

# Population Dynamics of *Ditylenchus destructor* on Peanut<sup>1</sup>

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**Abstract:** The population development of *Ditylenchus destructor* in the roots, pegs, hulls, and seeds of eight peanut (*Arachis hypogaea*) genotypes was studied in the greenhouse. Although all genotypes tested were good hosts for *D. destructor*, differences in host suitability were observed. Invasion of the plant parts by *Ditylenchus destructor* proceeded more slowly in genotypes with long growth periods. During the second half of the growth period of these genotypes, *D. destructor* populations emigrated from the hulls and seeds into the soil but reinfected the pods after a few weeks. The genotypes with the longest growth periods supported the highest number of nematodes when each genotype was harvested at its usual harvest time. The long-season genotypes supported low numbers of nematodes when harvested before crop maturity.

**Key words:** *Arachis hypogaea*, *Ditylenchus destructor*, nematode, peanut, population dynamics, potato rot nematode.

*Ditylenchus destructor* Thorne, commonly known as the potato rot nematode, is the most important seed-borne nematode of peanut (*Arachis hypogaea*) in the Republic of South Africa (4,8). *Aphelenchoides arachidis* is the only other nematode species associated with peanut that also invades the seeds (4,9). *Ditylenchus destructor* has a life cycle of 6–7 days at 28 C and a high reproductive potential (3). Inoculation of peanut callus tissue with 50 *D. destructor* resulted in a 600-fold increase in nematode numbers within 5 weeks (1). In greenhouse experiments, inoculation with 50 *D. destructor*/seedling caused significant yield suppression on peanut cultivar Sellie (10). *Ditylenchus destructor* has been reported mainly from temperate regions (localized areas in the United States, many parts of Europe, and the USSR) (4). It is important as a pest of potato tubers and bulbs of flowers (6), but it has not been reported in hulls and seeds of peanut outside South Africa.

Peanut is grown annually on ca. 200,000 ha in South Africa. Apart from the most widely grown cultivar, Sellie, two other cultivars, Norden and Harts, were released in

1988 (12,13). Several cultivars and breeding lines, including Selmani, Misga, and PC 137-K41, are being developed. With the exception of Sellie, the suitability of these genotypes as hosts of *D. destructor* is unknown.

The objective of this study was to determine the population dynamics of *D. destructor* in roots, pegs, hulls, and seeds of peanut. Since the length of the growth period (average days until maturation) of the host may affect the final number of nematodes recovered, genotypes with different growth periods were used in the investigation.

## MATERIALS AND METHODS

Three experiments were conducted in a greenhouse maintained at 25 C day-night temperature with a 13-hour photoperiod. The following procedures were used in each experiment. Nematode-free peanut seeds were planted in plastic pots filled with 3,000 cm<sup>3</sup> steam pasteurized sandy soil (85% sand, 8% silt, 7% clay) and supplemented with *Rhizobium* nitrogen-fixing bacteria. Seedlings were thinned to one per pot 2 weeks after planting and inoculated with 3,500 ± 100 *D. destructor* 3 weeks after planting. Inoculum of *D. destructor* of various life stages was obtained from monoxenic cultures (14). Nematodes in 10-ml aqueous suspensions were pipetted into a hole in the root zone of the seedlings. The plants were irrigated three times a week with 200 ml water and fertilized weekly with a nutrient solution (6.5% N, 2.7% P,

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13% K). At each sampling date, fresh weight of root, peg, hull, and seed per plant were determined. In the first experiment, nematodes were extracted from one 200-cm<sup>3</sup> soil sample per pot by means of a decanting and sieving method (5), with 710- $\mu$ m-pore and 45- $\mu$ m-pore sieves, followed by centrifugal flotation (7). Nematodes were extracted from 5 g fresh roots and 1 g pegs by a centrifugal-flotation method (2) and from 5 g fresh hulls and seeds by soaking the tissues in shallow water in petri dishes for 24 hours at room temperature (1). Since these methods do not recover all the nematodes present in the samples, correction factors were used to calculate the total number of nematodes (y) from the number extracted (x). These were  $y = 5.0x$  for roots and pegs,  $1.5x$  for soil,  $2.2x$  for seeds, and  $1.87x$  for hulls (1, unpubl. data).

