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Crop Rotation and Races of *Meloidogyne incognita* in Cotton Root-knot Management[1]

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Abstract: The influence of various crop rotations and nematode inoculum levels on subsequent population densities of *Meloidogyne incognita* races 1 and 3 were studied in microplots. Ten different 3-year sequences of cotton, corn, peanut, or soybean, all with cotton as the 3rd-year crop, were grown in microplots infested with each race. Cotton monoculture, two seasons of corn, or cotton followed by corn resulted in high race 3 population densities and severe root galling on cotton the 3rd year. Peanut for 2 years preceding cotton most effectively decreased the race 3 population and root galls on cotton the 3rd year. Race 1 did not significantly influence cotton growth or yield at initial populations of up to 5,000 eggs/500 cm^3 soil. At 5,000 eggs/500 cm^3, cotton growth was suppressed by race 3 but yield was not affected.

Key words: cropping sequences, *Gossypium hirsutum.*

Meloidogyne incognita is the most important nematode parasite of cotton because of its wide distribution and its involvement with other microorganisms in various disease complexes (9,11). Nematode control in infested cotton fields is often necessary to avoid yield suppression. Chemical nematicides are an effective method of nematode control but are relatively expensive and subject to various environmental constraints. Cultivar resistance to *M. incognita* could be an inexpensive and effective method of nematode control; however, due to the complex inheritance of resistance to *M. incognita* in cotton (13) and the expense of cultivar development, there are few agronomically acceptable, highly resistant cultivars.

Crop rotation for reducing nematode populations and suppressing crop damage has been recommended for many years (7). In many cotton-producing areas practical rotation crops are limited by environmental or economic factors. Care must be exercised in selecting appropriate rotation crops; they must be poor or nonhosts for the nematode, yet economically feasible to produce.

Selection of rotation crops to suppress *M. incognita* is difficult because of the existence of four physiological races that have extremely broad and different, but overlapping host ranges (10,15). These races are distributed worldwide and exhibit a relatively consistent response to a series of host differentials. A study of many *M. incognita* populations collected from widely separated geographical regions of the world indicates that race 1 is the most frequently encountered (10). Certain populations of this race are capable of limited reproduction on 'Deltapine 16' cotton; however, race 3 is the most aggressive race on cotton (6).

The objectives of this study were i) to determine the significance of nematode host races in rotations involving cotton, ii) to identify optimum 3-year sequences of four crop species including cotton for management of *M. incognita,* and iii) to investigate the relation of various initial nematode levels to cotton growth and yield.

Materials and Methods

A 3-year experiment was initiated in 1979. One hundred fiberglass microplots (78 cm d × 50 cm deep) (2) were established in a Varina sandy loam on the North Carolina State University Central Crops Research Station near Clayton, North Carolina. All plots were fumigated with methyl bromide (100 g/m^2). Plots were covered with polyethylene tarps for 1 week after the fumigant was applied and then allowed to aerate for 3 weeks before infestation with nematodes.

M. incognita populations 83-1 (race 1) and 178-3 (race 3) were selected from the International *Meloidogyne* Project Live Nematode Culture Collection for their consistent and typical performance in the North Carolina host differential test (14). Each population was increased on tomato

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TABLE 1. Cropping sequences studied for their influence on *Meloidogyne incognita* population dynamics.*

Year planted		
1979	1980	1981
Cotton	Cotton	Cotton
Corn	Corn	Cotton
Peanut	Peanut	Cotton
Soybean	Soybean	Cotton
Cotton	Corn	Cotton
Cotton	Peanut	Cotton
Cotton	Soybean	Cotton
Soybean	Peanut	Cotton
Corn	Soybean	Cotton
Peanut	Corn	Cotton

* Cotton 'Deltapine 16,' Corn 'Pioneer 3368A,' Peanut 'Florigiant,' and Soybean 'Forrest.'

(*Lycopersicon esculentum* Mill 'Rutgers') in greenhouse pots. Inoculum consisted of a mixture of heavily galled roots (chopped into 1–2-cm segments) and potting medium in which the plants had been grown for 70 days. Estimates of juvenile population density per unit volume were obtained by a combination of semiautomatic elutriation (4) and modified centrifugal flotation (1) of 500-cm³ inoculum subsamples. The root fraction trapped on the 40-mesh elutriator sieve was processed by the NaOCl method (5) for estimates of numbers of *M. incognita* eggs.

On 16 May 1979, 5 liters of race 1 inoculum, containing approximately 900,000 eggs and juveniles, were incorporated into the upper 15 cm of each of 50 microplots for each race. The inoculum density was approximately 10,000 eggs and juveniles/500 cm³ soil in the upper 15-cm soil layer.

