Table 1. A super paramagnetic iron oxide nanoparticle (SPION) based genomic DNA extraction from soil method was compared to a standard phenol-based method and a commercial kit. Approximately 10 second-stage juvenile *Meloidogyne hapla* were inoculated to 0.5 g of soil, and then air dried before performing the extraction. Five replicates of each method were conducted and the experiment was conducted twice, with results averaged across all replicates. Means followed by the same letter within columns are not significantly different at the 0.05 level.

Protocol	Total DNA yield (ng)	$A_{260/280}$[w]	$A_{260/230}$[x]	Detectable by PCR (%)
Phenol	306.1 ***a***	1.84 ***b***	0.37 ***b***	50
Kit	199.0 ***a***	1.56 ***a***	0.97 ***a***	90
SPION	3.26 ***b***	1.60 ***a***	0.25 ***b***	70
LSD[y]	112.7	0.26	0.25	
F =	15.6	4.62	18.7	
P =	< 0.0001	0.019	< 0.0001	
CV (%)[z]	**Phenol**: 66.5	**Phenol**: 23.8	**Phenol**: 87.1	
	Kit: 30.9	**Kit**: 14.7	**Kit**: 37.7	
	SPION: 70.6	**SPION**: 6.46	**SPION**: 11.7	

[w] The ratio of spectral absorbance at 260 and 280 nm ($A_{260/280}$) is a quantitative measure of protein contamination in a nucleic acid sample. A ratio of 1.80 in a sample of DNA is considered free of protein contaminants.

[x] The ratio of spectral absorbance at 260 and 230 nm ($A_{260/230}$) is a quantitative measure of residual salt contamination. Higher values indicate less residual salts.

[y] LSD, least significant difference.

[z] CV, coefficient of variation is the ratio of the standard deviation to the mean, quantifying dispersion of the data.

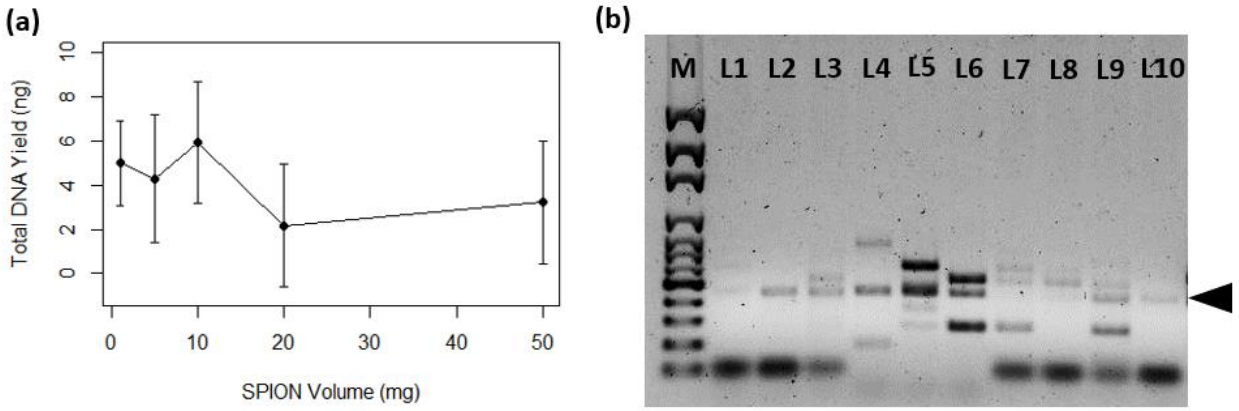

Figure 1. (a) Addition of increasing amounts of SPION up to 10 mg resulted in an increase in DNA yield. There was a marked decrease in DNA yield after 10 mg. (b) Resultant DNA from each SPION volume trial was amplified by PCR using the universal nematode primers rDNA2 and rDNA1.58s. Amplification products of *Meloidogyne hapla* are approximately 450-bp in size (arrowhead). Lanes 1 and 2: 1 mg SPION. Lanes 3 and 4: 5 mg SPION. Lanes 5 and 6: 10 mg SPION. Lanes 7 and 8: 20 mg SPION. Lanes 9 and 10: 50 mg SPION. M: 100-bp DNA ladder. Consistent amplification was noted following the addition of 10 mg of nanoparticles.

