Disease Note

Diseases Caused by Fungi and Fungus-Like Organisms

Fusarium verticillioides Causing Root and Stem Rot in Papaya (*Carica papaya*) in Mexico

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Mexico is the fifth-largest producer of papaya in the world with an estimated production of 1,134,753 metric tons per year (FAOSTAT 2022). In February 2022, in the center zone of Sinaloa State (Mexico), in a seedling-producing greenhouse, papaya seedlings were observed with an incidence (20%) of root and stem rot and necrotic tissue. Symptomatic tissues were collected from 10 papaya plants, which were cut into small pieces, 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 the dark for 5 days. Typical *Fusarium* spp. colonies were obtained from all root samples. Ten pure cultures were obtained by single-spore culturing and morphologically characterized on PDA and carnation leaf agar (CLA) media. On PDA, the colonies produced abundant white aerial mycelium, and the center of old cultures had yellow pigmentation (Leslie and Summerell 2006). Ten-day-old cultures grown on CLA medium produced slightly curved macroconidia, which showed zero to three septa, with some slightly sharp apices and basal cells with notches; the measurements were from 22.53 to 48.94 × 6.9 to 13.73 µm (n = 50). The microconidia were abundant, presented thin walls, and were oval and hyaline in shape, forming long chains and measuring 10.4 to 14.25 × 2.4 to 6.8 µm (n = 50). Chlamydospores were not observed. The translation elongation factor 1-alpha (*EF1-α*) gene (O'Donnell et al. 1998) was amplified by polymerase chain reaction and sequenced from the isolate FVTPPYCULSIN (GenBank accession no. OM966892). Maximum likelihood analysis was carried out using the *EF1-α* sequence (OM966892) and other species from the genus *Fusarium*. Phylogenetic analysis revealed that the isolate was *Fusarium verticillioides* (100% bootstrap). Furthermore, the isolate FVTPPYCULSIN was 100% similar with another reported *F. verticillioides* sequence (GenBank accession no. MN657268; Dharanendra Swamy et al. 2019). Pathogenicity tests were performed on 60-day-old papaya plants (cv. Maradol) grown on autoclaved sandy loam soil mix. Ten plants per isolate (n = 10) 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 (25 to 30°C). The assay was conducted twice. Root and stem rot similar to that observed on the infected plants in the greenhouse 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 of all inoculated plants and was identified again as *F. verticillioides* by sequencing the partial *EF1-α* 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 FVTPPYCULSIN was deposited in the fungal collection of the Faculty of Agronomy of the Autonomous University of Sinaloa. To our knowledge, this is the first report of root and stem rot of papaya caused by *F. verticillioides*. Papaya is an important fruit crop in Mexico, and the occurrence of this disease needs to be taken into account in papaya production.

References:

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