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MANIFESTATION OF HETEROSIS AND GENETIC PARAMETERS ASSOCIATED WITH IT FOR SOME VEGETATIVE AND EARLINESS TRAITS IN SQUASH

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ABSTRACT

The main objectives of this investigation were to determine the amounts of heterosis versus the mid-parents and the better parent, nature of gene action, heritability in both broad and narrow senses and correlation between each pair of traits. Four parental varieties of squash were crossed to obtain 12 F_1 hybrids according to a complete diallel crosses mating design.

The results revealed that the mean squares of genotypes which included four parental varieties and their hybrids were highly significant for all vegetative and earliness traits from the combined data. The results also cleared that mean values showed that no specific parent was superior for all studied traits. Generally, Eskandrani (P_1) was the best combiner for vein length (V.L.cm), number of leaves per plant (No.L./P.), fresh weight per plant (F.W./P.g) and dry weight per plant (D.W./P.g). Similarly, Zucchino mezza lung bianco (P_2) seemed to be the best combiner for leaf area (L.A.cm^2) trait. The results also indicated that the parent P_2 was the best combiner for all earliness traits. On the other hand, the performance of most $F_{1,1r}$ hybrids were variable and the results cleared that no hybrid gave the best results for vegetative and earliness traits. The results revealed that heterosis over mid-parents indicated the presence of highly significant values for all studied traits except for fresh weight per plant (F.W./P.g). The estimates of heterosis versus better parent showed highly significant values for most studied traits. The results showed the importance of general and specific combining abilities. GCA were larger than their corresponding estimates of SCA for vegetative and earliness traits. Reciprocal effects (r) were significant for most studied traits from the combined data. Estimation of genetic parameters showed that additive genetic variance was very important for most studied traits. The inheritance of these traits was mostly governed by additive genetic variance rather than non-additive and cytoplasmic genetic factors. In the same time, the estimates of heritability in broad sense were larger in magnitudes than their corresponding values in narrow sense.

Most pairs of traits exhibited positive genotypic and phenotypic correlation coefficients, such as: vein length (V.L.cm) with number of leaves per plant (No.L./P.), leaf area (L.A.cm^2), fresh weight per plant (F.W./P.g) and dry weight per plant (D.W./P.g). Also, number of first female flowering node (No.1stF.F.N) was significant correlated with date of first female flower (D.1stF.F.) and date of first male flower (D.1stM.F.). Therefore, plant breeders could design their programs, which make use of these advantages to select superior lines from the advanced segregating generations of the high yielding F_1 hybrids.

INTRODUCTION

Heterosis has been studied in all important vegetable crops as well as cucurbits. In squash and other cucurbits, heterosis was utilized aiming to increase the productivity and quality of traits. Many investigators studied heterosis among them, Kash and El-Diasty (1989) who studied heterotic effects in some squash hybrids. They observed heterosis values versus the mid-parents. They also cleared that the estimated values versus the better parent were significant for most studied traits. Abd El-Hadi (1995) studied six inbred lines and their 30 F_1 hybrids among them (including F_1 reciprocal hybrids) in agoor. He recorded the presence of highly significant values of heterosis versus the mid-parents. In this respect, Shamloul (2002) evaluated F_1 hybrids among new selected inbred lines of sweet melon. He indicated that the means of the F_1 hybrid significantly exceeded the means of the mid-parents for all vegetative traits. Similarly,Abd El-Maksoud *et al.* (2003) showed that the average means of the means of $F_{1,1r}$ hybrids and the average over all hybrids $F_{1,1r}$ exceeded their mid-parents for all studied traits except for sex ratio and days to first female flower, which were desirable lower forward increasing in female flower and earliness, respectively. In another study, Gabr (2003) estimated heterosis over mid-parents and the better parent. He indicated the presence of highly significant heterosis values over mid-parents for all studied vegetative traits in squash.

Concerning, GCA and SCA variances El-Diasty and Kash (1989) revealed that additive genetic variances were larger in magnitudes than that of the non-additive genetic variances for most vegetative traits. On the other hand, Awny *et al.* (1992) studied five cucumber inbred lines and their 10 F_1 hybrids. They cleared that specific combining ability variances were highly significant for leaves number and leaf area traits. They also added that there was no parent considered as the best combiner for all studied vegetative traits. In summer squash, El-Gendy (1999) reported that general combining ability and specific combining ability as well as reciprocal effects were significant for days to first female flower, numbers of fruits in the first seven pickings. In squash, Sadek (2003) illustrated that the non-additive genetic variances including dominance were the most important source of genetic variance. The results showed that both additive and non-additive genetic variances contributed in the inheritance of position of the first female flower, days to the first female flower and early yield as number and weight of fruits. Abd El-Hadi and El-Gendy (2004) studied four squash varieties and their 12 $F_{1,1r}$ hybrids. They cleared that the analysis of variance of diallel crosses mating design indicated that the mean squares of GCA, SCA, GCA × L and SCA × L showed highly significance for most studied traits at each location and over both locations. Recently, Abd El-Hadi *et al.* (2004) in squash showed that both GCA and SCA reveled highly significant values for all studied traits in the F_1 hybrids and F_2 generations except for F.W.(g) in the F_1 hybrids for GCA.