Table 2. The 100 g-SPION capture method was assessed for sensitivity in extracting DNA from *Meloidogyne hapla* within soil. Soil samples of 100 g were sterilized and inoculated with 1, 10, 10, or 1,000 *M. hapla* second-stage juveniles and air dried. The method was performed as described in the text for the 100 g-SPION capture method, and assessed for quantity (total yield) and quality ($A_{260/280}$ and $A_{260/230}$ ratios, and percent of samples detectable by PCR). Ten replicates per nematode quantity were processed. DNA yield increased as nematode inoculation number increased, with 1,000 nematodes producing significantly more DNA than the 1, 10, or 100 nematode groups. Means followed by the same letter within columns are not significantly different at the 0.05 level.

Nematodes per 100 g soil	Total DNA yield (ng)	$A_{260/280}$[w]	$A_{260/230}$[x]	Detectable by PCR (%)
1	0.74 ***a***	1.65	0.29	20
10	2.20 ***ab***	1.61	0.33	40
100	3.00 ***ab***	1.53	0.30	90
1,000	15.6 ***b***	1.58	0.36	90
LSD[y]	11.8	0.12	0.08	
F =	6.30	1.63	1.37	
P =	0.016	0.589 (ns)	0.268 (ns)	
CV (%)[z]	**One:** 66.1 **Ten:** 92.6 **Hundred:** 123.9 **Thousand:** 177.8	**One**: 5.94 **Ten:** 7.78 **Hundred:** 11.6 **Thousand:** 6.87	**One:** 17.9 **Ten:** 30.3 **Hundred:** 7.11 **Thousand:** 35.4	

[w] The ratio of spectral absorbance at 260 and 280 nm ($A_{260/280}$) is a quantitative measure of protein contamination in a nucleic acid sample. A ratio of 1.80 in a sample of DNA is considered free of protein contaminants.

[x] The ratio of spectral absorbance at 260 and 230 nm ($A_{260/230}$) is a quantitative measure of residual salt contamination. Higher values indicate less residual salts.

[y] LSD, least significant difference.

[z] CV, coefficient of variation is the ratio of the standard deviation to the mean, quantifying dispersion of the data.

