}$  ( $n = 40$ ); chlamydospores were not evident. The translation elongation factor 1 alpha (EF1- $\alpha$ ) gene (O'Donnell et al. 1998) was amplified by polymerase chain reaction and sequenced from the isolate FfscSINCUL (GenBank accession no. MK863033). Maximum likelihood analysis was carried out using the EF1- $\alpha$  sequence (MK863033) from the FfscSINCUL 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 60-day-old papaya plants (cultivar Maradol) grown on autoclaved sandy loam soil mix. Ten plants per isolate ( $n = 3$ ) were inoculated by drenching with 20 ml of a conidial suspension ( $1 \times 10^5$  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 (25 to 30°C). The assay was conducted twice. Root and stem rot similar to that observed on the infected plants in the field was observed on the papaya plants. No symptoms were observed on noninoculated control plants after 60 days. The pathogen was reisolated from the necrotic tissue from all inoculated plants and was identified again as *F. falciforme* (FSSC 3 + 4) (O'Donnell et al. 2008) by sequencing the partial EF1- $\alpha$  gene again and 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. The isolate FfscSINCUL was deposited in the fungal collection of the Faculty of Agronomy of the Autonomous University of Sinaloa. Although FSSC has been previously reported causing papaya stem rot in Brazil (Correia et al. 2013), this is the first report of root and stem rot of papaya caused by *F. falciforme* in Mexico. *F. falciforme* was previously reported in Mexico causing foot rot and wilt in tomato (Vega-Gutiérrez et al. 2019) and basal rot in onion (Tirado-Ramírez et al. 2018). Papaya is an important fruit crop in Mexico, and the occurrence of this disease needs to be taken into account in papaya production.

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The author(s) declare no conflict of interest.

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