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TRIPLE TEST CROSS ANALYSIS IN SESAME (*SESAMUM INDICUM* L.)

H.A. Dawwam[(1)], F.A. Hendawy[(1)], I.H. Darwish[(1)], S. A. Mohamed [(2)] and H.M. Ali[(1)]

1- Crop Science Department Faculty of Agriculture, Minuifya University
2- Oil Research Section, Field Crop Res. Inst. Agric. Res. Center. Egypt

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ABSTRACT: *Triple test cross analysis of four sesame crosses was used to detect and estimate the additive, dominance and epistasis genetic variation for days to the first flower, no. of branches/plant, plant height, capsule length, no. of capsules/plant, 1000 seed weight, seed yield/plant, oil content (%) and acid value. The variance between (L_1, L_2 and L_3) sets of triple test cross families was found to be highly significant for all traits in the four crosses investigated. The total epistasis was detected to be highly significant and significant for all traits in all crosses investigated except the height of the first capsule in the third and fourth crosses and acid value in the first cross. The mean square estimates due to sums (L_1+L_2+L_3)as test of additive genetic components were found to be highly significant for all traits studied in the four crosses except for number of capsules/plant in the fourth cross and 1000 seed weight in the second cross. While, the differences (L_1-L_2) as test of dominance genetic components were found to be highly significant for all traits studied in the four crosses except for number of branches/plant in the second cross ,plant height in the fourth cross and acid value in the first cross.*

Key words: *Triple test Cross , Additive, Dominance, Epistasis, Sesame .*

INTRODUCTION

Sesame (*Sesamum indicum* L.) is one of the most important oil seed crops, not only in Egypt but also in other parts of the world. In Egypt, sesame is considered as a food crop rather than an oil seed crop because most of seeds consumed directly, without oil extraction. The major obstacles to sesame's expansion in the new reclaimed soils its low yields and the absence of non-shattering cultivars suitable for mechanical harvesting

Triple test cross technique (Kearsey and Jinks, 1968 was used in order to investigate the role of additive, dominance and epistatic variation for seed sesame yield and some of its components. This biometrical method provides the breeders with unambigous estimates of epistasis and in the absence of epistasis, unbiased estimation of the additive and dominance genetic components also remains unaffected by differences in allele frequencies, degree of inbreeding and gene correlation. Moreover, epistatic interactions

have frequently been reported by many scientists in sesame (Sedek, 1999; and El-Hifney *et al.*, 2005).

The objectives of the present study are to establish : (1) the role of epistatic interaction in the inheritance of sesame yield and some of its components (2) the detection and estimation of additive and dominance components of genetic variation according to Kearsey and Jinks (1968), Jinks *et al.* (1969) and Jinks and Perkins (1970).

MATERIALS AND METHODS

This experiment was carried out at private farm in EL- Kassasein city, El-Tall- Kabeer district, Ismailia governorate, Egypt during the four successive summer seasons, 2003, 2004, 2005 and 2006. In the first season, the four crosses, Tushka 3 x Taka 3, Shandaweel 3 x Giza 24, 128 x Tushka 1 and M2A1 X 104 A 18-2, which will designated in the text as first, second, third and fourth cross, respectively, were made. The F1 plants of each cross were selfed in 2004 to produce F_2 seeds. In 2005 growing season, the obtained materials F_1, F_2 and the parental genotypes of each cross were sown. Twenty random F_2 plants of each cross were crossed, as males, back to its respective parents P_1, P_2 and F_1 (P_1 X P_2) to produce L1i (P_1 x F_2i), L_2i (P_2 x F_2i) and L_3i (F_1i x F_2i). In 2006, the sixty families (L_1 (20) + L_2 (20) + L_3 (20) of each cross with their respective parental genotypes were sown in a randomized complete block design with three replicates. The progenies were raised in single rows 4 meters long with 50cm between rows and plants within rows were 20cm apart. All normal agronomic practices were followed as usual for the ordinary sesame fields in the area. Data were recorded on five random competitive plants from each family in each replication.