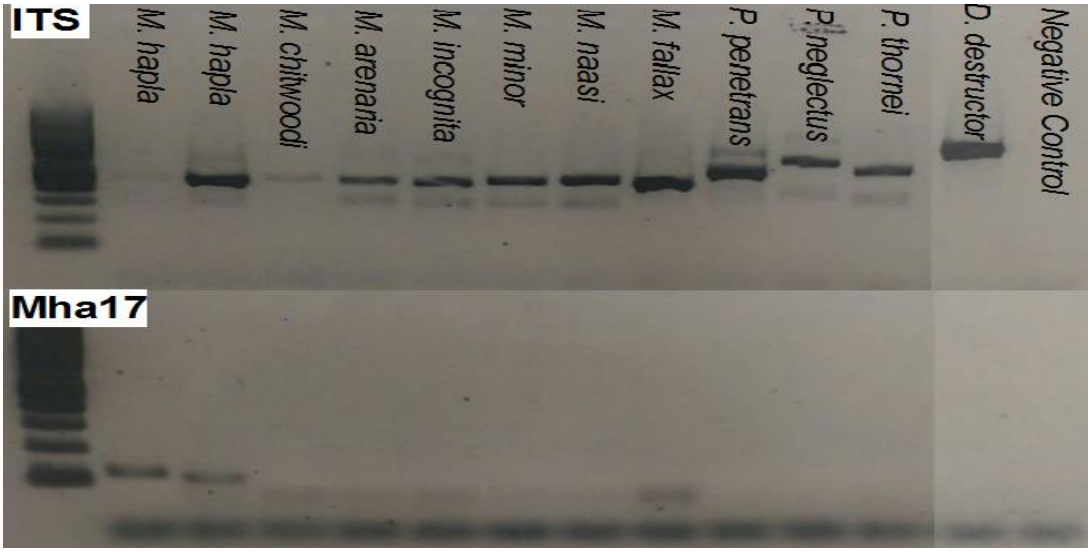

Figure 2. Results of primer and probe development revealed an optimal primer set that produced amplification only in *Meloidogyne hapla* DNA samples. This set (designated Mha17) is shown in the lower gel. Bands are visible only in lanes with *M. hapla* samples. The internal transcribed spacer (ITS, upper gel) was used as a positive PCR control.

Table 3. Initial (Pi) and final (Pf) populations of *M. hapla* second stage juveniles observed per 200 mL of soil from 100 points per field at planting and harvest, respectively. Manual counting was conducted using a microscope following a modified Whitehead tray extraction technique from soil collected in three potato fields in New York in 2016. Populations were highly variable within the field, with some locations having high populations, while other locations had no detectable nematodes. *P*-values indicate results of a paired *t*-test of initial and final populations across all sampling points within the field. ns = not significant at the 0.05% level.

		Lesion (*Pratylenchus* spp.)			Root knot (*Meloidogyne hapla*)		
		P_i	P_f	P_f/P_i	P_i	P_f	P_f/P_i
Field 1	Maximum	2,275	5,588		1,438	587.5	
	Minimum	94	75		0	0	
	Average	942.8	1,547	1.64	52.0	37.5	0.72
	P =	< 0.0001			0.387 (ns)		
Field 2	Maximum	554	999		1,588	23,337	
	Minimum	0	0		0	0	
	Average	76.8	81.5	1.06	72.0	2116	29.39
	P =	0.738 (ns)			< 0.0001		
Field 3	Maximum	506	787.5		1,038	20,588	
	Minimum	0	0		0	0	
	Average	72.0	57.7	0.80	115.3	3511	30.45
	P =	0.165 (ns)			< 0.0001		

