Journal of Agricultural Chemistry and Biotechnology

Complete Diallel Analysis for Nematodes Resistance in some Tomato Genotypes

Hamada, M. S.[1]; M. H. Abd El-Aziz[2*]; S. B. Gad[3]; and Manal M. Zaater[1*]

[1]Genetics Department, Faculty of Agriculture, Damietta University, Egypt.
[2]Genetics Department, Faculty of Agriculture, Mansoura University, Egypt.
[3]Zoology Department, Faculty of Agriculture, Mansoura University, Egypt.

Cross Mark

ABSTRACT

In this study a complete diallel analysis was done under the condition of nematode infection, using four different parental genotypes of Tomato. Mean squares of the studied genotypes were significant for all studied parameters, which proves the presence of a considerable amount of genetic variation among studied genotypes. Also, GCA and SCA mean squares were highly significant for all studied traits. This means that both GCA and SCA were important in the inheritance of these traits. Likewise, reciprocal effect mean squares were found significant for all the studied traits indicating that these traits are controlled by extra-nuclear factors in addition to the nuclear factors. Also, data showed that significant SCA effects in demand direction for most crosses in some studied traits. The estimations of $(\sigma^2 g_i)$ and $(\sigma^2 s_i)$ of the parental genotypes for all studied parameters indicated that the genotypes used in this study are of great importance to improve most of the studied traits. The estimation of genetic parameters and heritability for all studied traits proved the predominance of non-additive gene action in the inheritance of these traits. Results revealed that the cross (Cherry x Castle Rock) is a superior hybrid, and it could be selected in the breeding programs to resist nematode. Therefore, using this combination as started material for selection breeding program to produce resistant root-knot nematodes genotypes.

Keywords: Tomato, Root-Knot Nematode, Diallel, Combining ability, Gene action

INTRODUCTION

Tomato (*Lycopersicon esculentum*) is one of the most economically important vegetable crops in Egypt and all over the world. It is considered as an important source of vitamins A and C, minerals like Ca, P and Fe. Also, it is a rich source of antioxidants (mainly lycopene and β-carotene) which has a lot of health benefits, like reducing the risk of heart disease and cancer (Bhowmik *et al.,* 2012).

In Egypt, one of the most important pathogens which affect tomatoes and cause major economic damage is Nematode. It causes loss of yield ranges from 20 to 80% (Abd-Elgawad and Askary, 2015). The plant growth parameters correlated negatively with the initial population density of Nematode (Mekete *et al.*, 2003). Also, it reduces the photosynthetic rates (Bali *et al.*, 2018). These microorganisms penetrate the roots of plant species and migrate to the vascular cylinder, where they initiate a series of changes in the root, resulting in the formation of galls (or root knots) as well as the development of specialized feeding cells, called "giant cells," in their hosts. These alterations grossly affect nutrient partitioning and water uptake in the host (Roberts and May,1986). So, the use of resistant varieties is the most practical method to control these pathogens without increasing the cost of cultivation and provides an economically and environmentally viable approach for the management of nematodes. So, this investigation aimed to study the genetic parameters and the response of tomato genotypes (parents and their hybrids) to the infection by *M. incognita*. , to select suitable parents and hybrids able to resist Nematode to use them in the breeding programs in the future.

MATERIALS AND METHODS

An experiment involving Four parents of Tomato (*Solanum Lycopersicon*) viz., Advantage2 (P1), Cherry (P2), Fatma (P3), and Castle Rock (P4) and 12 single crosses including reciprocals (6 crosses and their reciprocals) were made among these parents according to complete diallel crosses mating design. The seeds were obtained denotaly from Dr. Sarah Elkomey, Vegetable Research Department, Horticultural Research Institute, Agricultural Research Center, Egypt. The Nematode infection part of this work was done in the summer season of 2019, at a private net house in Kafr Saad, Damietta under the supervision of the Dept. of Genetics, Fac. of Agric., Damietta University. All tomato seeds were germinated in sterilized soil.

Preparation of nematode inoculation

Eggs of *M. incognita* were obtained from a pure culture of *M. incognita* that was initiated by a single eggmass and propagated on coleus plants, *Coleus blumei* with the help of staff members of Agricultural Zoology Department, Faculty of Agriculture, Mansoura University, Egypt. These roots were washed by tap water, then soaked in 1.0% NaOCl and manually shaken for 60 s. After that, it was directly passed through sieves (500 mesh); the eggs were collected carefully after washing with tap water (Hussey and Barker, 1973). Finally, the number of eggs was counted and used for inoculating tomato seedlings in the following experiment. Experimental design

[*] Corresponding author.
E-mail address: mohahassan2005@gmail.com - manalzaater@gmail.com

The experiment was conducted under greenhouse condition (29±4°C) using the Randomized Complete Blocks Design with three replications. Forty-eight plastic pots (15 cm in diameter) filled in individually with 1000 g Sterile soil were transplanted with tomato seedlings. One week later, 3000 eggs of *M. incognita* were added to the plants.

Evaluation of traits

All the plants were harvested and uprooted after 45 days of nematode inoculation, and was used for determining the following traits:

Plant growth traits

The tomato plant growth traits included: fresh shoot lengths, fresh root length; fresh shoot and root weights; and shoot dry weight were measured and recorded (AOAC, 2005).