The experiment was arranged in a split-plot design with nematode populations as main plots and ten 2-year cropping sequences as subplots (Table 1). In year 3 (1981) of the experiment, all plots were planted to cotton. Each crop sequence was replicated five times. Plant species used in the crop sequences included cotton (*Gossypium hirsutum* L. 'Deltapine 16'), soybean (*Glycine max* Merr. 'Forrest'), corn (*Zea mays* L. 'Pioneer 3368A'), and peanut (*Arachis hypogaea* 'Florigiant'). Planting dates were 16 May 1979, 10 May 1980, and 5 May 1981. Each year seeds of the appropriate crops were planted in one row in the center of each plot, then thinned within 1 week after emergence to 8 cotton, 14 soybean, 6 corn, or 8 peanut plants per plot.

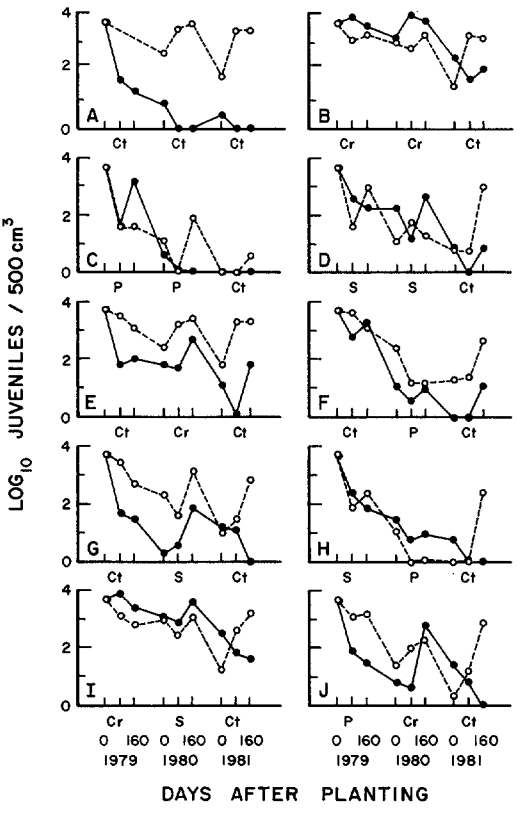

FIG. 1. Densities of *Meloidogyne incognita* race 1 (solid lines) and race 3 (broken lines) per 500 cm³ soil during various 3-year crop rotation sequences. Ct = cotton. Cr = corn. S = soybean. P = peanut.

Plots were limed and fertilized annually according to soil test recommendations for the crop to be planted. Soil samples for nematode assays were collected from the microplots at planting (except in 1979) and 80 and 160 days later. Each sample consisted of 10–12 cores (2.5-cm-d) from depths of 15–20 cm. A 500-cm³ subsample was processed by a combination of elutriation and centrifugal flotation, and egg masses were dispersed with NaOCl as described for inoculum preparation. Nematode numbers were transformed to $\log_{10}(x + 1)$ for statistical analysis.

In 1979 and 1980, all plants were cut at the soil line and removed from the plots at maturity. Roots were left undisturbed in the plots through the winter. Immediately before the subsequent crop was planted, plots were fertilized and lightly worked with

TABLE 2. *Meloidogyne incognita* race 3 population densities on cotton after various cropping sequences in microplots.

Cropping sequence 1979–1980	Juveniles*		Eggs*
	Pi	Pm	Pm
Cotton–cotton	58 a†	2,464 a	127 a
Corn–corn	28 abc	1,914 ab	75 abc
Peanut–peanut	0 c	0 b	0 c
Soybean–soybean	6 c	6 b	2 c
Cotton–corn	54 ab	1,722 ab	95 ab
Cotton–peanut	20 abc	0 b	4 c
Cotton–soybean	18 bc	140 b	12 c
Soybean–peanut	0 c	0 b	0 c
Corn–soybean	16 bc	420 b	39 bc
Peanut–corn	2 c	18 b	5 c

* Soil samples (500 cm^3) were taken at planting (Pi) or 80 days after planting (Pm).

† Means within columns followed by the same letter do not differ significantly at $P = 0.05$ by Duncan's multiple-range test.

TABLE 3. Deltapine 16 cotton root galling and yields in microplots infested with *Meloidogyne incognita* race 3 after various cropping sequences.

Cropping sequence	Root gall index*	1981 seed cotton yield (g/plot)
Cotton–cotton–cotton	4.8 a†	117.4 abc
Corn–corn–cotton	4.4 ab	114.2 bc
Peanut–peanut–cotton	0.2 e	151.8 a
Soybean–soybean–cotton	1.8 d	151.2 a
Cotton–corn–cotton	4.5 ab	108.8 c
Cotton–peanut–cotton	1.7 d	150.4 a
Cotton–soybean–cotton	3.1 c	131.6 abc
Soybean–peanut–cotton	0.2 e	129.6 abc
Corn–soybean–cotton	3.7 c	144.2 ab
Peanut–corn–cotton	1.5 d	131.0 abc

* Gall index based on 0–5 scale where 0 = no galls, 1 = 1–2, 2 = 3–10, 3 = 11–30, 4 = 31–100, 5 = >100 per root system.

