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DETECTION OF GENETIC COMPONENTS THROUGH TRIPLE TEST CROSS IN SOME QUANTITATIVE CHARACTERS OF SUMMER SQUASH (*cucurbita pepo* L.)

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ABSTRACT

The present study was carried out during five successive seasons during 2003-2005, at the experimental station farm (at Abies), of the Faculty of Agriculture, Alexandria university. To estimate the different kinds of genetic variance controlling the inheritance of some important and economical traits of summer squash, and to determine their relative sensitivity to different environments. The original genetic material of the present investigation consisted of 10 inbred lines of summer squash. Four of these pure inbred lines were used as parents of two main crosses. The two studied crosses were $P_1 \times P_2$ (cross II). In each of the two crosses, the two parents along with their F_1 were utilized as three testers to initiate, with a group of the other eight parental inbred lines (6 common in both crosses plus the two parents of the other cross), 24 triple test cross (TTC) families. The studied environments were the plant spacing of 30.45 and 60cm (as micro-environments) and the two different planting seasons June, 2004 and April, 2005 (as macro environments). The three tester, the eight parental inbred lines and the resultant 24 triple test cross families of each cross were evaluated for the various studied characters i.e. early fruit number/plant, early yield/plant, total fruit number/plant and average fruit weight, in the two studied seasons, using a split – plot system in randomized complete blocks design . The obtained results showed that the detection of both the additive and dominance genetic variances, indicated generally that both the additive and dominance gene effects contribute significantly to the genetic mechanisms involved in the inheritance of all studied characters, with relatively different magnitudes according to the character. The interactions additive × environment and dominance × environment reflected significant effects on average fruit weight, number of male flowers, sex-ratio and total yield/plant. Concerning the different types of the epistasis, the j + 1 – type of epistasis gave significant values for all studied characters, in either one cross or in both crosses; whereas, the i – type of epistasis was found significant in flowering and total yield characters, but in cross II only. The interaction effects of i-epistasis × environment were found significant on total yield characters, in cross I; while those of j+1 epistasis × environment were found significant on number of male flowers, sex – ratio, total yield/plant, in cross I, and on average fruit weight, in both crosses. Most of the studied parental inbred lines contributed significantly towards the total epistasis and played important positive or negative roles in affecting epistasis in all studied traits in both crosses.

INTRODUCTION

Summer squash *(Cucurbita pepo.* L.) is considered to be one of the most popular vegetable crops grown in Egypt. It is sown almost allover the year and eaten cooked as an immature fruit which is rich with fibers and vitamins or consumed for the mature seed as a snack which is a good source of fats and protein. According to the agricultural statistics, the total cultivated area with summer squash in 2004 was 91600 faddan (0.42 ha) in all seasons, which produced a total production of 678254 tons, with an average productivity of 7.40 tons/fed.

To improve the yield and yield attributes, knowledge of the genetic architecture of the parental material at hand has to be attained in order to plan a successful breeding program. Triple test cross analysis provides good information about the presence or absence of epistasis; that part of the genetic variance which is importance for controlling yield characteristics in breeding summer squash populations, yet still not well understood; in addition to estimating the additive and dominance components of genetic variance. A sound plant breeding program is usually dependent on such information, which reflect the relative importance of the additive and non-additive gene action components required for the improvement of quantitative characters.

The triple test cross (TTC) is a multiple mating scheme proposed by Kearsey and Jinks (1968), as an extension of Comstock and Robinson's (1948) North Carolina Design III. It is theoretically the best design for detecting and estimating the additive, dominance and epistasis components of variation for a quantitative trait. This design is so versatile that it can be applied to any population, regardless of its gene and genotype frequencies, as demonstrated by Jinks *et al.* (1969). Several modifications; such as those described by Jinks and Perkins (1972) and Jinks and Pooni (1980), were done to make the method applicable to more complex types of materials. Perkins and Jinks (1971) and Jinks and Virk (1977) provided information about the interaction between environments, and additive, dominance and epistatic effects of genes at the micro-and macro-environmental levels.

