

Meloidogyne enterolobii Found Infecting Root-Knot Nematode Resistant Sweetpotato in South Carolina, United States

W. B. Rutter^{1†} A. M. Skantar² Z. A. Handoo² J. D. Mueller³ S. P. Aultman⁴ P. Agudelo⁵

¹USDA-ARS United States Vegetable Laboratory, Charleston, SC 29414;

²USDA-ARS Mycology and Nematology Genetic Diversity and Biology Laboratory, Beltsville, MD 20705-2350;

³Edisto Research and Education Center, Department of Plant and Environmental Sciences, Clemson University, Blackville, SC 29817;

⁴Department of Plant Industry, Clemson University, Pendleton, SC 29670; and

⁵Department of Plant and Environmental Sciences, Clemson University, Clemson, SC 29634

Meloidogyne enterolobii (the guava root-knot nematode) is a highly polyphagous species that causes significant damage in a wide variety of crops worldwide ([Castagnone-Sereno 2012](#)). *M. enterolobii* has a well-documented ability to overcome many crop resistance genes that are effective against the more cosmopolitan *M. incognita* group (MIG) species endemic to the southern United States. In the continental United States, *M. enterolobii* was first reported in Florida ([Brito et al. 2004](#)) and more recently in North Carolina ([Ye et al. 2013](#)) infecting root-knot nematode resistant varieties of cotton and soybean. Herein we describe the first detection of this nematode infecting root-knot nematode resistant sweetpotato in South Carolina. In February 2018, a soil sample was collected as part of a Cooperative Agricultural Pest Survey for root-knot nematode species from a soybean field in Darlington Co., SC. The surveyed field had been rotated between soybean and sweetpotato for several years. Soil was sent to the USDA-ARS Laboratory in Beltsville, MD, for analysis. Total DNA was extracted from isolated juveniles, and amplicons generated from COII-16S rDNA, 28S D2-D3 rDNA, and rDNA intergenic spacer 2 were sequenced ([Skantar et al. 2008](#)). BLAST searches of these sequences against the NCBI nonredundant database found near perfect homology ($\geq 99\%$ identity) with multiple sequences from *M. enterolobii*. The morphology and morphometrics of second-stage juveniles and females, including the nature of perineal patterns, further established the identity of the species as *M. enterolobii*. During a follow-up survey, cured storage roots from the root-knot nematode resistant sweetpotato cultivar Covington were found displaying galling symptoms typical of a root-knot nematode. Ten individual females were excised from the infected storage roots and DNA extracted ([Holterman et al. 2012](#)). Single egg masses were used to inoculate susceptible tomato roots planted in sterilized soil, and these were cultured in an isolated growth

chamber to provide inoculum for further testing. Female DNA extractions were subjected to species diagnostic polymerase chain reaction and sequencing. Eight females produced amplification results consistent with *M. enterolobii* for four mitochondrial primer sets. Species identification was further confirmed by individually sequencing these amplicons. These sequences aligned with a combined identity of 99.5% to the published mitochondrial genome sequence of *M. enterolobii*. In contrast, these same sequences aligned with only 90.3, 89.7, and 90.4% combined sequence identity to the mitochondrial genome sequences from *M. incognita*, *M. javanica*, and *M. arenaria*, respectively. Greenhouse tests demonstrated that this isolate is highly virulent on the widely used MIG-resistant sweetpotato cultivar Covington (Yencho et al. 2008). There were no significant differences in observed galling (*t* test, *P* = 0.16, *n* = 6) or log normalized egg counts (*t* test, *P* = 0.39, *n* = 6) between Covington (galling = 54.5%, SD ± 18.9%; eggs/g of root = 9,670.5, SD ± 6,633.5) and the highly MIG-susceptible cultivar Beauregard (galling = 72.5%, SD ± 21.9%; eggs/g of root = 29,890.5, SD ± 22,122.4). The reproduction factor (eggs final/eggs initial) calculated for this isolate on Covington 46 days postinoculation was 30. *M. enterolobii* represents a significant threat to sweetpotato and other host crops in the southern United States.

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