



Genetic Parameters and Population of Coriander Reaction to *Meloidogyne incognita* Race 1

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Authors' contributions

This work was carried out in collaboration with all authors. Authors AMMS and KDSC designed the study, performed statistical analysis, wrote the protocol and wrote the first draft of the manuscript. Author CSRMM managed bibliographic searches. Authors DLN and MOS transcribed the final version, placed it in the journal's rules and was responsible for submitting it to the publication. Authors JLS and DM managed the analyzes of the study as well as the work. All authors read and approved the final manuscript.

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ABSTRACT

The genetic parameters provide indispensable information about the genetic behavior of the study population regarding the characters evaluated, providing subsidy to the breeder on the decision about the best selection method to adopt in order to realize a genetic gain and maintain adequate variability. In this sense, the present study was carried out to verify the reaction and to estimate genetic parameters of a population of coriander composed of two cultivars (Verdão and HTV Dom Luiz) and 49 half-siblings progenies parasitized by *Meloidogyne incognita* race 1. The experiment was conducted in a greenhouse in the Department of Agronomy of the Federal Rural University of Pernambuco. The 51 cultivars and progenies were arranged in a randomized block design with four

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replicates and each experimental plot was composed of eight plants. The sowing was carried out in a tray of 128 cell- expanded polystyrene filled with commercial substrate, 1,000 eggs/cell of the pathogen were inoculated on the same day of sowing. After 30 days of inoculation, the number of galls was quantified in the root system, the pathogen's eggs were extracted and, after the quantification of the eggs, the reproduction factor was estimated for each genotype. Data of the three characteristics were compared by Scott-Knott clustering test, then classified as resistant or susceptible, and genetic parameters estimated. The genotypes differed from each other at 1% probability level for all the characters under study. Heritabilities were high and positive with values of 75.91 for number of galls in the root system and 96.72 for the number of eggs. Based on the phenotypic and genotypic correlations, it was possible to select desired genotypes based on the number of galls in the initial selection cycles, making selection and recombination possible in the same cycle. Twelve (12) progenies were selected for their resistance to the pathogen.

Keywords: *Coriandrum sativum* L.; heritability; correlations; root-knot disease.

1. INTRODUCTION

Coriander is one of the 12 vegetables with the largest participation in the national market with a tendency to increase in the next few years [1]. It is widely cultivated in the Northeast region of Brazil [2]. The planted area of about 73,938 hectares and productivity of 15 t/ha, with revenues in the production of seeds and seedlings of \$10.99 and \$243.57 millions, respectively [1], reflect the economic importance of the crop in the country due to its market destinations. It ranges from the consumption of its leaves and fruits in raw state, to raw material for the food, pharmaceutical, alternative medicine [3] and perfume industries [4].

Several characteristics of the crop are to be improved, such as its resistance to early tillage [5], resistance to biotic and abiotic factors [6,7,8], as well as the inherent color, aroma and leaf texture. Among the diseases that affect the culture there is one caused by a species of the genus *Meloidogyne*, notably *M. incognita* race 1, the most harmful to coriander [9].

There are studies in the literature evaluating the reaction of cultivars and progenies of coriander to the attack caused by *M. incognita* race 1 searching to identify superior genotypes that can be a source of resistance to be explored in genetic improvement of the crop [10,11,9]. The evaluation of different cultivars is fundamental, since the increase of genetic variability is a strategy that must be explored in order to obtain gain from selection.

The study of genetic parameters of characters related to the infection caused by *M. incognita* race 1 is fundamental for the genetic

improvement of the crop, for the genetic parameter statistics that allow identifying the nature of the action of the genes involved in the control of the pest and to evaluate the efficiency of different breeding strategies, obtaining genetic gains and maintaining an adequate genetic basis of the breeding stock. Among the genetic parameters, the most important are additive and non-additive genetic variances, genetic correlations, and heritability [12]. In this way, the breeder must choose the best characters to be used in the selective processes, taking into account information such as the CVg/CVa and heritability. According to Costa et al. [13], heritability is a genetic parameter of extreme importance to the breeder, the estimation of the part of the phenotypic variance that is due to genetic effects and making possible the choice of the selection methods to be applied.

The objective of this work was to evaluate the reaction and to estimate the genetic parameters of two cultivars and 49 progenies of C2 half-sibs of coriander, regarding the parasitism caused by *M. incognita* race 1.