† Means within columns followed by the same letter do not differ significantly at $P = 0.05$ (root gall index) or $P = 0.1$ (seed cotton yield) by Duncan's multiple-range test.

a shovel. In 1981, all cotton root systems were removed from the soil, washed, and rated for root galling according to the following scale: 0 = none, 1 = 1–2, 2 = 3–10, 3 = 11–30, 4 = 31–100, and 5 = >100 galls/root system.

Inoculum density: In 1981, 48 additional microplots were fumigated with methyl bromide and inoculated with eggs of either *M. incognita* 83-1 or 178-3 in a water suspension. Eggs were applied in a 2-liter water suspension which was sprinkled uniformly over each plot surface and incorporated to 15 cm deep to give population densities of 500, 1,000, or 5,000 eggs/500 cm^3 soil. Plots were fertilized according to soil test recommendations, and seeds of Deltapine 16 cotton were planted on 7 May. Experimental design was a randomized complete block with six replications.

RESULTS

Population densities of both races of *M. incognita* in each 3-year crop sequence are plotted in Figure 1. In all sequences, race 1 attained lower population densities than race 3 by the end of the 1981 season. Race 1 populations were high on corn for 2 years (Fig. 1B) and increased on corn after cotton (Fig. 1E) or after peanut (Fig. 1J). Two years of soybean (Fig. 1D) or soybean following corn (Fig. 1I) maintained moderate to high levels of this race. Soybean following cotton increased population densities (Fig. 1G). With the exception of an increase in race 1 on peanut in 1979 (Fig. 1C), population densities of race 1 declined during years in which peanut was planted. A slight increase in densities occurred between 80 and 160 days after planting cotton in 1981 (Fig. 1B–F).

Following a decline in the population of race 3 during 1979, densities in the cotton monoculture plots reached the initial inoculation level (10,000/500 cm^3 soil) by 80 days in 1980 and 1981 (Fig. 1A). Corn planted for 2 consecutive years followed by cotton maintained a comparable population density to that seen in cotton monoculture (Fig. 1B). Both peanut (Fig. 1C) and soybean (Fig. 1D) for 2 consecutive years resulted in a decline in the population of this race. Alternating corn with cotton (Fig. 1E) or soybean with cotton (Fig. 1G) was not as effective in decreasing race 3 populations as was peanut alternated with cotton (Fig. 1F). A soybean–peanut rotation (Fig. 1H) resulted in a general population decline to undetectable levels by midseason in 1980. Corn followed by soybean did not substantially decrease race 3 populations (Fig. 1I), and corn following peanut increased population densities during the latter part of the 1980 season (Fig. 1J).

Numbers of race 3 juveniles in cotton monoculture plots at the beginning of the 1981 season and at 80 days postplanting

TABLE 4. Microplot population densities at 80 and 160 days after planting and cotton response to *Meloidogyne incognita* races 1 and 3 at various inoculation levels.*

Nematode race	Pi/500 cm³ soil	Nematode density†		Plant wt (g/plot)	Root wt (g/plot)	Root gall index‡	Seed cotton yield (g/plot)
		Pm	Pf				
Race 1	0	0 a§	0 a	137 a	29 a	0 a	81 a
	500	0 a	0 a	139 a	34 a	0.1 a	85 a
	1,000	0 a	120 a	142 a	31 a	0.1 a	85 a
	5,000	0 a	150 a	163 a	40 a	0.1 a	78 a
Race 3	0	0 b	0 c	202 ab	42 a	0 d	83 a
	500	21 b	1,160 b	199 ab	50 a	2.0 c	73 a
	1,000	120 b	2,970 b	243 a	53 a	3.2 b	75 a
	5,000	1,113 a	6,945 a	117 b	34 a	4.2 a	80 a

* Inoculum levels were calculated for 90 liters of soil (total volume of soil in upper 15 cm of each plot).
† Juveniles/500 cm³ soil. Pm = midseason density. Pf = density 160 days after planting.
‡ 0 = no galls, 1 = 1–2, 2 = 3–10, 3 = 11–30, 4 = 31–100, 5 = >100 per root system.
§ Column means within races followed by the same letter do not differ significantly by Waller-Duncan *k*-ratio *t*-test.

were significantly greater than after any of the other cropping sequences studied (Table 2). Initial populations (Pi) of less than 10 juveniles/500 cm³ soil occurred in plots where 2 years of peanut or soybean, soybean followed by peanut, or peanut followed by corn had been grown. By 80 days after planting, juvenile populations in cotton plots previously in cotton or corn monoculture or cotton followed by corn reached higher levels than in cotton following the other sequences. Egg densities in all plots were near or below the detectable level at planting in 1981. After 80 days, the greatest egg densities occurred in plots following cotton or corn monoculture or cotton followed by corn.

