Diseases Caused by Nematodes

First Report of Root-Knot Nematode *Meloidogyne enterolobii* on Cockscomb (*Celosia argentea* var. *cristata*) in Taiwan

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Cockscomb (*Celosia argentea*), a popular ornamental plant in the family Amaranthaceae, is commonly found in subtropical and temperate zones of Africa, South America, and Southeast Asia. It has been known to contain antiviral proteins, betalains, and anthocyanin, which can be applied in beneficial ways (Bodhipadma et al. 2010). In September 2020, a cockscomb plant (*C. argentea* var. *cristata*) showing typical galling root symptoms likely infected by root-knot nematodes (*Meloidogyne* sp.) was collected from a garden in Taichung, Taiwan, and a quick examination of several individuals using MK7F/R primers (Tigano et al. 2010) indicated that they were *Meloidogyne enterolobii*. A nematode population was established from a single egg mass and used for species identification and pathogenicity tests. Five perineal patterns of mature females from the single female population showed round to oval shapes with weak lateral lines. Dorsal arches were moderate to high, almost squared, with smooth ventral striae. Second-stage juveniles (J2s) were vermiform and had a slender tail and a tapering to a rounded tip with a distinct hyaline region at the tail terminus. Morphological measurements of 28 J2s revealed body length = 457.2 ± 20.6 (416.1 to 506.9) μm , body width = 16.0 ± 2.0 (13.4 to 20.3) μm , stylet length = 14.7 ± 0.5 (13.9 to 15.9) μm , dorsal gland orifice to the stylet base = 4.0 ± 0.5 (2.0 to 4.8) μm , and tail length = 56.0 ± 3.8 (47.4 to 60.3) μm . Female perineal patterns and morphometric data were similar to the original description of *M. enterolobii* (Yang and Eisenback 1983). DNA purified from approximately 1,500 J2s using a GeneMark Tissue & Cell Genomic DNA Purification Kit (GeneMark, Taiwan) was used to amplify the 18S rDNA fragment, D2-D3 expansion segments of 28S rDNA, and a COII region on mtDNA with primer sets 1A/MelR, D2A/D3B, and C2F3/1108, respectively (Powers and Harris 1993; Subbotin et al.

2006; Tigano et al. 2005). The 18S rDNA sequence (OK076893) of this study shares 99.94% nucleotide identity with those of *M. enterolobii* isolated from the United States (KP901058) and China (MN832688). The D2-D3 sequence of haplotype 1 (OK076898) shows 100% identity to those of *M. enterolobii* from China (MT193450) and Taiwan (KP411230). The sequence of haplotype 2 (OK076899) shows 99.86% identity to those of *M. enterolobii* from the United States (MN809527) and China (MN269945). The sequence of the COII region (OK086042) shows 99.86% identity to that of *M. enterolobii* from China (MN269945). Phylogenetic trees of the three gene sequences were plotted following Ye et al. (2021), revealing that the newly described root-knot nematode on cockscomb is grouped with other *M. enterolobii* isolates. DNA fragments amplified by primer sets Me-F/R (Long et al. 2006) and MK7F/R specifically targeting *M. enterolobii* yielded 236 and 520 bp, respectively. Pathogenicity tests were assayed from July to September 2021 on 3-week-old nematode-free cockscomb plants directly germinated from seeds of SkyStar (ASUSA SPIKE SEEDS, Taipei, Taiwan) in a 10.5-cm-diameter pot filled with 600 ml of sterilized peat moss/sand (1:1, v/v) soil in a 28°C walk-in chamber. Nematode eggs were extracted using 0.05% NaOCl as described by Vrain (1977), and cockscomb plants ($n = 3$) were inoculated by adding 6,000 eggs (10 eggs/cm³). Cockscomb plants treated with water were used as mock controls. The RF value of the inoculated plants was determined by the method of Belair and Benoit (1996) 45 days after inoculation, and the average was 4.13. No galls were observed on the roots of control plants. The results confirmed that cockscomb is a new host of *M. enterolobii*. To the best of our knowledge, this is the first report of *M. enterolobii* on *C. argentea* var. *cristata* in Taiwan.

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