A completely randomized design was used in the first experiment, with Sellie as an experimental plant. Eight plants were sampled at random from 6–24 weeks after planting at 3-week intervals. In the second experiment seeds of Harts and Misga (short-season genotypes), PC 137 and Sellie (medium-season genotypes), and Norden and Selmani (long-season genotypes) were planted in a randomized block. Eight plants of each genotype were sampled at 6, 9, 15, 18, 21, and 24 weeks after planting. In the third experiment, the genotypes Valencia 247 (medium-season), N. Rhodesia MS 20 (long-season), and MK 383 (very long-season), were used in a randomized block design. Three plants of each genotype were harvested every 3 weeks, from 6 to 27 weeks after planting.

Population data of the first experiment were subjected to analyses of variance in which the treatments were weeks after planting. Data of nematode counts were transformed to  $\log(x + 1)$  and means were compared by the Student-Newman-Keuls range test (11). The second and third experiments were analysed with a factorial model. The main effects were genotype and sampling date. Data were transformed to  $\log(x + 1)$  and *post hoc* comparisons of

means or groups of means were conducted by Scheffé's method (10).

## RESULTS

*Experiment 1:* Numbers of *D. destructor* in the roots of Sellie remained low throughout the growing period of the plants (Fig. 1A). Nematode populations in the pegs increased from an average of 30/g at 9 weeks to 18,300/g at 24 weeks after planting. At 18, 21, and 24 weeks, the pegs had more ( $P < 0.05$ ) nematodes than the roots.

Nematode numbers were greater ( $P < 0.05$ ) in the seeds and hulls than in the soil at 15 and 18 weeks after planting (Fig. 1B). Between 18 and 21 weeks, the nematode population increased in the soil and decreased in the seeds and hulls. Nematode numbers were greater ( $P < 0.05$ ) in the soil than in the seeds and hulls at 21 weeks. The nematode population then again decreased in the soil and increased in the seeds and hulls.

*Experiment 2:* Numbers of *D. destructor* in the roots of the six peanut genotypes remained low (av. 40/g) throughout the growing period of the plants and are not discussed. At 9 weeks almost no nematodes were found in the pegs, seeds, and hulls, since these plant parts had just begun to develop. The nematode population development is therefore discussed only from 15 weeks on.

In the pegs, significant interactions occurred between genotype and sampling date of the different genotypes. The genotype with the longest growth period, Selmani, exhibited a different pattern of population development, which gave rise to these interactions. Therefore the data were reanalyzed with the shorter season genotypes in one group (Fig. 2A) and Selmani in a separate group (Fig. 2C). There were no differences in nematode numbers in the pegs of the first group of genotypes (Fig. 2A). The population development of nematodes in these genotypes as a group (Fig. 2B) showed that the nematode numbers increased ( $P < 0.001$ ) between 15 and 18 weeks after planting. Between 18 and 21 weeks the nematode population re-

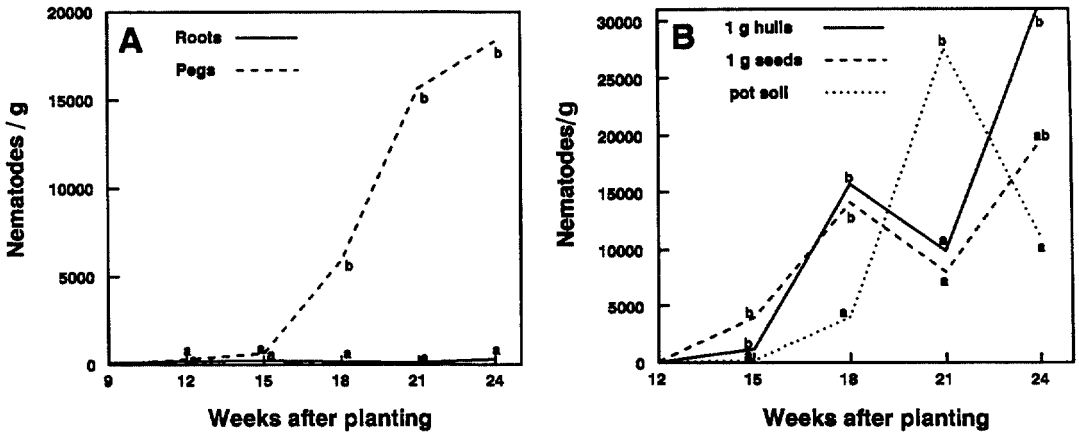


FIG. 1. Population development of *Ditylenchus destructor* on peanut cultivar Sellie. A) In roots and pegs. B) In hulls, seeds, and soil.