Biometrical analysis:

Test of epistasis and detection and estimation of additive and dominance components of genetic variations were carried out according to Kearsey and Jinks (1968), Jinks *et al.* (1969) and Jinks and Perkins (1970). The triple test cross families were firstly subjected to the convential two way analysis of variance for (L_{1i}, L_{2i} and L_{3i}) and (L_{ii} and L_{2i}) sets of families for each character separately The analysis provides a test of significance of the between families terms. The analysis provide a test for the between families terms .The within families replicates terms (L_{1i}, L_{2i} and L_{3i}) was used to test for the significancy of epistasis (L_{1i}+ L_{2i} -2 L_{3i}) and additive gene effects $\overline{L_{1i}} + \overline{L_{2i}} + \overline{L_{3i}}$) while the within ($L_{ii}$ and L_{2i}) types of edequate for testing the significance of dominance($\overline{L_{1i}} - \overline{L_{2i}}$) gene effects

Test for epistasis:

To test for epistasis, twenty values of (L_{1i}+ L_{2i} -2 L_{3i}) where i = 1 to 20 with 20 degrees of freedom were used i.e. to test for overall epistasis. The overall epistasis was partitioned into (I) type of epistasis (additive x additive) using one degree of freedom and (J and L) types of epistasis (additive x dominance) and (dominance x dominance), respectively using 19 degree of freedom.

The mean squares due to sums ($\overline{L_{1i}} + \overline{L_{2i}} + \overline{L_{3i}}$) and differences ($\overline{L_{1i}} - \overline{L_{2i}}$) for 19 degrees of freedom were used to detect the presence of additive and dominance genetic variation are employed to detect the additive genetic variance according to Comstock and Robinson (1952).

RESULTS AND DISCUSSION

All breeding methods depend largely on the heritable component of the genetic variance. The important task of the breeder is to take such components in consideration and partition it to its constituent parts which are important to crop improvement (Poehlman and Barthakur, 1972). The proper assessment and quantifying of the genetic components (additive, dominance and epistasis) would be of great help to the breeder to choose the appropriate breeding method. Most of the mating systems do not meet all the assumptions on which they are based Kearsy and Jinks (1968) have described the triple test cross analysis to overcome the mentioned problems. Such analysis can detect and allows estimation of the additive and dominance effects and provides an unambiguous test for epistasis. Moreover, it may be applied to any population irrespective of its gene frequency, mating system and linkage. in the light of all these advantages, the triple test cross analysis has been used in the present research work to study the genetic variation in an F_2 populations of four sesame crosses.

The early attempts to partition the genetic variance were done by Fisher (1918), where he classified genetic variance into three components, additive, dominance and epistasis. This classification was further developed by Hayman and Mather (1955), where they showed that epistasis could also be partitioned into three components additive X additive (I), additive X dominance (J) and dominance X dominance (L). Triple test cross technique provides the breeder unambiguous estimates of epistasis and in the absence of epistasis . The additive and dominance components also remains unaffected by differences in allele frequencies, degree of inbreeding and gene correlation in the parents.

The analysis of variances of the triple test cross families (L_1, L_2 and L_3) and (L_1 + L_2) for all traits i.e. days to the first flower, no. of branches/plant, plant height, capsule length, no. of capsules/plant, 1000 seed weight, seed

yield/plant, oil content (%) and Acid value in the four studied are presented in Table (1). The variance between (L_1, L_2 and L_3) and sets of triple test cross families were found to be highly significant for all traits studied in the four crosses under investigation The variance between (L_1 and L_2) sets of triple test cross were found to be highly significant for most traits studied in the four crosses under investigation, indicating the presence of substantial amount of the genetic variance which would be adequate enough for proceeding to further genetic assessment by means of the triple test cross analysis.

Tests for epistasis:

Analysis of variance for testing the presence of epitasis in the inheritance of all traits studied in the four crosses investigated are presented in Table (2). Presence of overall epistasis was evidenced by the significance of variance ($L_1i + L_2i - 2L_3i$).

The total epistasis was found to be highly significant for most traits studied in the four crosses under investigation, i.e., number of branches/plant and capsule length in the third cross, plant height in the first cross and oil content in the fourth cross, no significant was showed for the height to the first capsule in the last two crosses and acid value in the cross number one

Epistatic type (additive X additive) (I), epistatic type (additive X dominance) (j) and (L) type (dominance X dominance) interactions showed that mean squares estimates due to additive X additive (I) type were found to be highly significant for all characters studied in the four crosses under investigation except the height to the first capsule and plant height in the second cross, capsule length in the fourth cross and seed yield and oil content in the third cross. Both additives X dominance (J) epistatic type and dominance X dominance(L) epistatic type mean squares estimates were found to be highly significant for the height to the first capsule in the first and second crosses, capsule length in the first, second and fourth crosses, Plant height in the second and fourth crosses, number of capsules/ Plant in the second and third crosses, seed yield/ plant in the first three crosses,1000 seed weight in all four crosses, oil content % in the first and third crosses and acid value in the second cross.