Ismail (2003) carried out a study to investigate the interactions of two tomato triple test crosses (Money Moker × Castle Rock and Carmenco 200 × Peto 86) with three different micro-environments (30, 45 and 60cm plant spacings) to detect the different types of the genetic variance. The reported results indicated that Ms values for i type of epistasis (additive x additive) and i type × environments were found to be highly significant for all studied characters, except for early fruit weight and number, in the two crosses. While, j + 1 type and j + 1 × Env. were all highly significant, except early fruit number in first cross. Singh and Singh (1984) showed highly significant mean squares for j+1 type and its interaction with the environment in two studied tomato crosses. Also, there were significant estimates for i type epistasis × environemtnal for final plant height in first cross and for branch number in both crosses; while, j + 1 type of epistasis was more sensitive to environment in fruit yield characters. Singh *et al.* (1986a) studied the genetic parameters controlling the expression of seed yield and the yield components, using both the generation mean and triple test cross (TTC) analyses in two crosses of field pea. The estimates of the various genetic parameters indicated that the major component of the genetic variance was the additive component though the dominance component was also found to be significant. There was evidence of epistasis for most of the studied characters, specially that of i type. Many other previous studied were conducted on field crops, such as those of Singh *et al.* (1995) on wheat, Singh (1979) on barley, Singh (1980) on spring wheat, Ketata *et al.* (1976) on winter wheat, Wolf and Hallauer (1997) on Maize, Subbaraman and Rangasamy (1989) on rice and Tefera and Peat (1997) on t'ef. The reported results, generally, indicated that this genetical procedure is more appreciable and widely applicable for the genetical analysis of different populations; because it detects and estimates the epistatic components of variation; that provides unbiased estimates of the other genetical components; i.e., the additive and dominance components.

The present study was therefore undertaken on 12 parental genotypes of summer squash and their combinations To illustrate the relative importance of the different kinds of genetic variance controlling the inheritance of some important and economical straits of summer squash, and to determine their relative sensitivity to different environments.

MATERIALS AND METHODS

This study was carried out in five successive seasons during the years 2003-2005, at the experimental Station Farm (at Abies) of the Faculty of Agriculture, Alexandria University. This work was initiated to study the general performance in addition to estimating the genetic variance of some summer squash genotypes under different environmental conditions through a triple test cross design.

The original genetic material of the present investigation consisted of 10 inbred lines of summer squash (listed in Table 1). The parental inbred lines were at a high degree of homozygosity since they were previously selfed for six successive generations. Four of these inbred lines were used in this study as testers, in addition to their two F_1 hybrids, $P_1 \times P_2$ in cross I and $P_3 \times P_4$ in cross II, because they were the parents of the best hybrids for early yield and total yield, respectively, in a previous study of El-Sharkawy (2000) .The triple test cross (TTC) mating design of Kearsey and jinks (1968) was used in this study. Two groups of eight parental inbred lines each were used to generate the triple test cross families (their abbreviations and sources shown in Table 1).

Table (1): Abbreviations and sources of the summer squash parental inbred lines, used in two groups (crosses).

Lines	Group		Sources
	Cross I	Cross II	
P_1*	Tester	Parent	Derived from Eskandrani cultivar (from a breeding program in Nobaseed Company)
P_2	Tester	Parent	
P_3	Parent	Tester	
P_4	Parent	Tester	
P_5	Parent	Parent	Derived from Eskandrani cultivar (From Veg. Crops Dep., Alex. Univ.)
P_6	Parent	Parent	
P_7	Parent	Parent	Derived from Eskandrani cultivar (From open pollinated Veg. Crops De., Hort. Res. Center,. EL. Dokki)
P_8	Parent	Parent	Derived from Round zuccini cultivar, USA.
P_9	Parent	Parent	Derived from Early Straight Neck cultivar, USA.
P_{10}	Parent	Parent	Derived from Balady cultivar, Egypt.

* The originally 12 evaluated genotypes included these 10 parental inbred lines in addition to the two F_1 hybrids $P_1 \times P_2$ (used as a third tester in cross I) and $P_3 \times P_4$ (the third tester in cross II).

The experimental mating design consisted of crossing each of the eight parental inbred lines in each group to the two tester inbred lines and ot their F_1 resulting in 24 test cross; i.e. cross I consisted of P_1, P_2 and there F_1 as tester and the rest eight lines as parent .Cross II included P_3 , P_4 and there F_1 as testers and the rest as parents . Three plant spacings; i.e. 30cm (Env. 1), 45cm (Env. 2) and 60cm (Env. 3); were used in this study to represent the first type of environments (micro environment); while the other type of environments (macro environment) was represented by two different growing seasons; i.e. planting dates were on (1^{st} June 2004 and 1^{st} April 2005).

In the First season (April 2003), seeds of the four tester inbred lines, P_1, P_2, P_3 and P_4, were sown in the field on April 5, 2003 crossing among the four tester inbred lines were made

to produce enough seeds of F1 of each cross ,along with this selfed seeds from each tester inbred line were also obtained.

