Diseases Caused by Nematodes

First Report of *Meloidogyne hapla* Infecting Yunmuxiang (*Aucklandia lappa*) in China

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Yunmuxiang (*Aucklandia lappa*) is a tall, perennial herbaceous plant in the Compositae family, occurring mainly in Asia and Europe. Yunmuxiang originated in India and was introduced into China in approximately 1940. Since then, it has been widely cultivated in the southwest region of China for medicinal uses; it is included in the Chinese pharmacopoeia. Yunmuxiang is used primarily as a sedative, including for anesthesia (Ting et al. 2011). Severely stunted and withered yunmuxiang plants with rotted and galled roots were observed in a field in near the city of Lijiang (N 99°46'; E 27°18') in October 2019. These symptoms were typical of infection by root-knot nematodes. Second-stage juveniles (J2s) were collected from the soil in the root zone, and adult females were dissected from roots. Population densities of J2s ranged from 325 to 645 per 100 cm³. Morphological analysis and species-specific PCR were performed on the J2s and females. Morphological characteristics are as follows: for J2s ($n = 20$), body length = 360.5 ± 23.4 μ m, tail length = 47.2 ± 6.1 μ m, and stylet length = 10.4 ± 1.9 μ m, distance from dorsal esophageal gland opening to the stylet knot (DGO) = 3.96 ± 0.42 μ m; females ($n = 20$) were pear-shaped, body length = 565.23 ± 86.68 μ m,

maximum body width = 407.24 ± 60.21 μ m, stylet length = 9.93 ± 0.88 μ m, DGO = 4.76 ± 0.32 μ m, stylet median bulb width (MBW) = 29.67 ± 3.61 μ m, perineum morphology is low and low dorsal arch round, with a typical inferior protrusion near the anus. These morphological characteristics are consistent with *Meloidogyne hapla* as described by Hunt and Handoo (2009). To confirm species identification, DNA was extracted from females (Blok et al. 1997), and the ITS region was amplified using the primers 18S/26S (Vrain et al. 1992). Furthermore, species-specific SCAR primers JMV1/JMV hapla were used as described by Adam et al. (2007). PCR produced 768- and 419-bp sequences. Fragments were sequenced (MW512922 and MW228371, respectively) and compared with available sequences on NCBI. Sequences were 99.48% identical to the MT249016 and KJ572385 *M. hapla* sequences and 100% identical to the GQ395574 and GQ395569 *M. hapla* sequences, respectively. Morphological and molecular characterization supports the identification of the isolate found on *A. lappa* as *M. hapla*. Yunmuxiang seeds were planted in 20-cm diameter, 10-cm deep plastic pots containing 1,000 cm³ of sterilized soil. Seedlings were thinned to one per pot. At the two- to three-leaf stage, 10 pots were infested with 1,500 *M. hapla* J2s per seedling, using a sterilized micropipette. Plants were maintained at 20 to 25°C in a greenhouse. Control plants received sterile water, and the pathogenicity test was repeated three times. After 30 days, plants were removed from pots and the soil gently removed from the roots. A large number of galls (95.6 ± 2.5) and egg masses (33.5 ± 0.5) were found on each root system. Yunmuxiang was considered a good host for *M. hapla* in Lijiang. *M. hapla* is a major plant parasitic nematode with a wide geographic distribution and range of host plants, and it causes severe yield losses (Azevedo de Oliveira et al. 2018). Through investigation, this is the first report worldwide of *M. hapla* infecting *A. lappa*.

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