The (I), (J) and (L) types of epistasis were simultaneously significant for height to the first capsule in the first cross, capsule length in the first and second crosses, plant height in the fourth cross, number of capsules/ plant in the second and third crosses,1000 seed weight in all four crosses, seed yield in the first and second crosses and acid value in the second cross only.

Table (1): Mean squares of the analysis of variance (L_1, L_2 and L_3) and (L_1 and L_2) sets of triple test cross families for all traits studied in the four investigated crosses.

characters / Items	d.f	Days to the first flower				The height to first capsule				Number of branches/plant				Capsule length			
		Cross no.				Cross no.				Cross No.				Cross No.			
		I	II	III	IV	I	II	III	IV	I	II	III	IV	I	II	III	IV
Between L_1, L_2, L_3 families	59	3.96**	2.204**	2.79**	1.91**	69.42**	130.53**	82.98**	118.38**	0.149**	2.001**	0.83**	0.227**	0.037**	0.03**	0.07**	0.07**
Within families witnin replicates	720	1.05	0.79	0.905	0.46	25.8	59.75	40.92	19.39	0.07	0.9	0.24	0.07	0.0175	0.015	0.027	0.011
Between L_1, L_2 families	39	2.37**	1.17*	1.7**	2.52**	24.28**	137.6*	50.37**	120.36**	0.065**	1.36**	0.99**	0.18**	0.032**	0.029**	0.07**	0.08**
Within families within replicates	480	1.16	0.72	0.85	1.26	7.28	65.1	23.4	37.18	0.021	0.58	0.35	0.025	0.017	0.013	0.03	0.019

*,** significant at 0.05 and 0.01 levels, respectively.

Table (1): Cont.

characters / Items	d.f	Plant height				Number of capsule/plant				1000 seed weight				Seed yield/ plant			
		Cross no.				Cross no.				Cross No.				Cross No.			
		I	II	III	IV	I	II	III	IV	I	II	III	IV	I	II	III	IV
Between L_1, L_2, L_3 families	59	56.98**	112.38*	82.27**	92.37**	163.43**	405.57**	115.68**	272.19**	0.06**	0.018**	0.013**	0.018**	2.12**	2.76**	3.65**	7.9**
Within families within replicates	720	21.89	44.3	32.93	5.18	66.03	134.72	39.19	111.45	0.022	0.0067	0.0055	0.0034	0.95	0.93	0.27	3.76
Between L_1, L_2 families	39	60.01**	100.67*	30.18*	121.98**	132.87**	202*	105.00**	216.58**	0.034**	0.021**	0.011**	0.016**	1.36**	2.2**	1.39**	9.16**
Within families within replicates	480	25.43	58.6	18.66	8.40	67.48	102.49	40.46	24.56	0.011	0.0028	0.0051	0.0028	0.106	0.95	0.615	4.49

*,** significant at 0.05 and 0.01 levels, respectively.

Table (1): Cont.

characters / Items	d.f	Oil content %				Acid value			
		Cross no.				Cross no.			
		I	II	III	IV	I	II	III	IV
Between L_1, L_2, L_3 families	59	1.65**	0.68**	2.11**	3.04**	0.321**	0.0016**	0.00052**	0.0003**
Within families within replicates	720	0.49	0.25	0.14	1.3	0.0026	0.000059	0.00013	0.0001
Between L_1, L_2 families	39	0.59**	0.261*	2.77**	2.21**	0.335**	0.000128**	0.00018**	0.00051**
Within families within replicates	480	0.24	0.16	0.25	0.73	0.0095	0.000054	0.0000102	0.00016

*,** significant at 0.05 and 0.01 levels, respectively.

Table (2): Analysis of variance for testing the presence of epistasis in a triple test cross for all traits studied in the four crosses investigated.

characters / Items	d.f	Days to the first flower				The height to first capsule				Number of branches/plant				Capsule length			
		Cross no.				Cross no.				Cross No.				Cross No.			
		I	II	III	IV	I	II	III	IV	I	II	III	IV	I	II	III	IV
Epistasis (L_1+ L_2,-2 L_3)																	
Over all epistasis	20	7.72**	4.03**	4.85**	0.711	116.27**	166.95**	25.74	23.54	0.17**	3.10**	0.58*	0.32**	0.0515**	0.06**	0.055*	0.08**
(i) type	1	136.7**	60.23**	74.81**	2.34**	561**	26.74	344.25**	134.87**	2.21**	44.14**	6.3**	4.65**	0.149**	0.418**	0.73**	0.007
(j) + (L) types	19	0.93	1.07	1.17	0.63	92.86**	174.3**	8.99	17.68	0.063	0.94	0.29	0.1	0.046**	0.041**	0.019	0.09**
Within families within replicates	720	1.05	0.79	0.905	0.46	25.8	59.75	40.92	19.39	0.07	0.9	0.24	0.07	0.0175	0.013	0.027	0.011

*,** significant at 0.05 and 0.01 levels, respectively.

