Diseases Caused by Nematodes

First Report of Root-Knot Nematode *Meloidogyne enterolobii* on Poinsettia ‘Luv U Pink’ in Taiwan

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Poinsettias (*Euphorbia pulcherrima* Willd. ex Klotzsch.) originated in southern Mexico and northern Guatemala and are the most valuable potted flowering plant in the spurge family (Euphorbiaceae). The European Union and the United States are the two biggest poinsettia markets (Taylor et al. 2011), with a wholesale value of \$153 million in the United States in 2019. Root-knot galls of the poinsettia ‘Luv U Pink’ were collected from a production greenhouse located in Nantou County, Taiwan, in March 2021. No aboveground symptoms were observed. A nematode population was established from a single female and used for identification and fulfilling Koch’s postulates. The perineal patterns of five randomly picked females were round or ovoid with moderate to high dorsal arches, but no distinct lateral lines, and ventral striae were fine and smooth. The morphometric characters of second-stage juveniles (J2) included a vermiform body shape, a narrow, tapering tail with rounded tail tips, and a distinct hyaline tail end. Measurements of 20 J2 were: body length, 430 (398 to 473) µm; body width, 15.4 (13.4 to 17.8) µm; stylet length, 13.4 (13.0 to 14.0) µm; dorsal esophageal gland orifice to basal knob, 3.4 (2.8 to 3.9) µm; and tail length, 52.9 (47.6 to 62.2) µm. All morphometric data were consistent with the original description of *Meloidogyne enterolobii* (Yang and Eisenback 1983). Nematode DNA was extracted using the GeneMark Tissue & Cell Genomic DNA Purification Kit (GeneMark, Taiwan) from approximately 1,500 J2 and used for amplification of the 18S rRNA gene, the D2-D3 region of the 28S rRNA gene, and the mtDNA COII

region with primer sets 1A/MelR, D2A/D3B, and C2F3/1108, respectively (Power and Harris 1993; Subbotin et al. 2006; Tigano et al. 2005). The sequence of the 18S rRNA gene (accession no. MZ948800 haplotype 1 and MZ955998 haplotype 2) haplotype 1 shared 100% identity with that of *M. enterolobii* from the United States (KP901058) and China (MN832688) and haplotype 2 shared 99.8% identity with that of KP901058 and MN832688. The sequence of the D2-D3 region (MZ955995) shared 99% identity with that of *M. enterolobii* from the United States (KP901079). The sequence of the COII region (MZ964625) also shared 99% identity with that of *M. enterolobii* from the United States (AY446975) and China (MN840970). Phylogenetic trees of the three gene sequences plotted, as described by Ye et al. (2021), revealed that the newly described nematode was grouped with *M. enterolobii*. Sequence analysis of two fragments (236 bp and 520 bp) amplified with gene specific primers Me-F/R and MK7F/R, respectively (Long et al. 2006; Tigano et al. 2010), also confirmed the identity of *M. enterolobii*. To measure the reproductive factor (Rf), poinsettia Luv U Pink seedlings with eight true leaves were transplanted into three 12-cm-diameter pots each containing 6,000 eggs or water (mock control). Forty-five days after inoculation, the average Rf value of three inoculated plants was 6, and no galls were observed on mock control plant roots, confirming that poinsettias are a host of *M. enterolobii*. *M. enterolobii* has been reported in several *Euphorbia* species, including *E. heterophylla*, *E. prostrata*, *E. punicea*, and *E. tirucalli* (Han et al. 2012; Rich et al. 2009). To the best of our knowledge, this is the first report of *M. enterolobii* infecting *E. pulcherrima* ‘Luv U Pink’.

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