First Report of *Meloidogyne enterolobii* on *Ormosia hosiei* in China

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Ormosia hosiei is an evergreen tree that belongs to the family of Fabaceae. It is prized for its ornamental and medicinal value and rosewood. In November 2020, galls were observed on roots of stunted *O. hosiei* plants in the Nanning arboretum (22°43'38" N, 108°18'06" E), Guangxi, China. Disease incidence was approximately 80% (150 plants evaluated). Females were obtained by dissecting galls and second-stage juveniles (J2s) were collected from a single egg mass hatching. The female white body was pear to globular-shaped with a distinct neck region, while the perineal pattern usually was oval-shaped with a moderately high dorsal arch. J2 bodies were translucent with narrow tails and pointed tips, with hyaline tail termini. Those morphological characters were consistent with descriptions of *Meloidogyne enterolobii* (Brito et al. 2004; Yang and Eisenback 1983). Morphological measurements (mean, standard deviation, and range) of J2s ($n = 20$) included body length = 436.07 ± 12.5 (411.8 to 464.3) μm , body width = 16.01 ± 1.1 (14.6 to 17.7) μm , stylet length = 12.4 ± 0.8 (11.3 to 13.5) μm , dorsal esophageal gland orifice to the stylet base (DGO) = 3.8 ± 0.3 (3.3 to 4.3) μm , tail = 53.6 ± 4.3 (48.9 to 60.6) μm , and hyaline tail length = 15.9 ± 1.5 (13.6 to 18.3) μm . Measurements of females ($n = 20$) were: body length = 669.5 ± 43.8 (549.9 to 709.4) μm , body width = 641.9 ± 45.2 (559.3 to 732.8) μm , DGO = 5.3 ± 0.52 (4.6 to 6.1) μm , and stylet length = 14.9 ± 0.86 (13.8 to 16.8) μm . These measurements were also consistent with *M. enterolobii* (Yang and Eisenback 1983). The ITS rRNA gene sequence and D2-D3 expansion segment of 28S rDNA were amplified in the DNA of individual J2 using the primers 18S/26S (TTGATTACGTCCCTGCCCTT/TTTCACTCGCCGTTACTAAGG) and D2A/D3B (ACAAGTACCGTGAGGGAAAGT/TCGGAAGAACCACTACTA), respectively (Subbotin et al. 2006; Vrain

et al. 1992). The sequences were submitted in the NCBI with GenBank accession numbers MZ617284 (766 bp) and OK072889 (759 bp). The homology of the genes was 99 to 100% identical to that of *M. enterolobii* in ITS rRNA gene sequences MT406251, MG773551, and KF418369. The D2-D3 region of the 28S rRNA gene revealed 100% identity with *M. enterolobii* sequences from MT193450, MF467276, MZ541997, and so on. Neighbor-joining phylogenetic analysis showed that it was the most similar to *M. enterolobii*. For further confirmation, *M. enterolobii* species-specific primer pairs Me-F/Me-R (AACTTTTGTGAAAGTGCCGCTG/TCAGTTCAGGCAGGATCAACC) were used for amplification of the ribosomal intergenic spacer 2. An expected PCR fragment of approximately 236-bp was obtained (Long et al. 2006). A pathogenicity test was conducted in a greenhouse at 26 to 30°C. Eggs were multiplied in the greenhouse using a single eggmass hand-picked from infested *O. hosiei* roots. Twelve healthy 8-month-old *O. hosiei* seedlings were inoculated with 5,000 eggs/pot containing autoclaved soil mix (clay/substrate = 1:3, v/v), and six noninoculated seedlings were controls. After 10 weeks, the control plants displayed no symptoms. The roots of all inoculated plants showed galling symptoms. The reproduction factor (final population/initial population) was 5.2. Furthermore, the morphological and molecular identification of the nematode was identical to the original samples. *M. enterolobii* has a broad host range (Philbrick et al. 2020). To our knowledge, this is the first report of *M. enterolobii* parasitizing *O. hosiei* worldwide. This finding expands the host range of this nematode.

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