Infection parameters

Number of juveniles stage (J$_2$S) in soil/pot were extracted by sieving and modified Baermann technique (Goodey, 1957) counted by Hawksely counting slide under 100X magnification microscope, recorded, and then determined for each pot / replicate. Infected roots were washed with tap water, and then examined for recording number of eggmasses and galls per root system/replicate. The number of eggs in root extracted by soaking the root in 1.0% NaOCl and manually shaken for 60 s. After that, it was directly passed through sieves (500 mesh); the eggs were collected carefully after washing with tap water (Hussey and Barker, 1973). Finally, the number of eggs was counted under the microscope. R.F: Reproduction Factor was calculated according to the following formula: RF= Number of eggs and J$_2$ in roots and soil as a final population (P$_F$)/initial population (p$_i$), according to the modified quantitative scheme of Canto-Sáenz (Sasser *et al.*, 1984) and (Banora and Almaghrabi ,2019).

Statistical analysis

Data were subjected in order to test the significance of differences among the four parental varieties and 12 F$_1$ hybrids from 6 direct crosses and their reciprocals. Differences among genotypic means for all studied parameters were tested for significance using F test according to Steel and Torri (1960).

Sum of squares for genotypes was partitioned according to Griffing's Approach, method-1, model-1 Griffing (1956) into sources of variations due to GCA and SCA. The variances of GCA (σ^{2}g) and SCA (σ^{2}s) were obtained based on the expected mean squares for all studied parameters. Therefore, Additive (VA) and Non-additive (dominance and epistasis) (VD) genetic variances were estimated as follows: VA =2σ^{2}g, VD= σ^{2}s and Reciprocal variance was estimated as follow:

$$\sigma^2 r = 1/2 \ (Mr - Me)$$

where

σ^{2}r : is the variance of reciprocal effects.

M$_r$ and M$_e$: are the mean squares of reciprocal effect and error, respectively.

Average degree of dominance: (Dd) was estimated according to Matzinger and Kempthorne (1956) as follow:

$$Dd = \sqrt{\frac{2 \ \sigma^2 D}{\sigma^2 A}}$$

Estimates of heritability in both broad and narrow sense were calculated according to Singh and Chaudhary (1985):

$$h^2_{bs}\% = \frac{V_A + V_D}{V_A + V_D + \sigma^2_e} \qquad and \qquad h^2_{ns}\% = \frac{V_A}{V_A + V_D + \sigma^2_e}$$

Where: σ^2_e The variance of experimental error i.e. environmental variance.

We are considered the negative values equal Zero.

RESULTS AND DISCUSSIONS

This study was done to differentiate and reinforce the superiority among the different tomato genotypes under the stress of nematode infection for growth traits and infection parameters. For this purpose, four parents and their 12 hybrids of Tomato were infected by nematode then, all the studied parameters were determined. The results obtained from the evaluation of complete diallel crosses to evaluate the behavior of varieties in crosses also helped to partition the genotypic variance to its components. The genetic information of the studied traits aimed to help in carrying out a suitable breeding strategy for improving tomato genotypes able to be resistant to nematode infection. Therefore, the obtained results and their discussion will be presented in the following,

Data in Tables (1) and (2) illustrated the test of significance of mean squares of all genotypes, indicated the presence of highly significant differences among these genotypes in all the studied traits which suggested the presence of large variations among these genotypes and the planned comparisons for understanding the nature of variation and the determination of the amounts of heterosis for these traits are valid, and therefore could be made. Thus, the partitioning of the genetic variation into its components could be made through the analysis of complete crosses. Similar results were obtained by Hamada *et al.*, (2015).

Table 1.The analysis of variance and mean squares for growth traits.

S.O. V	d.f	S.L cm	R.L cm	P.L cm	S.W gm	R.W gm	P.W gm	S.D gm
Reps	2	42.146	187.9*	99.4	44.5	4.8	21.1	0.6
Geno(G)	15	1511.7**	204.8**	2276.9**	4550.3**	187.5**	5683.3**	50.1**
Error	30	42.74	41.9	98.2	47.0	12.2	47.9	1.31
Total	47							

*,**Significant at 0.05 and 0.01 levels of probability, respectively. S.L: Shoot length, R.L: Root length, P.L: Plant length and S.W: Shoot weight ,R.W :Root weight P.W: Plant weight and S.D : Shoot dry weight.

Table 2. The analysis of variance and mean squares for infection parameters.

S.O. V	d.f	(J2)/ soil	No. of galls	No. of eggmasses	No. eggs	R.F
Reps	2	21.1	55215.2	4284.0	785248.4	0.09
Geno(G)	15	71983.3**	1539362.5**	403764.4**	19723295.2**	2.27**
Error	30	63.9	32363.8	3393.5	355998.7	0.04
Total	47					

*, **Significant at 0.05 and 0.01 levels of probability, respectively. (J2)/ soil: number of juveniles/soil, No. galls: number of galls / root: No. of eggmasses: number of eggmasses / root, No. of eggs: Number of eggs /roots. R.F: Reproduction factor

The means of the four parents versus their F_1 hybrids and F_{1r} reciprocal hybrids were presented in Tables 3 and 4, respectively. The results showed that no specific parent was superior or inferior for all the growth studied traits. However, (P_2) was the best one for shoot length and total plant length. While (P_3) was the best genotype for shoot weight, root weight and total plant weight. Finally (P_4) exhibited the highest mean for root length. On the other hand, (P_1) was a superior parent for all the infection studied parameters which appears the least values. Also, the reproduction factor for this parent was 0.22 and the number of eggmasses was less than 20 which means that this parent is resistant (Yaghoobi *et al* .,1995). Regarding to F_1 hybrids and their reciprocal hybrids, the results showed that most of them generally exceed their two parents, which participated in the hybridization. It also appeared that some crosses exceeded their better parent, such as the combiners (P_2 x P_1), (P_4 x P_1) and (P_2x P_4) for all the growth studied traits. On the other hand, In general, the cross (P_2 x P_4) outstripped their better parent which appears the least values for all the infection parameters Also, the reproduction factor for this hybrid was 0.12 and the number of eggmasses was one which mean that this hybrid is resistant to nematode. Therefore, results showed that means of most hybrids from direct crosses differed significantly from that of their reciprocal crosses which indicate the presence of maternal effects in inheritance of these traits. Also, the cross (P_2 x P_4) is a superior hybrid, and it could be used in the breeding programs to select resistant nematode genotypes.