In the second and the fourth seasons November of 2003 and 2004the seeds of the tester inbreds, the F1,s and the other parental inbred line were sown. The selfing and crossing technique between the two tester inbred lines of each cross to produce the two F1,s again ,and among each of the three testers of each cross with the respective group of the eight parental inbred lines to produce 24 sets of families for each cross; i.e 8L1i ,8L2i ,8L3i. selfing also ,was done for each of the ten parental inbred lines to produce new seeds for the evaluation experiments in the successive growing seasons.

The evaluation of the used genetical materials was carried out in two seasons. Seeds of the sixty different genetic populations; 24 TTC families set (L_{1i}, L_{2i} and L_{3i}) for Each cross; i.e. 48 TTC families in both crosses together with 10 inbred lines (2 testers + 8 parents) and the two F1's of the two crosses ,were sown in two different growing seasons. The first one started on June 1st, 2004 and the second season was on April, 1st 2005, which represented the two macro environments. The experiments were conducted using a split – plot design with three replications. The main plots were devoted for the three different micro environments; i.e. the three plant spacings 30, 45 and 60 cm between plants. The different sixty genotypes were randomly distributed in the sub-plots of each micro environment. The sub-plot was one ridge of 4 m long and 1.5 m wide with an area of 6 square meters.

Recorded data:

1- Fruit number of early yield.

It was determined by summing the numbers of the harvested fruits in the first four harvest/ plant.

2- Early fruit weight/plant

It was recorded as the total weight of all harvest fruits (in gm) in the first four harvest, from all plants in each sub-plot, divided by the number of plants.

3- Total fruit number / plant

The total number of all harvested fruits from each sub/plot was divided by the number of plants.

4- Total yield /plant

Weight of the harvested fruits in each harvest was recorded and summed over all the harvesting season for each sub-plot and divided by number of plants to get total yield/plant (gm).

5- Average fruit weight / plant (g)

It was calculated by dividing the total weight of all harvested fruits of each sub-plot by its number.

Statistical analysis
Analysis of variance

Obtained data were statistical analyzed using then conventional two way analysis of variance for the split-plot system in a randomized complete blocks design in each season separately and combined over the two seasons. The comparisons among family mean, of each

cross, were conducted using Duncan's multiple range test at the 0.05 level of probability. The data were analyzed using SAS software, 1997 (SAS institute, release 6.12).

Triple test cross analysis under different environments

Triple test cross (TTC) analyses for crosses I and II; under the different planting spacings of 30, 45 and 60 cm in the two different growing seasons; were separately carried out for each cross and in each season, according to Jearsey and Jinks (1968), to detect additive, dominance and epistatic components of the genetic variation. The analysis, suggested by Jinks and Virk (1997), was flowed to obtain information about the interactions between environments and each of additive, dominance and epistatic effects of genes. Before proceeding to the biometrical analysis, the analysis of variance for L_1, L_2 and L_3 as well as L_1 and L_2 types of families were separately carried out to obtain the error variance for testing the additive, dominance and epistatic gene effects.

Testing of epistatsis

Kearsey and Jinks (1968) proposed the expression $L_{1i} + L_{2i} - 2L_{3i}$=D. the epistatic deviation D should equal zero in the absence of epistsis and will differ from zero if epistasis is present. The analysis of variaznce for the TTC provides two F-test for the presence of epistasis Perkins and Jinks, (1970). The source of variation due to tester with 2 d.f was partitioned into two orthogonal contrasts, one of which was $L_{1i} + L_{2i}$-$2L_{3i}$. The contrast L_{1i}+L_{2i}-$2L_{3i}$ was designated as epistasis in the TTC analysis and tests for the presence of i-type (additive x additive) epistasis effects. The tester x parent source of variation (14 d.f) was partitioned into two sources of variation, one of which was variation in $L_{1i} + L_{2i} - 2L_{3i}$ among parents, which was designated as epistasis x parent in the TTC and tests for j-1 type of epistasis (additive x dominance and dominance x dominance epistasis effects). A test of epistasis was conducted over environments to get information about the interaction of the two types of epistasis with environments. Parents and environments were considered random effects and testers were fixed effects.

Detecting of additive genetic variance

The variance component of among parents and their interaction with environments was employed to detect the additive genitive component and additive x environment genetic component, respectively, according to Comstock and Robinson (1952) from North Carolina design III method.

Detecting of dominance genetic variance

The variance component of the orthogonal contrast $L1_{ivs}$ L_{2i} among parents ($L1_{ivs}$ L_{2i}x parents) was used to detect the presence of dominance variance and their interaction with the environment (dominance x environment) according to Comstock on Robinson (1952) in North Carolina design III methods.