2. MATERIALS AND METHODS

The experiment was conducted in a greenhouse, in the Department of Agronomy of the Federal Rural University of Pernambuco (UFRPE), located at 8°54'47"S, 34°54'47"W, 6 m altitude, in the period from November to December 2017. The monthly average temperatures recorded by the weather station of Recife Curado (automatic) varied between 22.3 - 32.2°C, for minimum and maximum temperatures, respectively [14]. The experimental design was a randomized complete block design with four replicates, whose plot was composed of eight plants.

The reactions of two coriander cultivars (Verdão and HTV Dom Luiz) and 49 C2 progenies of coriander half-siblings inoculated with 1,000 eggs/cell at sowing were evaluated.

Of the evaluated progenies, 44 were obtained from the Verdão cultivar, by means of the evaluation of 2,000 plants sown on a tray of 128 cell- expanded polystyrene, inoculated with 1,000 eggs/cell of *M. incognita* race 1 at sowing and evaluated (counting of number of galls) at 30 days after inoculation. Plants with gall numbers lower than 10 were selected and transplanted to 2 L pots containing a substrate composed of soil and humus at a ratio of 3:1. The pots were placed in the open field at a spacing of 30 cm between plants in the row and 1 m between the rows, so that recombination occurred among the selected individuals. At harvest, each plant had its fruits collected individually and stored in properly identified paper bags, corresponding to the half-sib progenies C1. The progenies obtained in the first cycle were again evaluated with inoculation of 1,000 eggs/cell at sowing in a randomized block design with three replicates and a plot composed of 8 plants. The selection was carried out between and within the progenies in the same cycle, whose selection and recombination adopted the same criterion as the first selective cycle.

The other 5 progenies were obtained from the HTV Dom Luiz cultivar by the same procedure as the Verdão cultivar, with the exception of the inoculum density (4,000 eggs/cell) and the selection pressure, where the plants should have less than 5 galls in the root system to be selected. The highest density of inoculum in the Dom Luiz HTV cultivar was used because it presented greater tolerance to the pathogen when compared to Verdão in previous experiments.

Sowing was carried out in 128-cell expanded polystyrene trays containing the commercial substrate, placing two coriander seeds at a depth of approximately 0.5 cm, and then covering with the substrate. Subsequently, irrigation and inoculation of 1,000 eggs/cell of *M. incognita* race 1 were performed. Irrigation was carried out daily according to the water requirement, and fertigation was applied three times a week, preventing drainage with subsequent loss of inoculum.

After 30 days of sowing/inoculation, evaluation was performed. For this, the root system was washed in standing water to remove the

substrate. Then, the number of galls was quantified and the eggs were extracted from each individual plant according to methodology proposed by Hussey and Barker [15] and modified by Bonetti and Ferraz [16]. The eggs extracted were stored in properly identified containers and placed in a cold chamber until, the count was performed using a microscope (brand, manufacturer, city, country), increased 40X, and Peters' blade.

After quantification of the number of eggs, the reproduction factor (RF) for each sample was estimated as the ratio between the final population of the pathogen (number of eggs quantified in the sample) and the initial population of the nematode (1,000 eggs/cell). To classify the reaction of the cultivars and progenies of coriander to the pathogen, the scale of Oostenbrink [17] was used. Genotypes with $RF < 1$ were considered resistant, and those with $RF > 1$ were considered susceptible.

The data obtained were transformed by \sqrt{x} to meet the assumptions of the analysis of variance, and were submitted to it, with subsequent Scott-Knott grouping test at 5% probability, using the SISVAR statistical software [18]. The genetic parameters were estimated by the GENES statistical program [19].

3. RESULTS AND DISCUSSION

There were highly significant differences in the number of galls in the root system, number of eggs and reproduction factor among the evaluated genotypes. The coefficients of variation ranged from 11.65% to 16.86% (Table 1). Values of CV between 10 and 20% are considered as medium experimental precision [20], which according to Cargnelutti Filho and Storck [21] are not of concern.

For the number of galls in the root system, the means were divided into three groups. In the first group, the means varied between 3.75 and 6.75; in the second group of 8.00 - 11.25 and in the third group of 11.75 - 24.00 (Table 2). The means obtained in the three groups are inferior to those obtained by Santos et al. [9] evaluating the cultivars Verdão, Tabocas, Tapacurá, Palmeira and HTV Dom Luiz in the treatment that had as levels of the factors container and substrate, tray and Basaplant®. These results showed that it is possible to obtain promising progenies among those evaluated in the present study, based on this characteristic.