In order to understand the different types of genetic effects that control the inheritance of the different traits of tomato, the 6 F_1 hybrids and 6 F_1 reciprocal hybrids were setup in complete diallel crosses analysis of variance. The degree of freedom and sum squares due to crosses were partitioned into general combining ability (GCA), specific combining ability (SCA) and reciprocal effect. The combining ability importance in selective parents for hybridization has been stated by a lot of researchers in tomato. (Gautam *et al*., 2018) and (Vekariya *et al*., 2019). The results of the analysis of variances and the mean squares of combining ability for growth and infection parameters are presented in Tables 5 and 6, respectively.

The results exhibited that mean squares of general combining ability (GCA) and specific combining ability (SCA) were highly significant for all the studied parameters. These results indicated that both GCA and SCA were important in the inheritance of these parameters. Significant reciprocal effect mean squares were found for all the studied parameters indicating that these parameters

were controlled by extra-nuclear factors as well as nuclear factors.

Table 3. Mean performance of Parents and its F_1 hybrids for growth traits.

Parameters Genotypes	S.L cm	R.L cm	P.L cm	S.W gm	R.W gm	P.W gm	S.D gm
P_1	51.0	25.3	76.3	36.8	8.4	45.2	4.9
P_2	99.0	31.0	130.0	52.4	7.8	60.2	5.4
P_3	84.6	27.0	111.6	67.7	11.9	79.7	8.7
P_4	64.6	42.6	107.3	45.1	11.4	56.5	6.8
P_1 x P_2	79.6	47.3	127.0	66.6	15.2	81.7	8.6
P_2 x P_1	105.3	46.3	151.6	106.6	14.3	120.9	13.1
P_1 x P_3	67.0	28.6	95.6	92.3	9.3	101.6	11.3
P_3 x P_1	69.0	21.6	90.6	65.7	11.8	77.5	8.0
P_1x P_4	83.0	42.3	125.3	57.1	16.8	73.8	8.2
P_4 x P_1	89.0	46.6	135.6	76.4	36.2	112.6	11.7
P_2 x P_3	83.6	35.6	119.3	63.0	9.5	72.5	6.4
P_3 x P_2	88.6	34.0	122.6	88.3	15.1	103.5	12.1
P_2x P_4	131.6	44.3	176.0	178.1	25.0	203.0	19.9
P_4 x P_2	130	42.3	172.3	125.4	27.4	152.7	3.5
P_3 x P_4	62.0	37.0	99.0	44.5	8.5	53.0	4.2
P_4 x P_3	90.0	30.0	120.0	141.3	15.4	156.7	11.5
LSD$_{5\%}$	10.8	11.6	16.3	12.5	5.69	11.2	1.9

S.L: Shoot length, R.L: Root length, P.L: Plant length and S.W: Shoot weight ,R.W :Root weight P.W: Plant weight and S.D : Shoot dry weight.

Table 4. Mean performance of Parents and its F_1 hybrids for infection parameters.

Parameters Genotypes	(J2)/ soil	No. of galls	No. of eggmasses	No. eggs	R.F
P_1	40.3	22.3	8.7	621.73	0.22
P_2	243.3	169.3	122.0	1225.5	0.49
P_3	151.7	1743.7	379.7	7948.6	2.7
P_4	705.7	1676.3	432.7	4189.7	1.63
P_1 x P_2	251.3	869.7	212.3	4885.9	1.71
P_2 x P_1	347.3	954.3	156.7	5765.8	2.03
P_1 x P_3	150.7	468.7	238.7	3674.4	1.27
P_3 x P_1	101.3	664.3	169.3	3511.5	1.20
P_1x P_4	200.7	713.0	284.7	4864.2	1.69
P_4 x P_1	252.7	2311.7	1009.7	8367.5	2.87
P_2 x P_3	104.7	730.0	259.3	1473.3	0.53
P_3 x P_2	152.0	1033.7	301.7	4911.8	1.68
P_2x P_4	49.6	25.0	1	324.3	0.12
P_4 x P_2	207.7	2008.0	1375.0	7978.1	2.72
P_3 x P_4	255.7	852.0	412.0	2869.4	1.04
P_4 x P_3	179.3	26.0	5.6	2563	0.91
LSD5%	13.0	305.6	118.1	1029.0	0.34

(J2)/ soil: number of juveniles/soil, No. galls: number of galls / root: No. of eggmasses: number of eggmasses / root, No. of eggs: Number of eggs /roots. R.F: Reproduction factor.

Table 5 .The analysis of variance and mean squares for combining ability analysis for growth traits.

S.O.V	d.f	S.L cm	R.L cm	P.L cm	S.W gm	R.W gm	P.W gm	S.D gm
GCA	3	1225.7**	157.6**	1973.4**	979.8**	71.4**	1269.6**	7.6**
SCA	6	521.0**	81.5**	810.2**	2007.1**	81.4**	2607.6**	24.5**
Reciprocals	6	125.9**	10.4*	100.5*	1294.9**	39.1**	1493.7**	13.5**
Polled Error	30	9.5	9.3	21.8	15.7	2.7	10.7	0.2

*,**Significant at 0.05 and 0.01 levels of probability, respectively. S.L: Shoot length, R.L: Root length, P.L: Plant length and S.W: Shoot weight ,R.W :Root weight P.W: Plant weight and S.D : Shoot dry weight.