mained constant, but it decreased ( $P = 0.01$ ) between 21 and 24 weeks. The pegs of Selmani had fewer nematodes than did those of the other five genotypes (Fig. 2A, C). The numbers of nematodes in the sampling dates of Selmani did not differ from each other (Fig. 2D). Nematode numbers in pegs of Selmani, unlike those in pegs of the other genotypes, decreased between 18 and 21 weeks and increased again between 21 and 24 weeks.

Significant interactions between genotype and sampling date also occurred in the seeds of the different genotypes. This was due to a difference in population development between the short-season and

medium-season genotypes and the long-season genotypes. The short-season and medium-season genotypes were therefore analyzed as one group (Fig. 3A), and the long-season genotypes as a second (Fig. 3C). The nematode numbers in the seeds of the short-season genotypes, Harts and Misga, were lower ( $P = 0.01$ ) than those in the seeds of the medium-season genotypes, PC 137 and Sellie (Fig. 3A). Using 95% confidence intervals to compare the average nematode numbers, it appeared that there were more nematodes in the seeds of the short-season and medium-season genotypes than in the seeds of the long-season genotypes (Fig. 3A, C). Selmani also sup-

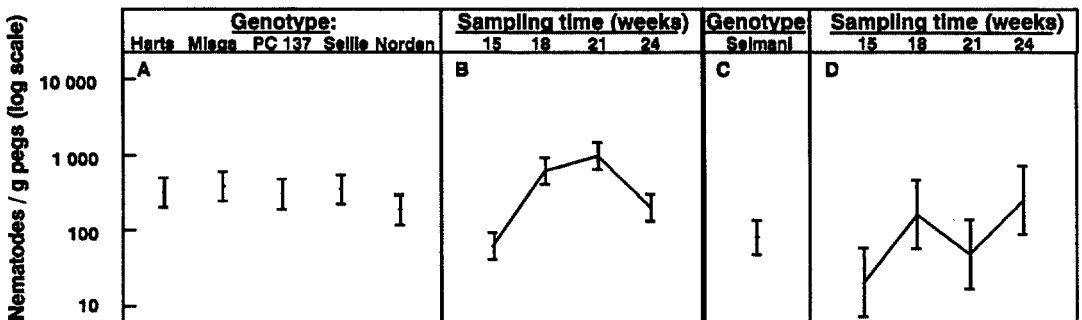


FIG. 2. Population development of *Ditylenchus destructor* in the pegs of different peanut genotypes. A) Mean population densities over four sampling dates for genotypes Harts, Misga, PC 137, Sellie, and Norden. B) Change in population density over time for genotypes Harts, Misga, PC 137, Sellie, and Norden. C) Mean population density on cultivar Selmani over four sampling dates. D) Change in population density on Selmani over time.