Table 1. Summary of the variance analysis of the number of galls in the root system (NGRS), number of eggs (NE), and the reproduction factor (RF) of two cultivars and 49 progenies of coriander inoculated with *Meloidogyne incognita* race 1

Source of variation	Degree of freedom	Square means		
		NGRS ⁺	NE ⁺	RF ⁺
Blocks	3	1.31	81.43	0.08
Genotypes	50	1.33 ^{**}	443.63 ^{**}	0.44 ^{**}
Error	150	0.32	14.57	0.02
QV%		16.86	11.65	11.68
Mean		3.36	32.75	1.04

⁺ Data transformed by \sqrt{x}

^{**} Significant at 1% probability, ^{ns} not significant

Table 2. Scott-Knott grouping test and reaction of two cultivars and 49 coriander progenies to *M. incognita* race 1 indicated by the number of galls in the root system (NGRS), number of eggs (NE), and reproduction factor (RF)

Genotypes	NGRS	NE	RF	Reaction*
67	3.75 a	265.25 a	0.27 a	Resistant
DP10	4.00 a	114.75 a	0.12 a	Resistant
58	4.75 a	311.75 a	0.32 a	Resistant
5	5.00 a	418.25 a	0.42 a	Resistant
69	5.50 a	160.75 a	0.16 a	Resistant
18	6.75 a	526.00 a	0.53 a	Resistant
DP11	8.00 b	225.75 a	0.23 a	Resistant
45	8.75 b	1107.50 b	1.11 b	Susceptible
51	9.00 b	857.75 b	0.86 b	Resistant
DP2	9.00 b	732.75 b	0.73 b	Resistant
8	9.50 b	746.00 b	0.75 b	Resistant
Verdão	9.75 b	1328.50 c	1.33 c	Susceptible
29	10.00 b	266.00 a	0.27 a	Resistant
4	10.25 b	2539.25 e	2.54 e	Susceptible
21	10.25 b	629.25 b	0.63 b	Resistant
31	10.25 b	576.00 a	0.58 a	Resistant
1	10.50 b	1159.50 b	1.16 b	Susceptible
40	10.83 b	750.25 b	0.75 b	Resistant
47	11.00 b	1037.50 b	1.04 b	Susceptible
64	11.19 b	487.00 a	0.49 a	Resistant
60	11.25 b	1445.00 c	1.45 c	Susceptible
54	11.25 b	1467.25 c	1.47 c	Susceptible
38	11.75 c	1556.25 c	1.56 c	Susceptible
19	11.75 c	879.75 b	0.88 b	Resistant
16	12.00 c	1902.75 d	1.90 d	Susceptible
15	12.44 c	1601.75 c	1.60 c	Susceptible
14	12.50 c	1564.00 c	1.57 c	Susceptible
49	12.50 c	1817.50 d	1.82 d	Susceptible
DP6	12.75 c	267.25 a	0.27 a	Resistant
HTV Dom Luiz	12.75 c	1711.50 d	1.71 d	Susceptible
33	13.00 c	1705.00 d	1.71 d	Susceptible
57	13.00 c	1542.25 c	1.54 c	Susceptible
3	13.50 c	1328.25 c	1.33 c	Susceptible
23	13.50 c	953.50 b	0.95 b	Resistant
42	13.50 c	1393.25 c	1.40 c	Susceptible
24	13.75 c	1503.00 c	1.50 c	Susceptible
44	13.75 c	1091.00 b	1.09 b	Susceptible
56	14.00 c	2596.25 e	2.60 e	Susceptible

Genotypes	NGRS	NE	RF	Reaction*
48	14.00 c	2358.50 e	2.36 e	Susceptible
22	14.25 c	676.00 b	0.68 b	Resistant
DP1	14.25 c	1273.25 c	1.28 c	Susceptible
20	14.50 c	820.50 b	0.82 b	Resistant
28	14.75 c	474.50 a	0.48 a	Resistant
46	14.75 c	1394.50 c	1.40 c	Susceptible
32	15.06 c	1348.63 c	1.35 c	Susceptible
12	15.25 c	1838.25 d	1.84 d	Susceptible
34	16.25 c	2337.50 e	2.34 e	Susceptible
53	16.75 c	1783.25 d	1.79 d	Susceptible
50	17.00 c	1945.50 d	1.95 d	Susceptible
52	17.00 c	2169.00 e	2.17 e	Susceptible
30	24.00 c	1876.75 d	1.88 d	Susceptible

* Oostenbrink scale (1966), resistant $FR < 1$ and susceptible $FR > 1$ genotypes.