Table 6. The analysis of variance and mean squares for combining ability analysis for infection parameters.

S.O.V	d.f	(J2)/ soil	No. of galls	No. of eggmasses	No. eggs	R.F
GCA	3	43716.3**	302671.7**	79707.3**	1501984.5**	0.19**
SCA	6	34179.2**	522503.9**	80931.0**	8720759.7**	0.99**
Reciprocals	6	3948.8**	608962.4**	215685.7**	6964327.3**	0.81**
Polled Error	30	21.3	10787.9	1131.2	118666.2	0.01

*, **Significant at 0.05 and 0.01 levels of probability, respectively. (J2)/ soil: number of juveniles/soil, No. galls: number of galls / root: No. of eggmasses: number of eggmasses / root, No. of eggs: Number of eggs /roots. R.F: Reproduction factor.

General combining ability effects (g_i) for each parental line were estimated and the obtained results for the studied parameters are shown in Tables 7 and 8. It could be seen from these Tables that (P_1) showed negative significance for shoot length ,plant length , shoot weight, total plant weight and shoot dry weight. (P_2) showed positive significance for all the growth traits except root length and root weight. (P_3) showed negative significance for shoot length, root length, plant length, root weight and plant weight. (P_4) showed positive significance for all the growth traits except shoot length and root length. It could be suggested that the parental genotypes (P_2) and (P_4) possess favorable genes to improve hybrids for growth traits under the condition of nematode infection.

Also, it could be seen from these Tables for the infection parameters that (P_1) showed negative significance for number of juveniles, number of galls and number of eggmasses, while (P_2) showed negative significance for number juveniles, number of galls, number of eggs and reproduction factor and (P_3) showed negative significance for number of juveniles and number of eggmasses . It could be suggested that these parental genotypes own favorable genes to improve hybrids acting towards nematode resistance.

Table 7. Estimates of general combining ability effects (gi) of each parental lines for growth traits.

Traits parents	S.L cm	R.L cm	P.L cm	S.W gm	R.W gm	P.W gm	S.D gm
P_1	-11.8*P	-0.7 P	-12.4*P	-14.4*P	-0.21P	-14.6 *P	-0.85 *P
P_2	16.0*G	2.9*G	18.9*G	9.9*G	0.02P	9.9 *G	0.96 *G
P_3	-7.4*P	-6.0*P	-13.4*P	-2.8P	-3.56*P	-6.4 *P	-0.83P
P_4	3.2P	3.8P	7.0*G	7.4*G	3.75*G	11.1 *G	0.72*G
SE(gi)	2.27	2.24	3.43	2.91	1.21	2.40	0.396
LSD (gi-gj)	4.86	4.81	7.37	6.25	2.60	5.15	0.851

*,**Significant at 0.05 and 0.01 levels of probability, respectively. S.L: Shoot length, R.L: Root length, P.L: Plant length and S.W: Shoot weight ,R.W :Root weight P.W: Plant weight and S.D : Shoot dry weight.
G (good) Denotes significant general combining ability effect in favorable direction.
P (poor) Denotes non-significant general combining ability effects in favorable direction, significant and non-significant general combining ability effects in unfavorable.

Table 8. Estimates of general combining ability effects (gi) of each parental lines for infection parameters.

Traits parents	(J2) / soil	No. of galls	No. of eggmasses	No. eggs	R. F
P_1	-39.0 *G	-138.4*G	-74.5*G	-34.3 G	-0.02G
P_2	-12.2 *G	-146.9*G	-16.8G	-599.6*G	-0.20*G
P_3	-56.3 *G	16.0P	-54.0*G	289.1 *P	0.08 *P
P_4	107.5*P	269.3*P	145.4*P	344.8 *P	0.15 *P
SE(gi)	2.769	62.3	20.18	206.7	0.069
LSD (gi-gj)	5.943	133.8	43.32	443.7	0.148

*, **Significant at 0.05 and 0.01 levels of probability, respectively. (J2)/ soil: number of juveniles/soil, No. galls: number of galls / root: No. of eggmasses: number of eggmasses / root, No. of eggs: Number of eggs /roots. R.F: Reproduction factor.
G (good) Denotes significant general combining ability effect in favorable direction.
P (poor) Denotes non-significant general combining ability effects in favorable direction, significant and non-significant general combining ability effects in unfavorable.

Specific combining ability and their reciprocal effects are demonstrated in Tables 9,10,11 and 12,

respectively. The results showed that significant SCA effects in desired direction were noticed for most crosses in some studied parameters as follows: The combiners (P_1 x P_4) and (P_2 x P_4) were good specific combiners which exhibited positive significant SCA effects for shoot length. These crosses involved (poor × poor) and (good x poor) general combiners as parents. While the combiner (P_1 x P_2) was good specific combiner which exhibited positive significant SCA effects for root length. This cross involved (poor × poor) general combiners as parents. for plant length; the crosses (P_1 x P_2), (P_1 x P_4) and (P_2 x P_4) respectively, have good specific combiners which exhibited positive significant SCA effects. These crosses involved (poor × good), (poor × good) and (good x good) general combiners as parents, respectively. Meanwhile, for shoot weight and total plant weight the combiners (P_1 x P_2), (P_1 x P_3), (P_2 x P_4), (P_3 x P_1) and (P_4 x P_2) were good specific combiners which exhibited positive significant SCA effects. These crosses involved (poor × good), (poor × poor), (good × good), (poor × poor) and (good x good) general combiners as parents, respectively. Also, the crosses (P_1 x P_4), and (P_2 x P_4) were good specific combiners which exhibited positive significant SCA effects for root weight. These crosses involved (poor × good) and (poor × good) general combiners as parents. For shoot dry weight, the combiners (P_1 x P_3), (P_2 x P_4), (P_3 x P_4), (P_3 x P_1) and (P_4 x P_2) were good specific combiners which exhibited positive significant SCA effects. These crosses involved (good × good), (good × poor), (good × good), (poor × good), (poor × good) and (good x good) general combiners as parents, respectively.

