Diseases Caused by Nematodes

First Report of Root-Knot Nematode *Meloidogyne enterolobii* Infecting Sweetpotato in the State of Rio Grande do Norte, Brazil

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The sweetpotato (*Ipomoea batatas* L., Convolvulaceae family) originated in Latin America and is currently cultivated worldwide. The storage roots, rich in calories, have made this crop one of the main caloric sources for low-income populations, especially in developing countries. Brazil annually produces about 805,000 t, with the northeast region responsible for 34% of this production (Albuquerque et al. 2020). In October 2019, sweetpotato plants cultivar Campina, from a field in the region of Touros, state of Rio Grande do Norte (RN), Brazil (5°12'31"S, 35°34'42"W), presented deformed storage roots, with galls, typical of root-knot nematodes. The roots were sent to the Nematology Laboratory (LabNema), where 14,032 eggs and 3,312 second-stage juveniles (J2s) of *Meloidogyne* sp., in 10 g of roots, were recovered. The species of adults was identified through morphological, biochemical, and phylogenetic analysis. The perineal region of females ($n = 10$) presented an oval shape, with a high and semitrapezoidal dorsal arch and streak-free perivulval region. The labial region of males ($n = 10$) presented high and rounded head cap, labial region slightly set off from the body, without annulations. The morphological characters were compatible with the original description of *Meloidogyne enterolobii* (Yang and Eisenback 1983). The phenotype of esterase isoenzymes showed two major bands (VS1 and S1) also characteristic of *M. enterolobii* (Esbenshade and Triantaphyllou 1985). Sequences of 18S rDNA (~1,200 bp) of individual females (Holterman et al. 2006) obtained from sweetpotatoes before (SPme1 and 2) and after inoculation (SPme3 and 6), and from guava, used as *M. enterolobii* species control,

were submitted to Bayesian analysis. The sequences presented genetic diversity among them resulting from seven single nucleotide polymorphisms and 99.4 to 99.9% identity with *M. enterolobii* sequences deposited in the NCBI GenBank (accession nos. MW209034 to MW209039). The pathogenicity test was carried out under greenhouse conditions, in which 3,000 eggs and J2s from the original population isolated of *M. enterolobii* were inoculated in sweetpotato seedlings (cv. Campina) ($n = 6$). After 3 months, the roots presented galls and deformations typical of root-knot nematodes, whereas non-inoculated plants did not present any symptoms. An average of 15,900 eggs and J2s of *M. enterolobii* (reproductive factor = 5.3) were recovered from the roots, proving that sweetpotatoes were a host of this species. *M. enterolobii* is known to cause great damage to sweetpotato (Ye et al. 2021). In Brazil, *Meloidogyne* nematode had been reported once, isolated from a sweetpotato field in the Ceará state, and the species suggested by the authors according to esterase electrophoresis was *M. enterolobii*. Nonetheless, the authors did not present taxonomic, isoenzyme phenotypes and molecular species identification integratively, nor included pathogenicity tests (Silva et al. 2016). Therefore, this is the first time that *M. enterolobii*, with reliable identification by different methods, including sequencing, was detected in commercial sweetpotato fields in the RN state and in Brazil. The local farmers reported that this nematode deforms the storage roots, which makes them useless for commercialization, resulting in minimal losses of 50% of production in the infested areas. Furthermore, as sweetpotatoes are vegetatively propagated, the spread of this nematode through planting material is favored. Considering the importance of this crop in Brazil, this report is essential for control measures of this pathogen to be taken in order to avoid its spread to other regions.

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