RESULTS AND DISCUSSION

1- General performance of the testers and the parental inbred lines:

In the present investigation, 12 genotypes of summer squash were evaluated for their morphological attributes to study the mean performances of the TTC tester and a group of parental inbred lines to be used to establish family sets of TTC, to through some light on the differences among the testers and a group of a random sample of summer squash parental inbred lines. Such differences among the evaluated genotypes and their interaction with the tested environments were arranged under the following sub-headings:

Early yield traits:

The results in Table 2, clearly, reflected favorable effects for the wide spacing on early yield potential, in both seasons, through the differences were not found significant. The 60 cm spacing treatment produced generally the highest values for the studied early yield traits in the two seasons.

For the average performance of the testers, it was noticed that the F_1 hybrid testers results in higher mean, values than those of their respective earlier productive parent in both seasons. in general the tester lines of the two crosses appeared to be different enough and proved to be valid as testers for these two traits. For concerning the parental inbred lines, the results showed the presence of significant differences among the lines in early fruit number and weight/plant. The two parents L_8 and L_5 appeared to be early producing parents in the first season; while, P_{10} and p_6 gave the significant higher values in second season, respectively. On the other hand, the inbred parental p_7 and p_9 were producing the poorest lines, in both seasons.

Total yield traits

The results, generally, reflected significant favorable effects for the wide spacing on yield potential/plant in both seasons. The 60 cm spacing treatment produced the highest total yield/plant in the two seasons. Meanwhile, the data in Table (3) illustrated that growing the plants of the different studied genotype at the narrowest spacing 30 cm increased the total productivity/ faddan as compared with the wider spacing. However, the differences were found high enough to be significant only in the second season, though the results of the first season reflected also the same general trend.

The comparison among the means of the various genotypes illustrated that the testers of both crosses reflected significant differences among them in all studied total yield characters in both seasons. The results, generally, illustrated that the F_1 testers, in the two crosses, surpassed their highest respective parent and showed heterosis in total fruit number and yield weight/plant, with the exception noticed in cross I in the second seasons. The highest averages fruit yield / plant were obtained from P_8, followed by those P_6 and P_5 in the first season, and from P_{10} and P6 followed by that of P_8 respectively, in the second season.

Table (2): Mean performances of the triple test cross testers and parental inbred lines for early fruit weight (gm)/ plant of summer squash under different micro environments (plant spacings) in both studied seasons.

Genotypes	First season			
	Env. 1	Env. 2	Env. 3	Gen. Avr.
Testers				
Cross I				
P_1	278.3 d-k*	419.0 c-i	444.3 b-h	380.5 CD
P_2	498.3 a-f	747.6 ab	439.0 b-h	561.6 AB
$P_1 \times P_2$	773.3 a	588.0 a-d	625.3 a-c	662.2 A
Cross II				
P_3	238.0 e-k	143.6 g-k	350.0 c-k	243.8 EF
P_4	235.0 e-k	300.0 c-k	400.0 c-j	311.6 D
$P_3 \times P_4$	401.6 c-j	455.0 b-g	560.0 a-e	472.2 BC
Parents				
P_5	66.6 jk	461.6 a-g	399.3 c-j	309.2 DE
P_6	116.6 h-k	173.3 f-k	169.0 f-k	153.0 E-G
P_7	108.3 h-k	50.0 k	88.3 i-k	82.2 G
P_8	246.6 e-k	412.6 c-i	368.0 c-k	342.4 CD
P_9	39.33 k	85.0 j-k	115.0 h-k	79.7 G
P_{10}	100.0 j-k	150.0 g-k	170.0 f-k	140.0 FG
Env. Avr.	258.5 A	332.1 A	344.0 A	
Genotypes	**Second season**			
	Env. 1	Env. 2	Env. 3	Gen. Avr.
Testers				
Cross I				
P_1	505.0 a-e	486.0 a-e	388.5 b-g	459.8 AB
P_2	569.5 a-c	492.5 a-e	375.0 b-h	479.0 AB
$P_1 \times P_2$	560.0 a-c	512.5 a-e	680.0 a	584.1 A
Cross II				
P_3	142.0 f-k	183.5 f-k	167.0 f-k	164.1 C
P_4	105.0 g-k	615.0 ab	487.5 a-e	402.5 B
$P_3 \times P_4$	325.0 b-j	415.0 a-f	510.0 a-e	416.6 AB
Parents				
P_5	67.5 i-k	87.5 h-k	260.0 d-k	138.3 C
P_6	529.5 a-e	331.5 b-i	375.0 b-h	412.0 B
P_7	25.0 k	37.5 jk	37.5 jk	33.3 D
P_8	156.5 f-k	248.0 e-k	170.0 f-k	191.5 C
P_9	25.0 k	40.0 jk	37.5 jk	34.17 D
P_{10}	285.0 c-k	588.0 ab	550.5 a-d	474.5 AB
Env. Avr.	274.5 A	336.4 A	336.5 A	