On the other side, The crosses (P_1 x P_4), (P_2 x P_3), (P_2 x P4), (P_3 x P_1), (P_3 x P_4), (P_2 x P_1), (P_4 x P_1), (P_3 x P_2), (P_3 x P_1) and (P_4 x P_2) were good specific combiners showing negative significant SCA effects for number of juveniles /soil which is desirable for nematode resistance. These crosses involved poor × poor general combiners as parents. For number of galls the crosses (P_1 x P_3), (P_3 x P_4), (P_4 x P_1), (P_3 x P_2), and (P_4 x P_2) also exhibited negative significant SCA effects. These crosses also involved (good × poor), (poor × poor), (poor × good), (poor × good) and (poor × good) general combiners as parents. Also, the crosses (P_3 x P_4), (P_4 x P_1) and (P_4 x P_2) exhibited negative significant SCA effects for number of eggmasses. These crosses involved (good × poor), (poor × good), (poor × good) and (poor × good) general combiners as parents. For number of eggs, the crosses (P_1 x P_3), (P_2 x P_3), (P_3 x P_4), (P_2 x P_1), (P_4 x P_1), (P_3 x P_2) and (P_4 x P_2) also showed negative significant SCA effects. These crosses also involved (good × poor), (good × poor), (poor × poor), (good x good) ,(poor × good), (poor × good) and (poor × good) general combiners as parents. Finally, for reproduction factor, ,the crosses(P_1 x P_3), (P_2x P_3), (P_3x P_4), (P_2x P_1),(P_4 x P_1), (P_3x P_2) and (P_4 x P_2) showed negative significant SCA effects. These crosses also involved (good × poor), (poor × poor), (good x good), (poor × good), (poor × good) and (poor × good) general combiners as parents. Similar results were obtained by Jassim and Abood, (2018).

Table 9. Estimates of specific combining ability effects (Sij) of each cross for growth traits.

Traits Crosses	S.L cm	R.L cm	P.L cm	S.W gm	R.W gm	P.W gm	S.D gm
P₁ x P₂	2.15	8.50 **	10.6 *	9.5**	-0.30	9.2 **	1.07
P₁ x P₃	1.06	-4.29	-3.2	14.6 **	-0.95	13.6**	1.61**
P₁ x P₄	8.40 **	5.25	13.6 **	-7.9	7.68 **	-0.3	0.39
P₂ x P₃	-8.52**	1.83	-6.7	-13.0 **	0.59	-12.4**	-0.55
P₂ x P₄	25.48**	0.54	26.0 **	52.6**	7.17 **	59.7 **	5.70 **
P₃ x P₄	-5.94 *	-0.42	-6.4	6.7	-3.47 *	3.2	-1.73 **
SE (sij)	2.11	2.09	3.20	2.71	1.13	2.23	0.202
LSD (sij-sjk)	6.41	6.35	9.71	8.23	3.423	6.79	1.12
LSD (sij-skl)	6.88	6.81	12.8	8.83	3.673	7.28	1.20

*,**Significant at 0.05 and 0.01 levels of probability, respectively. S.L: Shoot length, R.L: Root length, P.L: Plant length and S.W: Shoot weight ,R.W :Root weight P.W: Plant weight and S.D : Shoot dry weight.

Table 10. Estimates of specific combining ability effects (Sij) of each cross for infection parameters.

Traits Crosses	(J2) / soil	No. of galls	No. of eggmasses	No. eggs	R. F
P₁ x P₂	138.5**	305.6**	-59.8	1886.4 **	0.67 **
P₁ x P₃	9.2 **	-203.0 **	-3.0	-735.3 **	-0.24**
P₁ x P₄	-53.9 **	489.7 **	240.7 **	2232.0 **	0.73 **
P₂ x P₃	-15.3 **	120.9	15.6	-570.4 *	-0.20*
P₂ x P₄	-178.8 **	2.3	223.9 **	332.6	0.05
P₃ x P₄	-45.9 **	-738.0 **	-217.8 **	-1991.2**	-0.68**
SE (sij)	2.58	58.06	36.86	192.6	0.064
LSD (sij-sjk)	7.83	176.3	57.09	584.72	0.195
LSD (sij-skl)	8.40	189.2	61.26	627.47	0.209

*, **Significant at 0.05 and 0.01 levels of probability, respectively. (J2)/ soil: number of juveniles/soil, No. galls: number of galls / root: No. of eggmasses: number of eggmasses / root, No. of eggs: Number of eggs /roots. R.F: Reproduction factor.

Table 11. Estimates of reciprocal effects (rij) of each reciprocal cross (F1r) for growth traits.

