Diseases Caused by Nematodes

First Report of *Meloidogyne graminicola* on Tomato (*Solanum lycopersicum*) in Hainan, China

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Tomato (*Solanum lycopersicum*) is an important vegetable crop in Hainan Province, Southern China. In this area, rice and tomato rotation is the most common form of tomato cultivation. During March of 2021, in a field in Yazhou District, Sanya City, Hainan Province, leaves of some tomato plants (cv. Jinsheng) turned yellow, although no obvious dwarf plants were observed. The tomato plants with yellow leaves exhibiting obvious galls on the roots were collected. Several females and gelatinous egg masses of *Meloidogyne* spp. were found inside the cortex of the root galls after dissection. The perineal patterns of females ($n = 12$) were dorsoventrally oval with low and round dorsal arches lacking obvious lateral lines. Most of the striae were smooth and sometimes short, and irregular striae were observed within them. Morphological measurements of females ($n = 20$) included body length (L) = 569.2 ± 53.6 (457.6 to 662.7) μm , body width (BW) = 342.7 ± 69.8 (245.5 to 457.9) μm , stylet = 11.8 ± 0.7 (10.5 to 13.3) μm , dorsal pharyngeal gland orifice to stylet base (DGO) = 4.0 ± 0.2 (3.7 to 4.6) μm , vulval slit length = 24.1 ± 3.7 (16.7 to 30.7) μm , and vulval slit to anus distance = 16.0 ± 1.9 (12.6 to 19.3) μm . Second-stage juveniles (J2s, $n = 20$) had the following morphological characters: $L = 440.6 \pm 26.7$ (395.7 to 488.3) μm , $BW = 15.9 \pm 1.0$ (14.5 to 17.9) μm , stylet = 13.5 ± 0.8 (12.3 to 14.9) μm , tail length = 69.5 ± 3.7 (65.4 to 76.9) μm , and hyaline tail terminus = 21.0 ± 2.1 (17.3 to 24.9) μm . These morphological characters

matched the original description of *Meloidogyne graminicola* (Golden and Birchfield 1968). Ten individual females were transferred to 10 different tubes for DNA extraction. The species-specific primers Mg-F3 (5'-TTA TCGCATCATTTTATTG-3') and Mg-R2 (5'-CGCTTTGTTAGAAAATG ACCCT-3') were used for the identification of *M. graminicola* (Htay et al. 2016). For the 10 DNA samples, a 369-bp fragment was amplified by this pair of primers, confirming their identities as *M. graminicola*. The mitochondrial DNA region between COII and the IRNA gene was amplified using primers C2F3 (5'-GGTCAATGTTTCAGAAATTGTGG-3') and 1108 (5'-TACCTTTGACCAATCAGCT-3') (Powers and Harris 1993). A DNA fragment of 531 bp was obtained and the sequence (GenBank accession no. MZ576221) was 99.8% identical to the sequences of *M. graminicola* (GenBank accession nos. MH033621, MK616527, and MG356945). Part of the rDNA spanning ITS1, 5.8S gene, and ITS2 was amplified with primers 18S (5'-TTGATTACGTCCCTGCCCTT-3') and 26S (5'-TTTCACTCGCCG TTACTAAGG-3') (Vrain et al. 1992). The sequences from the ITS region were 790 bp (GenBank accession no. MZ312595) and were all 100% identical to the known sequences of *M. graminicola* (GenBank accession nos. MF320126, HM623442, and KY020414). In greenhouse tests, six 30-day-old tomato plants (cv. Jinsheng) were individually transplanted in pots ($V_{\text{sand}}:V_{\text{soil}} = 3:1$) and inoculated with 1,500 J2s hatched from the egg masses of collected *M. graminicola* samples per plant. Two noninoculated tomato plants served as negative controls. After 50 days, inoculated plants had galled roots similar to those encountered in the field and there were J2s and eggs within the galls. The nematode reproduction factor (RF = final population/initial population) was 5.3. No symptoms were observed on control plants. These results confirmed the nematode's pathogenicity on tomato. To our knowledge, this is the first report of a natural infection of tomato with *M. graminicola* in China.

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