Table (2): Cont.

characters / Items	d.f	Plant height				Number of capsules/plant				1000 seed weight				Seed yield/plant			
		Cross no.				Cross no.				Cross No.				Cross No.			
		I	II	III	IV	I	II	III	IV	I	II	III	IV	I	II	III	IV
Epistasis (L_1+ L_2,-2 L_3)																	
Over all epistasis	20	41.22*	119.82**	118.47**	40.48**	187.89**	800.39**	125.73**	466.9**	0.104**	0.024**	0.019**	0.02**	4.02**	3.6**	1.043**	9.63**
(i) type	1	129.85**	0.00016	2910.58**	360.98**	615.8**	3984.34**	230.7**	3738.01**	0.77**	0.191**	0.054**	0.09**	26.82**	7.52**	0.0061	95.46**
(j) + (L) types	19	36.7	126.13**	37.84	23.81**	65.37	474.9**	120.21**	136.85	0.06**	0.014*	0.017**	0.02**	2.82**	3.4**	1.09**	5.11
Within families within replicates	720	21.89	44.3	32.93	5.18	66.03	134.72	39.19	111.45	0.022	0.0067	0.005	0.0034	0.95	0.93	0.27	3.76

*,** significant at 0.05 and 0.01 levels, respectively.

Table (2): Cont.

characters / Items	d.f	Oil content %				A cid value			
		Cross no.				Cross no.			
		I	II	III	IV	I	II	III	IV
Epistasis (L_1+ L_2,-2 L_3)									
Over all epistasis	20	3.004**	1.28**	0.41**	4.81*	0.0011	0.00053**	0.0014**	0.005**
(l) type	1	19.4**	21.38**	0.06	68.01**	0.018**	0.003**	0.023**	0.007**
(j) + (L) types	19	2.14**	0.22	0.43**	1.48	0.00021	0.0004**	0.00021	0.002
Within families within replicates	720	0.49	0.25	0.14	1.3	0.0026	0.000055	0.00013	0.001

*,** significant at 0.05 and 0.01 levels, respectively.

But the higher values of (J) and (L) types of epistasis suggested that biparental matings might be attempted in F_2 and subsequent generations and selection might be postponed till relatively late generation. These results are in general agreement with those previously obtained by Sharaan and Ragab (1986), Sheiref (1997), Ramesh *et al.* (1998), Sedek (1999), El-Hifny *et al* (2005), El-Morshidy *et al.* (2005b) and Bakheit *et al.* (2005).

Detection and estimation of additive ($L_1+L_2+L_3$), N.C.M. III (L_1+L_1) and dominance (L_1-L_2) genetic variances:

The analysis of variance for sums (measuring additive genetic variance) and differences (measuring dominance genetic variance) and the estimation of additive and dominance genetic components are presented in Table (3).

The mean squares estimates due to sums ($L_1+L_2+L_3$) were found to be highly significant for all characters studied in the four crosses under investigation except for number of capsules/plant in the fourth cross and 1000 seed weight in the second crosses.

The mean squares due to N.C.M. III additive (L_1+L_2) were found to be highly significant for all characters studied in the four crosses under investigation except for days to the first flower in the second and fourth crosses, height to the first capsule in the fourth cross, number of branches in the second and third cross, capsule length in the third cross and plant height in the second cross and acid value in the first capsule.

The mean squares estimates due to differences (L_1 -L_2) as the test of dominance were found to be highly significant for all studied characters in the four crosses except for except for number of branches/plant in the second cross and acid value in the first cross.