Traits Crosses	S.L cm	R.L cm	P.L cm	S.W gm	R.W gm	P.W gm	S.D gm
P₂ x P₁	-12.8 **	0.50	-12.33**	-20.0 **	0.44	-19.6**	-2.23 **
P₃ x P₁	-1.0	3.50	2.50	13.3 **	-1.26**	12.1 **	1.66 **
P₄ x P₁	-3.0	-2.17	-5.17	-9.7*	-9.70 **	-19.4**	-1.76 **
P₃ x P₂	-2.5	0.83	-1.67	-12.7 **	-2.83 *	-15.5 **	-2.83 **
P₄ x P₂	0.83	1.00	1.83	26.6 **	-1.23	25.4**	2.86 **
P₄ x P₃	-14.0 **	3.50	-10.50 *	-48.4 **	-3.47*	-51.9 **	-3.68 **
SE (rij)	5.23	5.18	7.93	6.72	2.79	7.28	0.916
LSD (rij- rki)	9.72	9.63	14.74	12.49	5.19	10.30	1.70

*,**Significant at 0.05 and 0.01 levels of probability, respectively. S.L: Shoot length, R.L: Root length, P.L: Plant length and S.W: Shoot weight ,R.W :Root weight P.W: Plant weight and S.D : Shoot dry weight.

Table 12. Estimates of reciprocal effects (rij) of each reciprocal cross (F1r) for infection parameters.

Traits Crosses	(J2) / soil	No. of alls	No. of eggmasses	No. eggs	R. F
P₂ x P₁	-48.0**	-42.4	27.8	-440.0 **	-0.16 *
P₃ x P₁	24.7 **	-97.9	34.8	81.5	0.04
P₄ x P₁	-26.0 **	-799.4 **	-362.6**	-1751.6 **	-0.59 **
P₃ x P₂	-23.7**	-151.8*	-21.4	-1719.2 **	-0.58 **
P₄ x P₂	-79.0**	-991.5**	-687.0**	-3826.9**	-1.30 **
P₄ x P₃	38.2**	412.9	202.9	153.2	0.06
SE (rij)	6.39	143.9	46.61	477.4	0.159
LSD (rij- rki)	11.89	267.6	86.6	887.4	0.296

*, **Significant at 0.05 and 0.01 levels of probability, respectively. (J2)/ soil: number of juveniles/soil, No. galls: number of galls / root: No. of eggmasses: number of eggmasses / root, No. of eggs: Number of eggs /roots. R.F: Reproduction factor.

Tables 13 and 14 showed the estimation of general combining ability variances ($\sigma^2 gi$) and specific combining ability variances ($\sigma^2 si$) of each parental genotype for growth traits and infection parameters, respectively. The results demonstrated that the largest values of $\sigma^2 gi$ and $\sigma^2 si$ were detected in (P_4) for root weight and number of juveniles / soils which indicated that this parent has contributed to the inheritance of these parameters in some hybrids. While (P_4) showed high estimation only of ($\sigma^2 g_i$) for number of eggmasses which indicate that this parent contributed to the inheritance of this trait in some hybrids. Also, the results showed that the largest value of ($\sigma^2 g_i$) for shoot weight, total plant weight and shoot dry weight were detected in (P_1) which indicated that this parent has contributed to the inheritance of these parameters in some hybrids. As well, (P_2) showed high estimation only of ($\sigma^2 g_i$) for shoot length, total plant length, number of eggs and reproduction factor which indicate that this parent contributed to the inheritance of these parameters in some hybrids. Finally, (P_3) showed high estimation only of ($\sigma^2 g_i$) for root length which indicate that this parent contributed to the inheritance of these parameters in some hybrids. These explanations were in harmony with those obtained by Hamada *et al.,* (2015) and AL-Hamdany (2014).

Table 13. Variances of general combining ability effects ($\sigma^2 g_i$) and specific combining ability effects ($\sigma^2 s_i$) of each parental variety for growth traits.

Traits	S.L cm		R.L cm		P.L cm		S.W gm		R.W gm		P.W gm		S.D gm	
Parents	$\sigma^2 g_i$	$\sigma^2 s_i$	$\sigma^2 g_i$	$\sigma^2 s_i$	$\sigma^2 g_i$	$\sigma^2 s_i$	$\sigma^2 g_i$	$\sigma^2 s_i$	$\sigma^2 g_i$	$\sigma^2 s_i$	$\sigma^2 g_i$	$\sigma^2 s_i$	$\sigma^2 g_i$	$\sigma^2 s_i$
P₁	137.2	33.7	-0.87	54.7	151.6	144.7	205.4	175.0	-0.34	28.7	212.1	129.7	0.68	1.82
P₂	254.0	358.7	6.96	33.6	352.4	407.3	95.0	1503.3	-0.38	24.6	96.0	1897.7	0.89	16.82
P₃	54.0	50.0	34.7	6.61	177.5	37.5	5.8	206.1	12.3	5.4	39.4	170.3	0.65	2.81
P₄	9.1	385.8	13.1	10.1	46.2	544.6	52.4	1309.5	13.7	63.4	122.5	1960.4	0.47	9.37

S.L: Shoot length, R.L: Root length, P.L: Plant length and S.W: Shoot weight ,R.W :Root weight P.W: Plant weight and S.D : Shoot dry weight.

Table 14. Variances of general combining ability effects ($\sigma^2 g_i$) and specific combining ability effects ($\sigma^2 s_i$) of each parental variety for infection parameters.

Parameters	(J2)/ soil		No. of galls		No. of eggmasses		No. eggs		R. F	
Parents	$\sigma^2 g_i$	$\sigma^2 s_i$	$\sigma^2 g_i$	$\sigma^2 s_i$	$\sigma^2 g_i$	$\sigma^2 s_i$	$\sigma^2 g_i$	$\sigma^2 s_i$	$\sigma^2 g_i$	$\sigma^2 s_i$
P₁	1522.3	11074.2	18141.9	183827.5	-9946.7	30412.9	-6238.4	4503326.1	-0.0006	0.52
P₂	147.7	25672.0	20565.4	50623.8	348437.8	26613.8	352146.2	1960133.1	0.04	0.24
P₃	3162.1	1205.2	-755.4	296845.8	72477.5	23488.9	76185.9	2378380.7	0.00	0.27
P₄	11554.3	38786.1	71504.6	26877.3	107775.7	30100.1	111484.0	127282.8	0.02	0.001

(J2)/ soil: number of juveniles/soil, No. galls: number of galls / root: No. of eggmasses: number of eggmasses / root, No. of eggs: Number of eggs /roots. R.F: Reproduction factor.