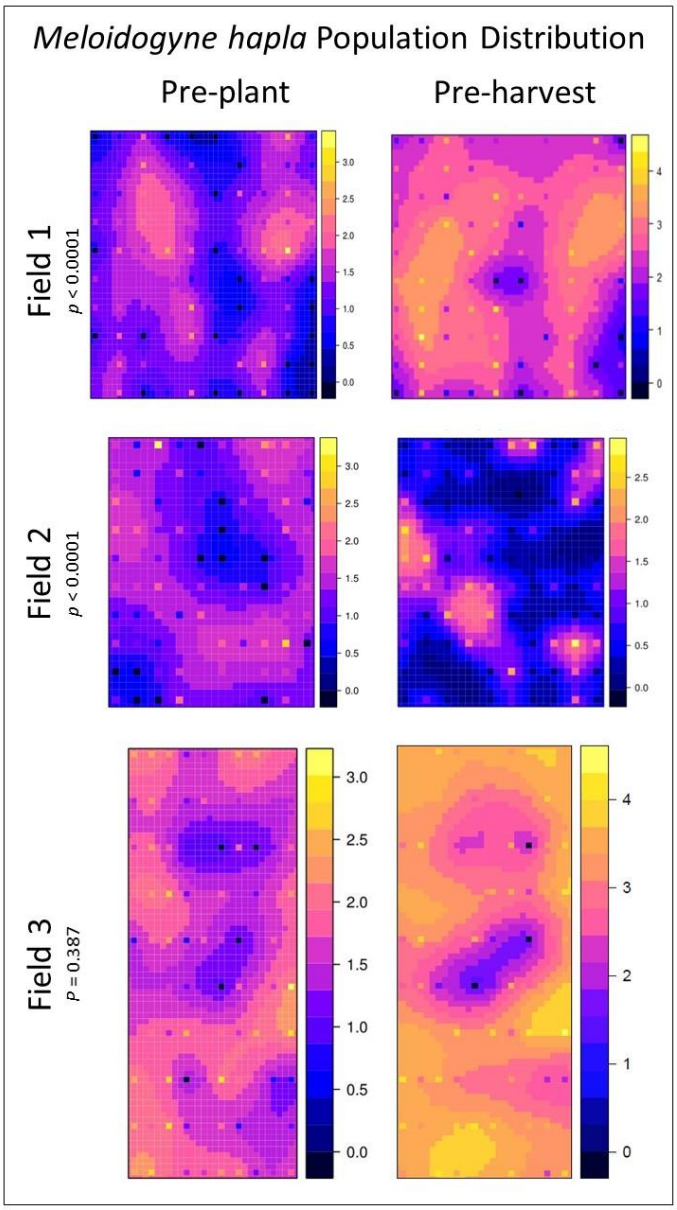

Figure 3. Spatial distribution of *Meloidogyne hapla* populations at planting and harvest within three potato fields in New York as determined by manual counting and interpolation with ordinary kriging. Marks on the scale indicate a 10-fold increase. Populations were highly variable across the field and a significant increase in populations were observed for Fields 1 and 2 between the two sampling times.

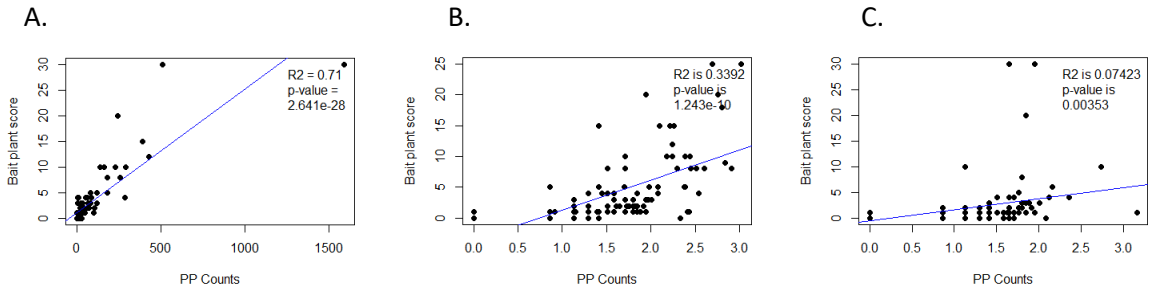

Figure 4. Regressions between *Meloidogyne hapla* populations assessed by manual counting at planting and root galling severity in tomato bait plants for each of the three potato fields (A, B, and C) in New York in 2016. Pre-plant (PP) nematode counts (actual counts for field A, and logarithmic expression for fields B and C) are plotted along the x-axis and bait plant root galling score as a percentage is plotted along the y-axis.

Table 4. Association between total tuber weight (kg) and populations of *Meloidogyne hapla* and *Pratylenchus* spp. combined at the two sampling times for the three potato fields sampled in New York in 2016. Probability values presented parenthetically. ns = not significant at the 0.05% level.

	Pearson's Correlation Coefficients for *Meloidogyne hapla* and *Pratylenchus* spp. Populations Combined	
	Tuber Weight and Initial Populations	**Tuber Weight and Final Populations**
Field 1	0.047 (p = 0.642) (ns)	0.287 (p = 0.0038)
Field 2	- 0.16 (p = 0.108) (ns)	0.26 (p = 0.0098)
Field 3	0.17 (p = 0.094) (ns)	0.32 (p = 0.041)

Table 5. Effect of potato cultivar on tuber yield, shoot fresh weight, number of tubers, tuber diameter, root fresh weight, root galling score, and reproduction factor in a glasshouse trial conducted at Geneva, New York in 2017. Cultivar was significant for each of the response variables, indicating the potato cultivars tested in this bioassay exhibited variable growth habits across inoculation levels. Values followed by different letters within a column are significantly different at the 0.05 level. Data is presented here after being back-transformed.