*** Values followed with a common alphabetical letter, within a comparable group of means, do not significantly differ, using Duncan's multiple range test at 0.05 level of significance**

Table (3): Mean performances of the triple test cross testers and parental inbred lines for total fruit weight/ plant of summer squash under different micro environments (plant spacings) in both studied seasons.

Genotypes	First season			
	Env. 1	Env. 2	Env. 3	Gen. Avr.
Testers				
Cross I				
P_1	656.0 l-o*	863.6 j-n	1195.0 e-j	904.9 F
P_2	1033.3 h-l	1275.0 d-j	1387.6 c-j	1232.0 CD
$P_1 \times P_2$	1369.6 c-i	1661.3 b-d	2481.6 a	1837.6 A
Cross II				
P_3	525.0 no	970.0 i-m	1420.0 c-i	971.7 EF
P_4	858.0 j-n	1100.0 g-k	1500.0 b-g	1152.7 DE
$P_3 \times P_4$	1068.3 g-l	1400.0 c-i	1733.3 bc	1400.6 BC
Parents				
P_5	749.6 k-n	1113.0 f-k	1607.6 b-e	1156.8 DE
P_6	875.0 j-n	1211.6 e-j	1556.6 b-f	1214.4 CD
P_7	583.3 m-o	500.0 no	874.3 j-m	652.6 G
P_8	1206.6 e-j	1474.0 b-h	1885.3 b	1522.0 B
P_9	266.6 o	633.3 l-o	975.0 i-m	625.0 G
P_{10}	470.0 no	657.0 l-o	1240.0 d-j	789.0 FG
Env. Avr.	805.1 C	1071.5 B	1488.0 A	
Genotypes	**Second season**			
	Env. 1	Env. 2	Env. 3	Gen. Avr.
Testers				
Cross I				
P_1	1145.0 b-h	1079.5 c-h	1078.5 c-h	1101.0 B-D
P_2	1723.0 ab	1399.0 a-d	1465.0 a-d	1529.0 A
$P_1 \times P_2$	1345.0 a-e	1267.5 a-f	1510.0 a-d	1374.0 AB
Cross II				
P_3	550.0 h-j	912.5 d-i	1221.0 b-g	894.5 C-E
P_4	650.0 g-j	1277.5 a-f	1312.5 a-e	1080.0 B-D
$P_3 \times P_4$	11.0 c-h	1550.0 a-c	1850.0 a	1500.0 A
Parents				
P_5	421.0 ij	702.5 f-j	1272.5 a-f	798.7 DE
P_6	1146.5 b-h	981.5 c-i	1106.5 c-h	1078 B-D
P_7	550.0 ij	752.5 e-j	1537.5 a-c	946.7 C-E
P_8	772.5 e-j	1031.5 c-h	1405.0 a-d	1069.7 B-D
P_9	235.0 j	650.0 g-j	1087.5 c-h	657.5 E
P_{10}	745.0 e-j	1375.0 a-d	1538.0 a-c	1219.3 A-C
Env. Avr.	865.2 C	1081.5 B	1365.3 A	

*** Values followed with a common alphabetical letter, within a comparable group of means, do not significantly differ, using Duncan's multiple range test at 0.05 level of significance**

2- detecting of additive, dominance and epistasis genetic components:

The aforementioned results of the present study; on two groups of summer squash triple test cross families, cross I ($P_1 \times P_2$) and cross II ($P_1 \times P_2$), tested under three micro-environments (30, 45and 60 cm plant spacing) and two macro-eviroments (late summer season planting on June 1st, 2004 and summer season planting on April1st, 2005 Tables (4,5) showed that the detections of both the addative and dominance genetic variances for the different studied characters indicated that both the addative and dominance gene effects contributed significantly to the genetic mechanisms involved in the inheritance of all studied characters. The estimated values of the addative genetic parameter were found highly significant in all the characters, in both crosses. The interaction effects of addative× environment were found significant for total yield/ plant, in cross II. The effects of the dominance× enviroment interaction were found significant for, total yield and average fruit weight, in both crosses. These results, generally, agreed with those of Feleafel *et al.* (2001), Hassan *et al.* (1984) and Abd EL-Hafez *et al.* (1997).