Tables 15 and 16 exhibited the genetic parameters, which included additive (VA) , dominance (VD) and reciprocal effects (Vr) variances in addition to heritability in broad sense ($h^2b\%$) and in narrow (h^2n %) sense , as well as dominance degree ratio (D) which were determined for growth and infection parameters . The ratio σ^2_g/σ^2_S was lower than one for all studied traits, which indicated the importance of non-additive gene effect in these parameters. Similar results were obtained by Hamada *et al.,* (2015) and Mohamad *et al.*, (2007). Also, the results showed that the magnitudes of non-additive genetic variances (VD) were larger than their symmetric estimates of additive genetic variances (VA) for all the growth and infection parameters. This suggests that dominance genetic variance played a great role in the inheritance of all these studied parameters. To confirm these results, the degree of dominance (Dd) has been calculated, it exceeded one for all studied parameters. Likewise, the estimation of heritability in broad sense ($h^2bs\%$) were larger than their ones in narrow sense ($h^2ns\%$) for all studied parameters. Moreover, the broad sense heritability estimates ($h^2bs\%$) were more than 88.1 % and larger than their corresponding narrow sense heritability ($h^2ns\%$) which ranged from 3.8 % to 37.5% for all studied parameters. These results confirm that non-additive gene action is the predominance in the inheritance of these studied parameters. Furthermore, the reciprocal variance (σ^2r) was positive and lower than non-additive genetic variance for all studied parameters which indicate that these parameters were not only controlled by nuclear genetic factors, but also the cytoplasmic genetic factors play an important role in its inheritance. Similar results were obtained by Hamada *et al.,* (2016).

Table15. The relative magnitudes of different genetic parameters for growth traits.

Traits Parameters	S.L cm	R.L cm	P.L cm	S.W gm	R.W gm	P.W gm	S.D gm
σ^2_g/σ^2_S	0.299	0.27	0.3	0.06	0.11	0.06	0.037
VA	302.9	35.9	485.2	239.1	16.8	313.4	1.8
VD	506.8	67.5	777.4	1983.6	77.3	2591.6	24.1
Vr	55.8	1.8	33.9	635.7	17.5	738.9	6.5
VE	14.25	14.0	32.8	23.5	4.1	16.0	0.4
D	1.83	1.9	1.8	4.1	3.0	4.1	5.2
$H_b\%$	98.3	88.1	97.5	99.0	95.9	99.5	98.3
$H_n\%$	36.8	30.6	37.5	10.6	17.1	10.7	6.8

S.L: Shoot length, R.L: Root length, P.L: Plant length and S.W: Shoot weight ,R.W :Root weight P.W: Plant weight and S.D : Shoot dry weight.

Table16. The relative magnitudes of different genetic parameters for infection parameters

Traits Parameters	(J2) / soil	No. of galls	No. of eggmasses	No. eggs	R. F
σ^2_g/σ^2_S	0.160	0.071	0.123	0.02	0.022
VA	10923.7	72970.9	19644.0	345829.6	0.04
VD	34157.9	511716.0	79799.8	8602093.5	0.98
Vr	1963.7	299087.2	107277.3	3422830.5	0.40
VE	21.3	10787.9	1131.2	118666.2	0.013
D	2.50	3.745	2.850	7.1	6.678
H2b%	99.95	98.2	98.9	98.7	98.7
H2n%	24.2	12.3	19.5	3.8	4.2

(J2)/ soil: number of juveniles/soil, No. galls: number of galls / root: No. of eggmasses: number of eggmasses / root, No. of eggs: Number of eggs /roots. R.F: Reproduction factor.

CONCLUSION

Based on these results, it could be concluded that, most of the studied parameters were shown to be mainly controlled by non-additive effects and cytoplasmic genetic factors. Good performance of the obtained hybrids may be referred to additive × additive, additive × dominance, and dominance × dominance (epistatic interactions). Therefore, it is possible to suggest using the hybridization then selection method to improve tomato genotypes to be able to resist root- knot nematodes. As found in this study, some crosses have the ability to resist nematode, with considering using more resistant parents in these methods.

REFERENCES

Abd-Elgawad M.M.M. and T.H. Askary (2015). Impact of phyto nematodes on agriculture economy. In: "Agents of Phyto nematodes "(T.H. Askary, P.R.P. Martinelli, eds). Biocontrol, CAB International, 23 pp.

AL-Hamdany, S. Y. H. (2014). Estimation of heterosis, combining ability, gene action, genotypic and phenotypic correlation in peas (*Pisum sativum L.).* Jordan Journal of Agricultural Sciences. 10 (2): 273-294.

Association of Official Analytical Chemists (AOAC) (2005). Association of Official Analytical Chemists. Official Methods of Analysis of AOACInternational, 18th ed. Official Methods of Analysis, Maryland, USA.

Bali S., P. Kaur, A. Sharma, P. Ohri, R. Bhardwaj, M. N. Alyemeni, L. Wijaya and P. Ahmad (2018). Jasmonic acid-induced tolerance to root-knot nematodes in tomato plants through altered photosynthetic and antioxidative defense mechanisms. Protoplasma 255 (2): 471−484.

Banora, M.Y. and O. A. Almaghrabi (2019). Differential response of some nematode-resistant and susceptible tomato genotypes to *Meloidogyne javanica* infection. Journal of Plant Protection Research,59(1): 113-123.

