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First Report of the Root-Knot Nematode *Meloidogyne enterolobii* Parasitizing Watermelon from Veracruz, Mexico

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Disease Notes

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In early April 2012, a sampling of watermelon crop *Citrullus lanatus* (Thunb.) Matsum & Nakai, 1916 cv. Sunsugar took place as part of the National System of Epidemiological Phytosanitary Surveillance (SINAVEF-MEX). This sampling was conducted at Riachuelos locality, Tecolutla, Veracruz, located at the geographic coordinates: 20.42008° N and 96.9627° W, within 50 meters of the Gulf of Mexico. Plants showed yellowing, stunting, and high levels of infection expressed by extensive galling on the roots. These symptoms were reproduced in the greenhouse on watermelon cv. Sunsugar. Egg masses were extracted to obtain juveniles (J2). Female necks and perineal patterns were mounted as well as males and J2 to take measurements of selected morphometric characters. To determine the nematode identity based on a morphological species concept, the following characters were considered. Females: stylet length, DGO and perineal pattern; males: stylet length; J2: body, stylet, tail, and hyaline tail terminus length. The morphometric analysis showed that those values corresponded to the original description of the root-knot nematode *Meloidogyne enterolobii* Yang & Eisenback, 1983 (=*M. mayaguensis* Rammah & Hirschmann, 1988) (1,2,3,4). For confirmation of this finding, a molecular diagnosis was

performed using markers located in rDNA and mtDNA by PCR amplification and DNA sequencing. The rDNA region analyzed was the expansion segments D2-D3 of the 28S gene (primers D2A and D3B). This produced an amplified product of 780 bp. With regard to mtDNA, an amplification of the marker located between the genes COII/16S (primers C2F3 and 1108) resulted in a fragment of 705 bp that is specific for *M. enterolobii* (1). Sequences of the amplified products were compared with sequences from GenBank (NCBI). The sequences of both markers exhibited 99 and 100% identity with sequences corresponding to *M. enterolobii* isolates from Florida, Puerto Rico, and China. Maximum likelihood phylogenetic trees of rDNA and mtDNA sequences demonstrated that the Mexican isolate of *M. enterolobii* grouped among other isolates exclusive of other *Meloidogyne* species. The detection of this nematode in Veracruz, Mexico, expands the previously known worldwide distribution. It represents a serious threat due to the high level of aggressiveness shown in watermelon, which was so severe that growers had to change to a different crop. To our knowledge, this is the first report of the root-knot nematode *M. enterolobii* infecting watermelon cv. Sunsugar in Veracruz, Mexico.

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