The results obtained here would indicate that epistasis is an integral component of genetic architecture of all traits studied in the four crosses investigated and hence, detection, estimation and consideration of this component is important for formulation of the most efficient breeding programs to improve these traits in the four crosses studied. If epistasis is ignored, no precise conclusion could be drawn about the relative importance of additive, dominance genetic components would be biased by epitasis to unknown extent as in the present materials. Consequently, non-allelic inter action, depicted for all traits studied in the four crosses. Investigated could be manipulated through recurrent selection technique for the improvement of theses traits. Recurrent selection had also been suggested for non allelic inherited traits in sesame by Sedek (1999) and El- Hifny *et al.* (2005). Since both additive and dominance gene effects were found to be significant for all traits studied in the four crosses investigated, simple selection procedure in early generation may not contribute significantly to the improvement of these traits. The additive genetic components in these traits can be successfully exploited through pedigree method of selection because of major contribution of additive gene effects in late generations of segregating populations.

Table (3): Mean squares of (sums) additive ($L_1+L_2+L_3$) and N.C.M III (L_1+L_2) and (differences) dominance (L_1-L_2) for all traits studied in four crosses investigation.

characters / Items	d.f	Days to the first flower				The height to first capsule				Number of branches/plant				Capsule length			
		Cross No.				Cross No.				Cross No.				Cross No.			
		I	II	III	IV	I	II	III	IV	I	II	III	IV	I	II	III	IV
Additive ($L_1+L_2+L_3$)																	
Between ($L_1+L_2+L_3$) families	19	4.8**	1.53**	3.95**	19.42**	187.26**	219.26**	449.28**	136.32**	0.17*	2.06*	1.14**	0.47**	0.8**	0.16**	0.93**	5.41**
Within families within replicates	720	1.05	0.79	0.905	0.46	25.8	59.75	40.92	19.39	0.7	0.9	0.24	0.07	0.0175	0.015	0.027	0.011
N.C.M. additive (L_1+L_2)																	
Between (L_1+L_2) families	19	397.1**	0.505	3.6**	2.32	50.56**	255.25**	95.95**	70.03	0.114**	0.76	0.55	0.35**	0.054**	0.078**	0.03	0.205**
Within families within replicates	480	1.16	0.72	0.85	1.26	7.85	65.1	23.46	37.18	0.021	0.58	0.35	0.025	0.017	0.013	0.03	0.019
Dominance (L_1-L_2) families																	
Between (L_1-L_2) families	19	2.48*	2.04**	2.3**	3.75**	49.15**	220.81**	472.4**	149.18**	0.097**	1.043	1.72**	0.48**	0.068**	0.03**	0.118**	0.517**
Within families within replicates	480	1.16	0.72	0.85	1.26	7.85	65.1	23.46	37.18	0.021	0.58	0.35	0.025	0.017	0.013	0.03	0.019

*,** significant at 0.05 and 0.01 levels, respectively.

Table (3): Cont.

characters / Items	d.f	Plant height				Number of capsules/plant				1000 seed weight				Seed yield/plant			
		Cross No.				Cross No.				Cross No.				Cross No.			
		I	II	III	IV	I	II	III	IV	I	II	III	IV	I	II	III	IV
Additive (L'_1+ L'_2+ L'_3)																	
Between (L'_1+ L'_2+ L'_3) families	19	113.79**	176.73**	88.44**	245.76**	498.2**	1234.8**	265. 69**	160.53	0.07**	0.106	0.041**	0.35**	7.47**	7.68**	2.84**	16.92**
Within families within replicates	720	21.89	44.3	32.93	5.18	66.03	134.72	39.19	111.45	0.022	0.067	0.0055	0.0034	0.95	0.93	0.27	3.76
N.C.M. additive (L'_1+ L'_2)																	
Between (L'_1+ L'_2) families	19	55.28*	77.41	57.2**	175.27**	2658.46**	721.38**	154.63**	261.55**	0.04**	0.078**	0.012*	0.04**	3.44**	4.58**	6.67**	20.29**
Within families within replicates	480	25.43	58.6	18.66	8.4	67.48	102.49	40.46	24.56	0.01	0.0028	0.0051	0.0028	0.106	0.95	0.61	4.49
Dominance (L'_1- L'_2) families																	
Between (L'_1- L'_2) families	19	54.66*	393.5**	227.05**	287.84**	284.08**	300.22**	210.98**	503.66**	0.02*	0.03**	0.017**	0.028**	2.78**	4.31**	2.22**	60.25**
Within families within replicates	480	25.89	58.6	18.66	8.4	67.48	102.49	40.46	24.56	0.01	000028	0.051	0.0028	0.106	0.95	0.61	4.49

*,** significant at 0.05 and 0.01 levels, respectively.

Table (3): Cont.