Bhowmik, D., K.P. Sampathkumar , S.Paswan and S. Srivastava (2012). Tomato –a natural medicine and its health benefits. J. of pharmacognosy and phytochemistry 1:33-43.

Gautam, N., M. Kumar, D. Kumar, S. Kumar, A. Vikram, R. K. Dogra and Shikha Sharma (2018). Combining ability and gene action studies for important quality traits in tomato (*Solanum lycopersicum L.).* International Journal of Chemical Studies, 6 (2): 1992-1996.

Goodey, B. J. (1957). Laboratory methods for work with plant and soil nematodes. Technological Bulletin 2.

Hamada, M. S., M. H. Abd El-Aziz and Manal M. Zaater (2015). Nature of gene action for some economic parameters and combining ability for some economic parameters of Okra. J.Agric. Chem.and Biotechn., Mansoura Univ.Vol. 6 (3): 53– 63.

Hamada, M. S., A. F. Hamaiel, S.M.Faried and Sara A. A. Elkomey, (2016). Nature of gene action for some economic characters of tomato (*Lycopersicon esculentum L.*) Vareities J. Agric. Res. Kafr El-Sheikh Univ. 42(2) :24-33.

Hussey, R.S. and K.R. Barker (1973). A comparison of methods of collecting inoculate of *Meloidogyne spp.*, including a new technique. Plant Diseases Reproduction 57:1925-1928.

Jassim , H. F. and I.D. Abood (2018).Identification of *Mi1.2* Resistance gene in some Tomato Hybrids from diallel cross against root-knot nematode caused by *Meloidogyne spp.* Research Journal of Pharmaceutical, Biological and ChemicalSciences.9(1):927:933.

Matzinger, D. F. and O. I. Kempthorne (1956). The modified diallel table with partial inbreeding and interactions with environment. Genetics, 41:822–833.

Mekete T., W. Mandefro and N. Greco (2003). Relationship between initial population densities of *Meloidogyne javanica* and damage to pepper and tomato in Ethiopia. Nematologia Mediterranea 31 (2): 169–171.

Mohamad A. A., A. N. M. Amin and S. I. Towfiq (2007). Estimation of heterosis, general and specific combining ability using diallel cross in maize (*zea mays l.*). Mesopotamia J. of Agric. 35 (3)1-14.

Roberts, P. A. and D. May (1986). Meloidogyne incognita resistance characteristics in tomato genotypes developed for processing. Journal of Nematological 18:353-359.

Sasser J.N., C.C. Carter and K.M. Hartman (1984). Standardization of Host Suitability Studies and Reporting of Resistance to Root-knot Nematodes. North Carolina State Graphics, Raleigh, NC, USA, 7 pp.

Singh, R. K. and B. D. Chaudhary (1985). Biometrical methods in quantitative genetic analysis. Kalyani publisher, New-Delhi revised edition, India.

Steel, R. G. and J. H. Torri (1960). Principles and procedures of statistics. McGraw Hill Book Company. INC, New York.

Vekariya, T.A., G. U. Kulkarni, D. M. Vekaria, A. P. Dedaniya and J.T. Memon (2019). Combining Ability Analysis for Yield and its Components in Tomato (*Solanum lycopersicum L.*) Acta Scientific Agriculture ,3 (7): 185-191.

Yaghoobi, J., I. Kaloshian, Y. Wen and V.M. Williamson (1995) Mapping a new nematode resistance locus in *Lycopersicon peruvianum*. Theor Appl Genet 91:457-464.

التحليل الدائري الكامل للمقاومة للنيماتودا في بعض التراكيب الوراثية لنبات الطماطم

محمد سعد حماده[1]، محمد حسن عبد العزيز [2] ، سمير برهام جاد[3] و منال محمد السيد زعتر[1]

[1]قسم الوراثة – كلية الزراعة – جامعة دمياط – مصر.

[2]قسم الوراثة – كلية الزراعة – جامعة المنصورة– مصر.

[3]قسم الحيوان الزراعي– كلية الزراعة – جامعة المنصورة – مصر.

في هذه الدراسة تم إجراء التحليل الدائري الكامل تحت ظروف العدوى بنيماتودا تعقد الجذور وذلك باستخدام أربعة أنواع من التراكيب الوراثية المختلفة للطماطم. كانت قيم متوسط مربعات التراكيب الوراثية عالية المعنوية لجميع الصفات المدروسة مما يؤكد على وجود تباين وراثي كبير بين التراكيب الوراثية المستخدمة .كذلك كانت تقديرات متوسط مربعات القدرة العامة والخاصة على التآلف عالية المعنوية بالنسبة لجميع الصفات المدروسة مما يوضح أن كلا النوعين من القدرة على التآلف هام بالنسبة لتوارث هذه الصفات المدروسة .أيضاً كانت تقديرات متوسط مربعات تأثيرات الهجن العكسية معنوية لجميع الصفات المدروسة مما يوضح أن هذه الصفات يتحكم فيها عوامل وراثية لا نووية بالإضافة للعوامل الوراثية النووية .كذلك أوضحت النتائج وجود قدرة خاصة على التآلف معنوية في الاتجاه المرغوب لمعظم الهجن الناتجة في بعض الصفات المدروسة .كذلك أثبتت تقديرات المقاييس الوراثية و معامل التوريث دور الفعل الجيني غير المضيف في توارث الصفات المدروسة. وأوضحت النتائج أن الهجين (شيري x كاسل رووك) هو هجين متفوق و يمكن اختياره كبداية لبرنامج تربية بالانتخاب للتوصل إلى تراكيب وراثية محسنة ولها القدرة علي مقاومة نيماتودا تعقد الجذور .