



Pathotypic variation between isolates of *Meloidogyne enterolobii* collected from Sweetpotato in North and South Carolina (United States)



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Introduction

M. enterolobii (*M.e.*) has become a serious problem in the Southeastern United States (US). *M.e.* has a wide host range similar to other closely related species, such as *M. incognita* (*M.i.*). Despite their similarities, many of the host resistance genes that are effective against *M.i.* are ineffective against *M.e.* We conducted greenhouse assays to identify new sources of resistance that are effective against multiple isolates of *M.e.* In the process, we found evidence of pathotypic variation between *M.e.* isolates.

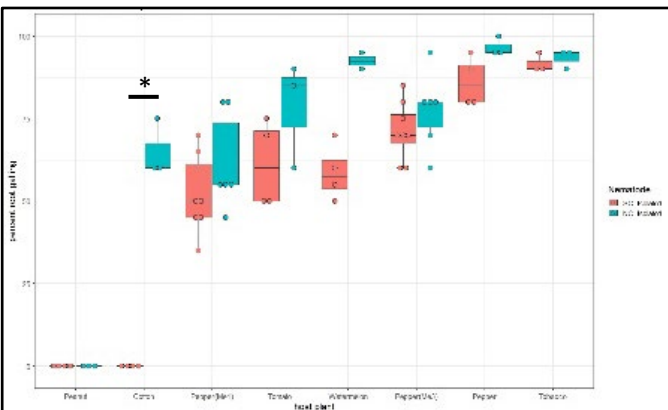


Fig 1. *M.e.* isolates 'SC.1' and 'NC.1' were collected from separate sweetpotato fields in the Carolinas. Both isolates caused severe galling on most of the *M.i.* host panel, as well as *M.i.* resistant pepper genotypes. Interestingly, only NC.1 produced galling on *M.i.* susceptible cotton cv. 'Delta Pine 61'

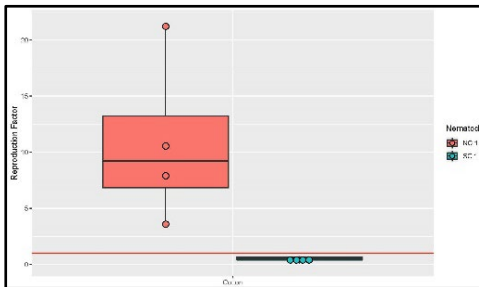


Fig 2. Side-by-side infection assays using both isolates demonstrated that SC.1 doesn't effectively damage or reproduce on cotton cv. 'Delta Pine 61'

Table. Data from select sweetpotato accessions screened against both isolates. All resistant accession were consistent between isolates. However, differences were observed between susceptible controls

Sweetpotato cultivar	Isolate SC.1		Isolate NC.1		Classification
	% Galling	Eggs/gram root	% Galling	Eggs/gram root	
COVINGTON	49.7 ± 3.8	12,864.0 ± 3,516	47.1 ± 5.9	9,570.0 ± 3,785.5	SUSCEPTIBLE
BEAUREGARD	52.7 ± 4.5	20,462.0 ± 4,169	27.5 ± 3.0	1,028.8 ± 263.0	SUSCEPTIBLE
Tanzania	0.0 ± 0.0	31.9 ± 15.8	0.0 ± 0.0	5.7 ± 3.3	RESISTANT
Regal	0.3 ± 0.3	33.8 ± 18.3	3.0 ± 2.0	16.4 ± 11.3	RESISTANT
Porto Rico	0.5 ± 0.3	60.7 ± 39.8	1.5 ± 1.5	5.8 ± 3.6	RESISTANT

Conclusions and Future Directions

- Consistent with previous reports, *M.e.* isolates in the US are not affected by *M.i.* resistance genes in pepper.
- The recent appearance of different *M.e.* pathotypes in the US indicates that this species has a high level of pathogenic variability similar to other parthenogenic species
- New *M.e.* resistant crop varieties will be needed to manage this pest, but overuse of individual resistance genes is likely to result in the selection of virulent *M.e.* strains.

Additional Information and Resources

- [Focused Investigations on the Distribution and management of *Meloidogyne enterolobii*: FindMenematode.org](#)
- Rutter et. al. Plant Disease 2021. 105(10): 3147-3153