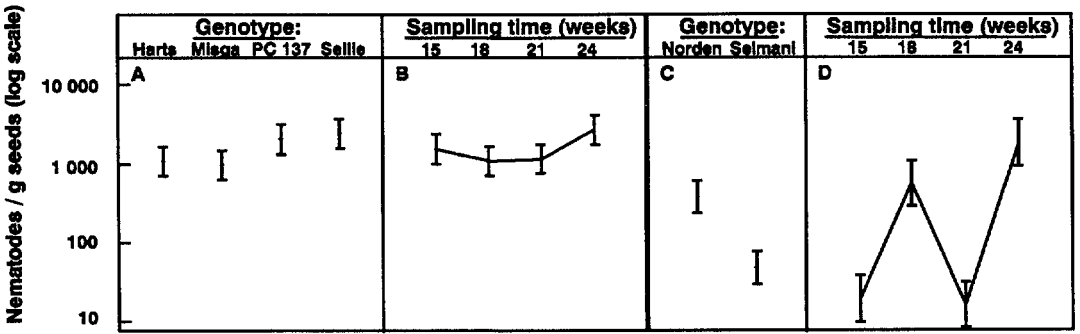


FIG. 3. Population development of *Ditylenchus destructor* in the seeds of different peanut genotypes. A) Mean population densities over four sampling dates for genotypes Harts and Misga (short-season) and PC 137 and Sellie (medium-season). B) Change in population density over time for genotypes Harts, Misga, PC 137, and Sellie. C) Mean population density on genotypes Norden and Selmani (long-season) over four sampling dates. D) Change in population density of Norden and Selmani over time.

ported fewer ( $P < 0.001$ ) nematodes than did Norden (Fig. 3C). Nematode numbers in the seeds of the short-season and medium-season genotypes remained constant over the four sampling dates (Fig. 3B). In contrast, the nematode numbers in the seeds of the long-season genotypes, Norden and Selmani, were lower ( $P < 0.001$ ) at 15 and 21 weeks than at 18 and 24 weeks (Fig. 3D).

Significant interactions between genotype and sampling date also occurred with regard to nematode numbers in the hulls. These interactions also appeared to be related to length of growing season. Therefore the data were again analysed as two groups: the shorter season genotypes

(growth periods 17 to 20 weeks) and the longer season genotypes (growth periods 21 to 24 weeks). Nematode population levels in the hulls of the first group were similar (Fig. 4A). In the second group (Fig. 4C), however, the numbers of nematodes in the hulls of Sellie were greater ( $P < 0.001$ ) than in Norden, whereas Norden, in turn, maintained greater ( $P < 0.001$ ) numbers of nematodes than did Selmani. The population development in the hulls of the shorter season genotypes (Fig. 4B), showed that fewer ( $P < 0.001$ ) nematodes were found at 15 weeks than at 18 weeks and at 21 weeks than at 24 weeks ( $P < 0.001$ ). The population levels in the longer season group decreased at 21 weeks so that

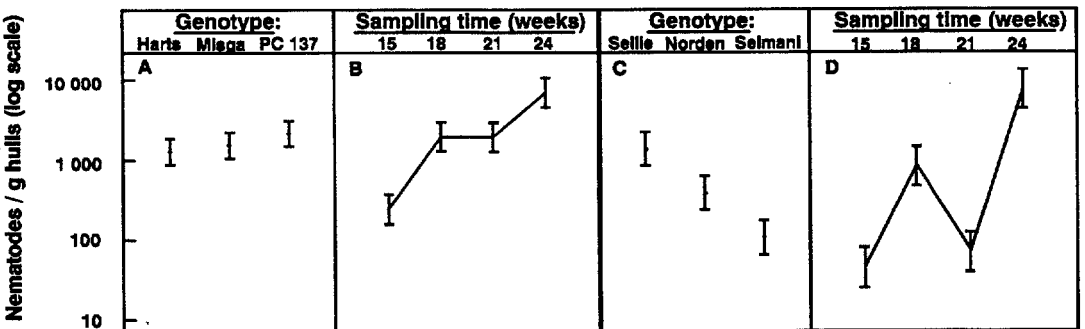


FIG. 4. Population development of *Ditylenchus destructor* in the hulls of different peanut genotypes. A) Mean population densities over four sampling dates for shorter season genotypes Harts, Misga, and PC 137. B) Mean of the change in population density over time for genotypes Harts, Misga, and PC 137. C) Mean population density on longer season genotypes Sellie, Norden, and Selmani over four sampling dates. D) Change in population density of Sellie, Norden, and Selmani over time.