Characters / Items	d.f	Oil content %				A cid value			
		Cross No.				Cross No.			
		I	II	III	IV	I	II	III	IV
Additive (L'_1+ L'_2+ L'_3)									
Between (L'_1+ L'_2+ L'_3) families	19	3.64**	5.95**	2.2**	4.71**	0.0052*	0.0001**	0.0426**	0.00039**
Within families within replicates	720	0.49	0.25	0.14	1.3	0.0026	0.00005	0.00013	0.0001
N.C.M. additive (L'_1+ L'_2)									
Between (L'_1+ L'_2) families	19	0.88**	0.56**	1.38**	3.7**	0.0002	0.00052**	0.00089**	0.00031*
Within families within replicates	480	0.24	0.16	0.25	0.73	0.0095	0.000054	0.0000102	0.00016
Dominance (L'_1- L'_2) families									
Between (L'_1- L'_2) families	19	1.55**	0.49**	1.9**	8.41**	0.0008	0.00078**	0.00055**	0.011**
Within families within replicates	480	0.24	0.16	0.25	0.73	0.0095	0.000054	0.0000102	0.00016

Generally, for exploitation of all types of gene action, bi-parental approach inters crossing and/or recurrent selection may be practical for developing high yielding in sesame lines in advanced generations. Similar conclusion was also drawn by Kassem *et al.* (1979) Sherief (1997). Bakheit *et al.* (2005) and El- Hifny *et al.* (2005).

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تحليل التربل تست كروس في السمسم

حسان عبد الجيد دوام[1] – فتحى أحمد هنداوى[1] – إبراهيم حسينى درويش[1] – سامى عطية محمد[2] – حمودة محمد أحمد على[1]

١ – قسم المحاصيل– كلية الزراعة – جامعة المنوفية

٢– قسم الزيت– معهد بحوث المحاصيل الحقلية– مركز البحوث الزراعية– الجيزة.

الملخص العربي

اجريت هذه الدراسة في المواسم الصيفية ٢٠٠٣، ٢٠٠٤، ٢٠٠٥، ٢٠٠٦ وذلك بغرض كشف التفاعل غير الاليلي لصفات ميعاد ظهور أول زهرة– ارتفاع أول كبسولة– عدد الأفرع/ نبات– طول الكبسولة– ارتفاع النبات– عدد الكبسولات/ نبات– وزن الألف بذرة– محصول البذور/ نبات– نسبة الزيت– رقم الحموضة في اربعة هجن من السمسم وهي:

(توشكى٣ ×طاقة٣)، (شندويل ٣× جيزة٢٤)،(١٢٨× توشكى١) و(M2A1×١٠٤ع ١٨–٢)

وقد استخدم لهذا الغرض طريقة تحليل تربل تست كروس طبقا لـــ

Kearsy and Jinks (1968), Jinks *et al.*(1969) and Jinks and Perkins (1970).

ويمكن تلخيص النتائج المتحصل عليها في الأتي:

١– كانت قيم التباين بين عائلات التهجين الثلاثي الاختبارى (L_1,L_2,L_3) وكذلك (L_1,L_2) عالية المعنوية فى كل الصفات المدروسة فى الهجن الأربعة تحت الدراسة.

٢– كان الفعل الجيني التفوقي عالي المعنوية لكل الصفات في الهجن الأربعة المدروسة فيما عدا صفة ارتفاع أول كبسولة في الهجين الثالث والرابع ورقم الحموضة في الهجين الأول. وكان التباين الراجع إلى طراز التفوق المضيف × المضيف (I) عالي المعنوية لكل الصفات في الهجن الأربعة المدروسة فيما عدا صفة ارتفاع أول كبسولة وارتفاع النبات في الهجين الثاني وطول الكبسولة في الهجين الرابع ومحصول البذور ونسبة الزيت في الهجين الثالث. بينما كان طرازي التفوق المضيف× السيادي (J) و السيادي × السيادي (L) عاليا المعنوية لمعظم الصفات المدروسة في كل الهجن فيما عدا ميعاد التزهير وعدد الأفرع/ النبات في كل الهجن

وارتفاع أول كبسولة في الهجين الثالث والرابع وارتفاع النبات في الهجين الثالث وعدد الكبسولات / النبات في الهجين الرابع ومحصول البذور في الهجين الرابع ونسبة الزيت في الهجين الثالث والرابع ورقم الحموضة في الهجين الأول والثالث والرابع.

٣-ساهم كل من الفعل الجيني المضيف والسيادي بدور فعال في توارث جميع الصفات تحت الدراسة.