Concerning the detection of epistais, the analysis of the TTC mating design in cross I and cross II families indicated that the epistatic effects were important in the inheritance of several traits. The F-test for the epistasic types in the TTC analysis of variance indicated that the addative× additive effects were present for total fruits number and total yield / plant in cross II. The addative× dominance and dominance× dominamve (j+L-type of epistasis) appeared important in the inheritance of early fruits characters, in both crosses; for total fruits number and total fruit weight / plant, in cross I; and for average fruit weight, in cross II. Gamble (1960) reported that additive× dominance gene effects were detected more frequently for plant height and ear length in maize.

The obtained results, generally illustrated that the expressions of both types of epistasis (i-episrasis and j+ 1-epistasis) were found in many cases to be significantly affected by environments. The interaction (i-type of epistasis× enviromnet) reflected significant effects on the inheritance of total fruit number and total fruit weight/ plant in cross I. the (j+1- type of epistasis× environment) interaction was found significant in determining the performance of total yield/ plant, in cross II, and average fruit weight, in both crosses. On tomato, Ismail (2003) found that the estimated variance components of the epistasis× environments interactions were found highly significantly for the inheritance of all studied traits except early fruits number. The obtained results of the present study revealed also that the interaction effects main effect, except for the performance of total fruits number, in cross I.

The obtained estimates for the epistatic deviation means Tables (6,7) indicated the direction and relative magnitudes to indentify those lines which interacted with the testers L_1 and L_2 in each cross to produce significant total epistais. The tested parental inbred lines P_9, P_8 and P_6, for early fruits number; P_8, for early yield/plant; P_6, and P_9 for total fruits number; P_9 for total yield/ plant; and P_3 and P_5, for average fruit weight; showed insignificant contributions towards the total epistasis in both crosses, respectively. On the other hand, all the other tested parental inbred lines, in both crosses played important positive or negative roles in affecting the total epistasis in all the studied traits. It should be mentioned here that the experimental size required to detect epistasis through TTC depends largely on the gene dispersion in the first (L_1) and second (L_2) tester parents. Jinks and Pooni (1980) and the number of diverse genotype used in the study Ketata *et al.* (1976). Therefore, more diverse summer squash genetypes are suggested to be included in studies designed for the detection of epistasis through TTC technique.

Table (4): Triple test cross analysis of variance for early yield characters of summer squash, measured over environments

Sources of variation	d.f.	Cross I		Cross II	
		Fruits number of early yield	Early Yield/ plant	Fruits number of early yield	Early Yield/ plant
Environments	5	4.51*	401905**	11.54**	444649**
Testers	2	20.54	530291*	5.30	197947
L_{1i} vs L_{2i}	1	39.88	1047717**	6.03	231133
$L_{1i}+ L_{2i}- 2L_{3i}$ (i-epistasis)	1	1.21	12866	4.57	164762
Env. × Tester	10	1.52	36886	1.19	30719
Env. × L_{1i} vs L_{2i}	5	1.24	14808	1.55	43092
Env. × $L_{1i}+ L_{2i}- 2L_{3i}$ (Env. × i- epistasis)	5	1.80	58965	0.83	18346
Parents (additive)	7	19.07**	358670**	20.47**	321019**
Env. × parents (Env. × additive)	35	1.31	34932	1.24	29644
Tester × parents	14	11.61**	155416**	9.01**	150032**
L_{1i} vs L_{2i} × parents (dominance)	7	15.36**	185125**	3.68*	80746*
$L_{1i}+ L_{2i} - 2L_{3i}$ × parents (j+ 1- epistasis)	7	7.86**	125707**	14.33**	219318**
Env. × tester × parent	70	1.43	36642	1.49	33550
Env. × (dominance)	35	1.35	33835	1.49	31150
Env. × (j+ 1- epistasis)	35	1.51	394449	1.49	35951
Error	207	1.59	29887	1.13	26326

***, ** Significant at 0.05 and 0.01 level of significance, respectively.**

Table (5): Triple test cross analysis of variance for total yield/ plant characters of summer squash, measured over environments