Means followed by the same lower case letter in the column do not differ statistically by the Scott-Knott test at 5% probability

For the number of eggs, the means varied from 114.75 to 2596.25; forming five groups within this range. The reproduction factor had a trend similar to the number of eggs, since it was directly proportional to this variable. The first group was formed by reproduction factors from 0.12 to 0.58; being all the genotypes classified as resistant and presenting the smallest means, being therefore, those indicated for selection. In the second group, composed of reproductive factors from 0.63 to 1.16, individuals with $RF < 1$ and $RF > 1$ were present. However, because they were statistically different from the first group, which presented the lowest means, genotypes with $RF < 1$ will not be selected. In the other three groups, the reproduction factors were all higher than one, and the selection of such progenies is not recommended.

The RF values of the progenies of group "a" ($0.12 \leq RF \leq 0.58$) were lower than those obtained for the cultivars Verdão ($RF = 1.33$) and HTV Dom Luiz ($RF = 1.71$). These progenies also showed smaller RFs than those found by Santos et al. [9], which presented 1.54; 1.59; 1.69; 2.01 and 2.42 for the cultivars HTV Dom Luiz, Tapacurá, Verdão, Palmeira and Tabocas, respectively. Diniz et al. [11] also obtained a superior result to those found in the present study, where the cultivar Verdão showed a $RF = 2.4$ when inoculated with 1200 eggs of *M. incognita* race 1 at 15 days after sowing and evaluated at 45 days after inoculation. Thus, the progenies belonging to the group "a", presented superior behavior regarding the resistance to *M. incognita* race 1, being promising to give continuity to the program of genetic improvement of the culture.

As for the genetic parameters, in all analyzed characters there is a greater contribution of the genetic variation to the variation presented by the phenotype, indicating that there is actually genetic variability among the evaluated progenies, simplifying the selection process and making selection possible (Table 3). This fact was very important because, according to Borém and Miranda [22], the greater the proportion of variability resulting from the environment in relation to phenotypic variability, the more difficult it is to perform genotype selection effectively, reducing the efficiency of the selective process carried out by the breeder.

The coefficients of genetic variation (CVg) were 14.97 and 31.62 for the number of galls in the root system and the reproduction factor, respectively. The coefficient of genetic variation allows inferring about the genetic variability among the characters, and aids the selection of superior genotypes for it evidences the levels of genetic variability present in different genotypes, environment, and characters [23]. Therefore, the estimation of the genetic variance between family means (progenies) is fundamental and indispensable for the breeder, since the success of a breeding program depends on the existence of genetic variability in the base population [12].

The heritability presented values from 75.91 (NGRS) to 96.72 (NE), which were considered high. The attainment of high estimates of heritability indicates that it is possible to select superior genotypes [5]. Therefore, it is possible to obtain a genetic gain (or resistance to *M. incognita* race 1) with the selection based on the number of galls in the system, the number of eggs, and reproduction factor.

Table 3. Genetic parameters estimated for the number of galls in the root system (NGRS), number of eggs (NE), and reproduction factor (RF)

Genetic parameters	Characters		
	NGRS	NE	RF
V_g	0.25	107.27	0.107
V_e	0.08	3.64	0.004
V_p	0.33	110.91	0.111
h^2	75.91	96.72	96.70
CV_g	14.97	31.62	31.62
CV_a	16.86	11.62	11.68
CV_g/CV_e	0.89	2.71	2.71

Phenotypic variance (V_p), environmental variance (V_e), genetic variance (V_g), heritability (h^2), coefficient of genetic variance CV_g , coefficient of environmental variance (CV_e), and mean between coefficient of genetic and environmental variance (CV_g/CV_e).