Root gall indices on cotton infected with race 3 at the end of the 1981 season were highest following cotton or corn monoculture or cotton followed by corn (Table 3). The race 3 populations in cotton plots (1981) following a cotton–soybean or corn–soybean sequence caused significantly lower gall indices than in plots following 2 years of cotton, 2 years of corn, or a cotton–corn rotation. Soybean–soybean, cotton–peanut, or peanut–corn resulted in slight cotton root galling by race 3 in 1981. After peanut–peanut or soybean–peanut, cotton root gall indices were lower than in any other crop sequence.

At $P = 0.05$, there were no significant differences in seed cotton yields with any cropping sequence, but at $P = 0.1$, significantly greater yields were found after peanut–peanut, soybean–soybean, or cotton–peanut (Table 3). Seed cotton yields following a cotton–corn sequence were the lowest of all sequences.

Inoculum density: Race 1 populations were low or undetectable at harvest regardless of initial inoculum level (Table 4). Root gall indices were low in all treatments. No significant suppression of cotton plant weight or seed cotton yield occurred in any of the race 1 treatments.

In race 3 plots, levels of 500 or 1,000 eggs/500 cm³ soil did not suppress cotton top weights. Top weights were lower, however, at 5,000 eggs/500 cm³, but seed cotton yields were not affected. Root gall indices increased in severity as inoculum level increased.

DISCUSSION

The nematode population data from this study confirm the report of differences in reproductive ability between races 1 and 3 of *M. incognita* on cotton (6). In all crop sequences which included cotton, population densities of race 1 were low. Race 3, on the other hand, reproduced well on cotton. In field rotation studies including cotton, corn, peanut, and tobacco, populations of *M. incognita acrita* increased after cotton or corn but not after peanut (12). In that study, one population of *M. incognita acrita* reproduced well on both cotton and tobacco, while another population reproduced only on cotton, results commonly associated with races 4 and 3, respectively, of *M. incognita* (14).

Corn and cotton were suitable hosts for race 3. Race 1 appeared to be capable of greater reproduction on corn than race 3

(Fig. 1B). Peanut has been reported as a nonhost for all races of *M. incognita* (14), and in our studies, populations of both races generally declined under peanut.

Although cotton is a poor host for race 1, slight population increases occurred between midseason and harvest during 1981 on cotton in several of the plots (Fig. 1B, D–F). However, gall indices in all cases were very low. This study illustrates the influence of good-, poor-, or non-host crops on *M. incognita* race 3 population levels. Either peanut, a nonhost, or soybean, a poor host, resulted in low initial and midseason population densities (Table 2) and relatively low root gall indices (Table 3) in the subsequent cotton crop. The data presented here indicate that one peanut or soybean planting was as effective as 2 years in either crop in reducing race 3 populations for the next cotton crop.

Both cotton and corn were good hosts of race 3 in this study. Cropping sequences which included either or both of these crops resulted in more severe root galling on cotton, during the 1981 season, than did sequences in which peanut or soybean were used (Table 3). Care should be exercised in any corn–cotton rotation where the presence of race 3 is suspected.

Agricultural producers many times make nematode management decisions with little or no consideration of the *Meloidogyne* race present. Soil assays for nematodes are useful in determining nematode control measures including selection of rotation crops, but are of no help in determining races. *M. incognita* is the only major *Meloidogyne* species of economic importance in cotton in the United States, and within this species less than 25% of the populations studied through the International *Meloidogyne* Project are capable of appreciable reproduction on cotton (6,10).

These data indicate that where aggressive races occur, crop rotation or other nematode management procedures may be necessary for cotton production. The race 1 data shown here, as well as earlier studies with all four races on resistant and susceptible cotton (6), indicate that the nonaggressive races (races 1 and 2) probably will not be a limiting factor in cotton production.

Our work concerned the management of only *M. incognita* through cropping sequences because this species is the most economically important plant-parasitic nematode in many areas where cotton is produced (11). However, since field communities of plant-parasitic nematodes are usually polyspecific in nature (8), crop rotation for management of one species may result in increased populations of other potentially damaging species (3,8). Further studies on the influence of cropping sequences on nematodes other than *M. incognita* are needed.

We have demonstrated the significance of cropping sequences on the population dynamics of a major cotton parasite. An awareness of the occurrence of races within this species and a knowledge of the races common to a particular region should provide the basis for rational nematode management decisions.

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