Sources of variation	d.f.	Cross I			Cross II		
		Total fruits No/ plant	Total yield/ plant	Average fruit weight	Total fruits No/ plant	Total yield/ plant	Average fruit weight
Environments	5	53.52**	2178337**	2048.6**	69.30**	2380268**	1365.7*
Testers	2	123.88**	3145068**	669.2	42.89*	164855*	1223.7
L_{1i} vs L_{2i}	1	245.82**	6238830**	1315.4	4.37	382663	2150.2
$L_{1i}+ L_{2i}- 2L_{3i}$ (i-epistasis)	1	1.95	51307	23.0	81.42**	1747048**	297.3
Env. × Tester	10	6.19*	258895*	680.5	2.45	71351	341.2
Env. × L_{1i} vs L_{2i}	5	1.21	50963	812.2	2.04	81381	452.8
Env. × $L_{1i}+ L_{2i}- 2L_{3i}$ (Env. × i- epistasis)	5	11.17**	466828**	548.8	2.85	61322	229.6
Parents (additive)	7	42.87**	1175207**	1515.8**	48.53**	1393933**	1438.2**
Env. × parents (Env. × additive)	35	2.56	81305	468.4*	3.50	146155*	495.5*
Tester × parents	14	24.20**	553136**	826.1*	10.98**	501115**	1714.6**
L_{1i} vs L_{2i} × parents (dominance)	7	29.69**	651658**	1100.1*	14.98**	781669**	2211.3**
$L_{1i}+ L_{2i} - 2L_{3i}$ × parents (j+ 1- epistasis)	7	18.71**	454615**	552.2	6.98	220561	1218.0*
Env. × tester × parent	70	2.83	127544**	512.0**	3.65	135119*	476.6**
Env. × (dominance)	35	3.28	171508**	503.8*	3.65	150775*	431.2**
Env. × (j+ 1- epistasis)	35	2.39	83581	520.2**	3.65	119462*	522.0**
Error	207	2.84	71854	264.6	3.17	84980	257.4

***, ** Significant at 0.05 and 0.01 level of significance, respectively.**

Table (6): Average epistatic deviations (L_{1i}+ L_{2i}- $2L_{3i}$) of individual summer squash studied inbred lines for early yield characters, in both studied crosses.

Tested inbred Parents	Early fruits no/ plant	Early fruits weight/ plant
	Cross I ($P_1 \times P_2$)	
P_3	4.54**	527.00**
P_4	- 0.37	195.40**
P_5	- 0.84**	- 166.40**
P_6	- 2.92**	- 471.40**
P_7	- 2.04**	- 128.01**
P_8	0.36	8.74
P_9	0.12	148.60**
P_{10}	- 3.54**	- 403.80**
Average	- 0.58*	- 36.20
	Cross II ($P_3 \times P_4$)	
P_1	5.06**	566.30**
P_2	- 0.71*	- 117.00**
P_5	3.11**	527.40**
P_6	0.51	292.20**
P_7	1.24**	195.60**
P_8	3.15**	419.90**
P_9	2.02**	343.00**
P_{10}	- 7.23**	- 852.00**
Average	0.89	171.90**

*, ** Significant at 0.05 and 0.01 level of significance, respectively.

Table (7): Average epistatic deviations (L_{1i}+ L_{2i}- $2L_{3i}$) of individual summer squash studied parental inbred lines for total yield characters, in both studied crosses.

Tested inbred Parents	Total fruits no/ plant	Total yield/ plant	Average fruit weight
		Cross I ($P_1 \times P_2$)	
P_3	7.96**	1189.10**	- 4.35
P_4	- 9.52**	351.10**	28.82**
P_5	- 2.64**	- 626.20**	- 6.77
P_6	- 0.70	- 144.70**	- 8.64**
P_7	0.92**	502.80**	38.31**
P_8	- 1.27**	- 473.30**	- 23.35**
P_9	- 0.56	- 250.00**	- 16.26**
P_{10}	- 5.67**	- 640.40**	28.93**
Average	- 1.44**	- 11.40	4.58
		Cross II ($P_3 \times P_4$)	
P_1	6.26**	1122.40**	17.31**
P_2	2.58**	260.50**	- 20.62**
P_5	5.80**	934.80**	9.90**
P_6	0.37	129.20	18.00**
P_7	2.77**	502.10**	11.70**
P_8	4.14**	329.50**	- 30.90**
P_9	3.22**	97.50	- 64.40**
P_{10}	0.37	445.00**	- 23.90**
Average	3.18**	447.60**	- 35.11**

** Significant at 0.01 level of significance, respectively.

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الملخص العربي

تقدير المكونات الوراثية للصفات الكمية من خلال اختبار الهجن الثلاثية فى قرع الكوسة

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أجريت هذه الدراسة في خمسة مواسم زراعية متتابعة خلال الفترة ٢٠٠٣-٢٠٠٥ وذلك لتوضيح ودراسة أنواع التفاعل في مجموعتين من الهجن الثلاثية الاختبارية لهجينين في قرع الكوسة، وذلك تحت ظروف بيئية مختلفة بمزرعة كلية الزارعة – جامعة الإسكندرية بأبيس.