Heritability values obtained in the present study were higher than those estimated by Diniz [24] in a study carried out to evaluate the cultivars Portuguese, Tabocas, Tapacurá, Verdão, Palmeira, HTV-9299 parasitized by *M. incognita* race 1, where the estimated heritability was 48.83 for the number of galls and 70.85 for the number of eggs. Heritability estimates vary according to several factors such as characteristic, estimation method, population diversity, endogamy level of the population, evaluated sample size, number and type of environments, experimental unit considered and precision in the experimental conduction, and data collection [22]. Therefore, even by taking into account the same characteristics in the same species, there will be variation in the values of heritability obtained in different populations and experiments. In addition, it will be necessary to estimate such parameter for each working population and to adopt other parameters to complement the information provided by the heritability, aiming at helping the decision maker of the breeding, with the CV_g/CV_e ratio being an option to be adopted.

As the CV_g/CV_e ratio was superior to a unit for number of eggs and reproductive factor (2.71), and close to 1 for the number of galls in the root

system (0.89), selection based on these characters was made possible. This is because, according to Cruz et al. [25], there is a favorable situation to obtain a genetic gain with the selection when the CV_g/CV_e ratio tends to 1.0 or is greater than 1.0 since the genetic variation exceeds the environmental variation. Thus, as the CV_g/CV_e and heritability are parameters that indicate the success in the selection of superior genotypes [26], and both parameters obtained in the present study were high, it is possible to obtain a genetic gain in the selection of the superior progenies in the population studied. Moreover, these progenies can be used in the search for genotypes that may be a source of resistance to *M. incognita* race 1 to be used in coriander breeding programs.

All genotypes that presented the lowest averages for number of galls in the root system were in the group of the lowest values of reproduction factor (0.12 - 0.58). Based on the correlations between the characters under study, it was verified that all are positively related to each other (Table 4).

The phenotypic and genetic correlations between the number of galls in the root system and the number of eggs and reproductive factor were all

Table 4. Phenotypic, genetic, and environmental correlation coefficients for the number of galls in the root system (NGRS), number of eggs (NE) and reproduction factor (RF)

	Character	NGRS	NE	RF
NGRS	Rp	-	0.71**	0.71**
	Rg	-	0.81**	0.81**
	Re	-	0.23 ^{ns}	0.23 ^{ns}
NE	Rp	-	-	1.0**
	Rg	-	-	1.0**
	Re	-	-	0.99*

** significant at 1% probability, ^{ns} not significant.

highly significant, positive, and strong, with a Rg value of 0.81 (NGRS x NE, NGRS x RF) and a Rp value of 0.71 (NGRS x NE; NGRS x RF) for the genetic and phenotypic correlations, respectively. High genetic correlation indicates that the characters involved were affected by the same genes or are closely linked genes [27]. This fact was important because it has indicated that the indirect selection based on the number of galls in the root system, a non-destructive mode that allows recombination of the selected individuals both within and between the progenies, may be an option to be adopted in the initial selection cycles. Therefore, the reproduction factor could be used as a criterion for selection in more advanced cycles.

The genetic, phenotypic and environmental correlations between the number of eggs and the reproductive factor were very significant. All correlations were very strong and positive as expected, since the reproduction factor is estimated from the number of eggs, being directly proportional to it. Although these characters were highly correlated, the use of the reproductive factor was important because it provides information on the behavior of the pathogen population. This allows the identification of the genotypes that allow the nematode population to increase in the soil, besides allowing the classification of the genotypes as susceptible or resistant on the scale of Oostenbrink [17], optimizing the selective process carried out by the breeder.

4. CONCLUSION

The inoculation at sowing with 1,000 eggs/cell of *M. incognita* race 1 and evaluation at 30 days after inoculation was efficient in differentiating the evaluated genotypes, promoting reduction of time and optimization of resources.

The high values of heritability and CVg/CVe obtained indicate that the number of galls in the root system, number of eggs, and reproductive factors can be used to make selection of promising genotypes resistant to the pest, allowing gain with the selection and attainment of superior bred populations.

With the strong genetic correlations between the number of galls in the root system and the reproduction factor, it is possible to select based on the number of galls in the initial cycles of breeding programs in order to obtain genotypes resistant to *M. incognita* race 1 and selection and

recombination between and within progenies in the same selective cycle. However, it is indispensable to the extraction of eggs and estimation of the reproduction factor in more advanced cycles in the breeding programs of coriander. The selection of 12 superior genotypes, namely the progenies 67, DP10, 58, 5, 69, 18, DP11, 29, 31, 64, DP6, and 28 for future breeding program for resistance to the pest was made.

COMPETING INTERESTS

Authors have declared that no competing interests exist.

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