	Yield (g)	Shoot fresh weight (g)	Number of tubers	Tuber Diameters (mm)	Root fresh weight (g)	Root galling score	Reproduction factor (Pf/Pi)
Adirondack Blue	216.7 ***abc***	231.4 ***ef***	4.64 ***cde***	4.91 ***a***	48.1 ***c***	0.54 ***b***	9.3 ***abc***
Atlantic	186.8 ***bcd***	328.9 ***cd***	3.73 ***de***	4.66 ***ab***	62.1 ***c***	0.50 ***b***	9.7 ***abc***
Eva	212.4 ***abc***	344.7 ***cd***	6.15 ***bc***	4.41 ***abc***	140.8 ***b***	0.75 ***b***	6.6 ***abc***
Lamoka	175.9 ***bcd***	391.6 ***bc***	2.93 ***e***	5.00 ***a***	69.3 ***c***	2.87 ***a***	14.5 ***ab***
Nordana	223.3 ***ab***	235.1 ***ef***	8.07 ***b***	3.69 ***d***	65.7 ***c***	0.27 ***b***	8.0 ***abc***
Norland	168.1 ***cd***	174.2 ***f***	5.64 ***cd***	3.92 ***cd***	42.3 ***c***	0.38 ***b***	3.1 ***bc***
NY140	177.0 ***bcd***	298.0 ***de***	4.64 ***cde***	4.31 ***abcd***	71.5 ***bc***	0.86 ***b***	13.3 ***ab***
Reba	135.1 ***d***	473.9 ***b***	4.00 ***cde***	3.96 ***bcd***	73.9 ***bc***	0.80 ***b***	16.0 ***a***
Snowden	137.8 ***d***	414.8 ***bc***	5.57 ***cd***	3.62 ***d***	95.1 ***bc***	0.58 ***b***	14.3 ***ab***
Upstate	217.6 ***abc***	168.6 ***f***	21.3 ***a***	2.68 ***e***	27.2 ***c***	0.33 ***b***	7.9 ***abc***
Waneta	262.8 ***a***	282.3 ***de***	4.42 ***cde***	4.89 ***a***	75.9 ***bc***	0.62 ***b***	10.4 ***abc***
Rutgers (Tomato)	---	656.9 ***a***	---	---	392.1 ***a***	1.86 ***ab***	1.2 ***c***
HSD =	52.4	89.4	2.2	0.70	69.3	1.87	12.1
F =	11.8	52.2	100.7	44.2	48.7	3.89	3.12
P =	< 0.0001	< 0.0001	< 0.0001	< 0.0001	< 0.0001	< 0.0001	0.0008

Table 6. Effect of *Meloidogyne hapla* population density across cultivars on potato tuber yield, shoot fresh weight, number of tubers, tuber diameter, root fresh weight, root galling score, and reproduction factor in a glasshouse trial conducted at Geneva, New York in 2017. Plants were inoculated with either 500 *M. hapla* J2 nematodes ('Medium' level), 1500 *M. hapla* J2 nematodes ('High' level) or 0 *M. hapla* J2 nematodes ('Control' level, inoculated with sterile water). Inoculation level was significant for yield, root galling score, and reproduction factor. Values followed by different letters within a column are significantly different at the 0.05 level. Data is presented here after being back-transformed.