١- دراسة السلوك العام للآباء والمختبرات المستخدمة في الدراسة تحت بيئات مختلفة (مسافات زراعة مختلفة وفي موسمين زراعيين مختلفين).

٢- تقدير الفعل الجيني ومكونات التباين الوراثي من فعل إضافي وسيادي وتفوق التي تحكم توريث بعض الصفات الاقتصادية في قرع الكوسة باستخدام نظام الهجن الثلاثية الاختبارية.

استخدمت في هذه الدراسة عشر سلالات أبوية من محصول قرع الكوسة، من بينها أربع سلالات أبوية لهجينين متميزين هما P_1xP_2 (cross I), $P_3x\ P_4$ (cross II) ولقد استخدم الأبوان وكذلك الجيل الأول بينهما في كل هجين كثلاث مختبرات، وذلك بالإضافة إلى ثاني سلالات أبوية أخرى (ست مشتركة بالإضافة للأبوين في الهجين الآخر)، وذلك لتكوين عائلات الهجن الاختبارية الثلاثية (٢٤ عائلة منها ١٢ تمثل هجناً فردية و٨ تمثل هجناً ثلاثية). ولقد تم تقييم مجموعتي عائلات الهجينين تحت ظروف بيئية مختلفة وكانت البيئات المستخدمة هي ٣٠ و ٤٥ و ٦٠سم كمسافات زراعة (بيئات محددة النطاق) أما البيئات الواسعة النطاق فكانت الزراعة في موسمين زراعيين مختلفين، وهما يونيو ٢٠٠٤ وأبريل ٢٠٠٥.

تم تقييم مجموعتي التراكيب الوراثية المختلفة لعائلات الهجن الاختبارية الثلاثية بالإضافة إلى الآباء المختبرة الثلاثة والسلالات الأبوية الثماني في كل هجين، وكان التصميم المستخدم نظام القطع المنشقة في تصميم القطاعات العشوائية الكاملة مع استخدام ثلاث مكررات في الموسم ومكررتين في الموسم الثاني، حيث مثلت كل عشيرة وراثية بقطعة تجريبية مساحتها ٦م^2، ووزعت مسافات الزراعة الثلاث في القطع الرئيسية، وخصصت القطع المنشقة للعشائر الوراثية. و كانت اهم النتائج المتحصل عليها هي ان سلوك التراكيب الوراثية الابوية المستخدمة في الدراسة تحت بيئات مختلفة اظهرت اختلافات معنوية. مما يؤكد مناسبة التراكيب المستخدمة لاجراء هذه الدراسة. أظهرت التباينات الراجعة لتأثيرات الإضافة والسيادة قيماً معنوية عالية في كل الصفات المدروسة مما يؤكد أهمية الدور الذي تلعبه كل من التفاعلات الجينية الإضافية وغير الإضافية في توارث وسلوك الصفات تحت الدراسة، مع اختلاف الأهمية النسبية كل نوع تبعاً للصفة المدروسة. وكانت التفاعلات لكل من الإضافة والسيادة مع البيئة معنوية في متوسط وزن الثمرة والمحصول الكلي للنبات. بالسبة لطرز التداخل (j+i. espistasis) فقد عكست قيماً معنوية في كل الصفات المدروسة في أي من الهيجينين أو في كليهما، أما بالنسبة لطراز التدخل (i-epistasis) فقد أعطى قيماً معنوية في صفات المحصول الكلي في الهجين الثاني، أما بالنسبة للتفاعل بين البيئة وطرز التداخلات السابقة، فقد وجد أن التفاعل بين الطراز (-i)× البيئة كان معنوياً في صفات المحصول الكلي في الهجين الأول، وأما الطرز (-i+1)× البيئة فقد وجدت معنوية في صفات المحصول الكلي في الهجين الثاني، وصفة متوسط وزن الثمرة في كل من الهجينين، وقد أظهرت النتائج أن معظم السلالات الأبوية المدروسة قد لعبت دوراً معنوياً موجباً أو سالباً في ظهور الانحرافات الراجعة للتفوق (أو التداخل) في كل الصفات المدروسة وفي كل من الهجينين.