

## Diseases Caused by Fungi and Fungus-Like Organisms

### First Report of Mango Malformation Disease Caused by *Fusarium proliferatum* in Mexico

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Mango (*Mangifera indica* L.) is the most economically important fruit in the tropical and subtropical regions of the world. Mexico is ranked the fourth largest mango producer worldwide with an approximate production of 2,396,675 t in 2019 (FAOSTAT 2020). Sinaloa is the principal mango production state in Mexico with 410,147 t in 2020 (SIAP 2021). Mango malformation disease (MMD) is one of the main limitations in the production of this crop worldwide, causing serious losses in yield. During December 2017 to April 2018, symptoms of MMD were observed in commercial mango in the municipality of El Rosario (Sinaloa, Mexico). These symptoms included malformed and compacted inflorescences, and abnormal development of vegetative shoots with shortened internodes at an incidence of 25%. Tissue samples from 15 symptomatic trees were superficially disinfested with 2% sodium hypochlorite and transferred to potato dextrose agar (PDA). Typical *Fusarium* spp. colonies were obtained from all samples. Fifteen pure cultures were obtained by single-spore culturing. White to cream-colored aerial mycelia of typical *Fusarium* colonies were observed from all samples on PDA (Leslie and Summerell 2006). From 10-day-old cultures grown on carnation leaf agar medium, macroconidia ( $n = 50$ ) were hyaline, relatively slender with a curve, four to five septate, and measured  $39.5$  to  $76.8 \times 5.7$  to  $9.5 \mu\text{m}$ . The microconidia ( $n = 50$ ) were hyaline and pyriform, without septa, and measured

$8.1$  to  $10.6 \times 5.1$  to  $6.9 \mu\text{m}$ . Chlamydospores were observed. The EF1- $\alpha$  gene (O'Donnell et al. 1998) was amplified by PCR and sequenced from the isolates. The EF1- $\alpha$  sequence from one representative isolate (128FRSIN) was deposited in GenBank with the accession number MK932806. Maximum-likelihood analysis was carried out using the representative EF1- $\alpha$  sequence for *Fusarium proliferatum* (MK932806) and other *Fusarium* species. Phylogenetic analysis revealed the isolate most closely related was *F. proliferatum* (100% bootstrap). The molecular identification was also confirmed via BLAST on the Fusarium ID and Fusarium MLST databases. The pathogenicity tests were carried out on healthy 3-month-old mango plants. Twenty plants and five shoots per plant were inoculated with  $20 \mu\text{l}$  of the conidial suspension ( $1 \times 10^6$  conidia/ml) (Freeman et al. 1999). Twenty plants served as noninoculated controls. Plants were maintained for 365 days under greenhouse conditions ( $25$  to  $30^\circ\text{C}$ ). The assay was conducted twice. Symptoms of multiple vegetative shoots and shortened internodes were observed 4 months after inoculation on the infected plants with an average disease of 4.5 in the first trial and 4.4 in the second assay according to the disease severity scale outlined by Iqbal et al. (2006). No symptoms were observed on noninoculated control plants after 365 days. One isolate per plant was isolated again from the plants with malformation symptoms ( $n = 20$ ) and was identified again as *F. proliferatum* by morphological and molecular characteristics. *F. proliferatum* was identified as the causal agent of MMD in China by Zhan et al. (2010). To our knowledge, this is the first report of *F. proliferatum* causing MMD in Mexico. The development of management strategies to prevent crop loss is required in this important mango production area.

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