	Yield (g)	Shoot fresh weight (g)	Number of tubers	Tuber Diameters (mm)	Root fresh weight (g)	Root galling score	Reproduction factor (Pf/Pi)
High	199.0 ***a***	325.0	6.26	3.69	112.9	1.87 ***a***	10.9 ***b***
Medium	173.7 ***b***	324.1	6.02	3.64	99.6	0.86 ***b***	17.7 ***a***
Control	204.3 ***a***	337.8	6.20	3.86	91.7	0.0 ***c***	0.0 ***c***
HSD =	19.7 g	31.8	0.81	0.23	24.6	0.66	4.31
F =	7.29	0.441	0.05	1.81	1.95	22.5	48.2
P =	0.001	0.644 (ns)	0.95 (ns)	0.16 (ns)	0.147 (ns)	< 0.0001	< 0.0001

Table 7. Effect of the interaction between cultivar and *Meloidogyne hapla* population density on potato tuber yield, shoot fresh weight, number of tubers, tuber diameter, root fresh weight, root galling score, and reproduction factor in a glasshouse trial conducted at Geneva, New York in 2017. The interaction term was only significant for fresh root weight, root galling score, and reproduction factor. Values followed by different letters within a column are significantly different at the 0.05 level. Data is presented here after being back-transformed.

Cultivar	Inoculation Level	Root fresh weight (g)	Root galling score	Reproduction factor (Pf/Pi)
Adirondack Blue	High	64.9 *bc*	0.8 *bc*	13.1 *abcd*
	Medium	44.6 *bc*	1.0 *bc*	14.9 *abcd*
	Control	30.6 *bc*	0.0 *c*	0.0 *d*
Atlantic	High	80.5 *bc*	0.6 *c*	15.9 *abcd*
	Medium	49.2 *bc*	1.0 *bc*	13.3 *abcd*
	Control	56.7 *bc*	0.0 *c*	0.0 *d*
Eva	High	162.0 *b*	1.5 *bc*	8.3 *bcd*
	Medium	153.5 *bc*	1.0 *bc*	11.6 *bcd*
	Control	84.6 *bc*	0.0 *c*	0.0 *d*
Lamoka	High	91.6 *bc*	7.2 *a*	14.1 *abcd*
	Medium	54.2 *bc*	1.4 *bc*	29.4 *abc*
	Control	60.5 *bc*	0.0 *c*	0.0 *d*
Nordana	High	78.4 *bc*	0.4 *c*	12.6 *abcd*
	Medium	46.8 *bc*	0.4 *c*	11.3 *bcd*
	Control	71.9 *bc*	0.0 *c*	0.0 *d*
Norland	High	63.1 *bc*	1.0 *bc*	4.1 *d*
	Medium	21.4 *c*	0.4 *c*	5.27 *cd*
	Control	46.6 *bc*	0.0 *c*	0.0 *d*
NY140	High	60.4 *bc*	1.6 *bc*	10.3 *bcd*
	Medium	80.1 *bc*	1.0 *bc*	29.7 *abc*
	Control	71.9 *bc*	0.0 *c*	0.0 *d*
Reba	High	88.9 *bc*	1.4 *bc*	16.5 *abcd*
	Medium	80.2 *bc*	1.0 *bc*	31.5 *ab*
	Control	53.6 *bc*	0.0 *c*	0.0 *d*
Snowden	High	93.1 *bc*	1.0 *bc*	6.1 *cd*
	Medium	94.7 *bc*	1.0 *bc*	36.7 *a*
	Control	*98.1 bc*	0.0 *c*	0.0 *d*
Upstate	High	23.8 *c*	0.6 *c*	6.8 *bcd*
	Medium	34.4 *bc*	0.4 *c*	16.9 *abcd*
	Control	25.7 *c*	0.0 *c*	0.0 *d*
Waneta	High	47.4 *bc*	1.0 *bc*	21.1 *abcd*
	Medium	84.0 *bc*	1.0 *bc*	10.3 *bcd*
	Control	92.2 *bc*	0.0 *c*	0.0 *d*
Rutgers (Tomato)	High	428.8 *a*	4.4 *ab*	1.6 *d*
	Medium	364.2 *a*	1.0 *bc*	2.0 *d*
	Control	383.2 *a*	0.0 *c*	0.0 *d*
HSD =		143.2	3.8	24.7
F =		1.64	2.82	2.43
P =		0.048	0.0001	0.0009