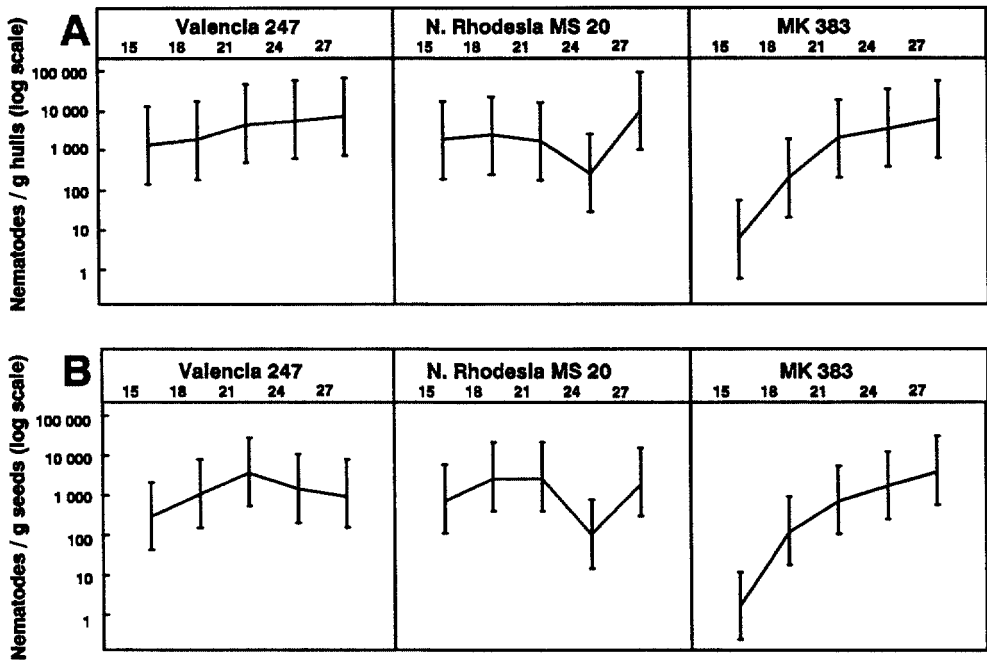


FIG. 5. Population development of *Ditylenchus destructor* on three peanut genotypes representing a medium (21 weeks), long (24 weeks), and very long (27 weeks) growth period. A) In hulls. B) In seeds.

fewer nematodes ( $P < 0.001$ ) were found in the hulls at 15 and 21 weeks than at 18 and 24 weeks (Fig. 4 D).

*Experiment 3:* The population development patterns in the hulls and seeds of the medium-season genotype, Valencia 247, and the long-season genotype, N. Rhodesia MS 20, differed, although there were no significant differences in nematode numbers between the sampling dates for both genotypes (Fig. 5). The hulls and seeds of MK 383, sampled at 15 weeks, had fewer ( $P < 0.05$ ) nematodes than those sampled 21–27 weeks after planting.

#### DISCUSSION

Although the pattern of nematode population development differed according to growth period, all genotypes tested were good hosts for *D. destructor*. The significant drop in nematode numbers in the hulls and seeds 21 weeks after planting, and the simultaneous increase of numbers in the soil, suggests that the nematodes migrate during that growth stage of the cultivar Sellie. This migration may be caused by physio-

logical changes in the hulls and seeds during maturation of the plant. A complex process of the time and mode of entry and development of *D. destructor* in roots, pegs, hulls, and seeds of Sellie was observed previously (9). Of the total final population, 2% of the nematodes were recovered from the roots, 4% from the pegs, 6% from the soil, 33% from the seeds, and 55% from the hulls. The preference of *D. destructor* to colonize hulls and seeds has been reported (8).

The migration of the nematodes between the hulls and seeds differed between the genotypes. The relationship between population levels in hulls and seeds often changed during the course of the trial, except in Selmani where the number of nematodes remained higher in the hulls than in the seeds. These patterns did not correspond with the growth periods of the genotypes.

The long-season genotypes supported fewer nematodes than did the shorter season genotypes. The decrease in nematode numbers in hulls and seeds of the longer

season genotypes near the end of the season, occurred in all three experiments (except in the very long-season genotype, MK 383).

The data presented, indicate that advancing the harvest dates of the long-season genotypes may prevent major nematode buildup. Repetition of these trials in the field is important to confirm the greenhouse experiments. Further research is necessary to investigate the possibility of physiological changes with plant maturation of the various peanut genotypes. This could cause the characteristic population dynamics found on genotypes of various growth periods, in particular the significant decrease of nematode numbers in the long-season genotypes.

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