Abd El-Hadi *et al.* (2001) in sweet melon reported that total yield per plant and length of fruit were positively correlated with weight of fruit. In squash, Abd El-Maksoud *et al.* (2003) reported that most pairs of traits exhibited negative (genotypic and phenotypic) correlation coefficient, while the following pairs of traits showed positive correlation coefficient i.e. sex ratio, days to the first female flower, early yield as weight and number of fruits in the 7 picking per plant total yield as total number and weight of fruits per plant. They also added that selection program for improving one or more of these traits would improve the others. In this respect, Abdel Sayyed *et al.*

(2003), in sweet melon, evaluated correlations between fruit quality characters. They found that flesh texture were negatively correlated with flesh flavor and aroma, while, positive genotypic correlations were detected between flesh flavor and each of flesh aroma and total acceptability.

MATERIALS AND METHODS

The genetic materials used in the present investigation included four varieties of squash belong to *Cucurbita pepo*, L. These varieties were: Eskandrani (P_1), Zucchino mezza lung bianco (P_2), White Bush Scallop (P_3) and Zucchino nano verde di Milano (P_4). The seeds of these parental varieties were obtained from different countries i.e.: (P_1) from Egypt, (P_2) from Germany, (P_3) from United States of America (U.S.A.) and (P_4) from Italy. All these varieties represented a wide range of variability in most studied traits.

Plants from each parental varieties were self-pollinated for three successive generations to obtain an inbred from each variety. In the summer season of 2002, all single crosses including reciprocals were made among these four varieties according to a complete diallel crosses mating design to produce 6 F_1 hybrids and 6 F_1 reciprocal hybrids. In addition, the four parental varieties were also self-pollinated to obtain enough seeds from each variety.

In the two summer seasons of 2003 and 2004 all the 16 genotypes obtained from the last season were evaluated in field trial experiment at El-Baramoun Station, Vegetables Research Station, Mansoura.

In the two growing seasons of 2003 and 2004 all 16 genotypes were evaluated in a field trial. The experimental design was the randomized complete blocks design with three replications. Each block consisted of 16 plots. Plot or the experimental unit was one ridge 5.0 m. long and 1.0 m. wide. The distance between hills was long 0.5 m. apart. Therefore, each ridge contained 10 hills. Data were recorded for the following vegetative and earliness traits: vein length (V.L.cm), number of leaves per plant (No.L./P.), leaf area (L.A.cm^2), fresh weight per plant (F.W./P.g), dry weight per plant (D.W./P.g), number of first female flowering node (No.1stF.F.N), date of first female flower (D.1stF.F.) and date of first male flower (D.1stM.F.).

Differences among genotypic means for all studied traits were tested for significance according to F-test. The form of analysis of variance and the expectations of mean squares were as outlined by Steel and Torrie (1960).

The amounts of heterosis were determined as the percentage deviation from the means of the F_1 hybrids (F_1), F_1 reciprocal hybrids (F_{1r}) and all $F_{1,1r}$ hybrids from the average of all parents (mid-parents) or the better parent.

In this investigation four varieties were utilized in a complete diallel crosses mating design to estimate general combining ability (G.C.A.) and specific combining ability (S.C.A.). In addition, the variances of reciprocal effect (r) could be also obtained. The procedures of these Analysis were described by Griffing (1956) method I. The estimates of GCA variance (٢ںg) and SCA variance (٢ںs) could be expressed in terms of genetic variances according to Matzingar & Kempthorne (1956) and Cockerham (1963).

RESULTS AND DISCUSSION

The results of the analysis of variances and the mean squares for all genotypes are presented in Table 1. Tests of significance revealed that the mean squares of the genotypes showed highly significance for all studied traits in both years and from the combined data. This finding indicated the presence of real differences among them except Y_2 for No.1stF.F.N which was only significant. In addition, the significant mean squares of genotypes suggested that the planned comparisons to understand the nature of variation and determinate the amounts of heterosis for these traits were valid.

Table 1: Analysis of variances and mean squares for vegetative and earliness traits for each year and the combined data.

S.V.	d.f	V.L.cm			No.L./P.			L.A.cm^2			F.W./P.g		
		Y_1	Y_2	Comb.	Y_1	Y_2	Comb.	Y_1	Y_2	Comb.	Y_1	Y_2	Comb.
Years	1	-	-	1.22	-	-	0.03	-	-	0.06	-	-	6
Rep.	2	0.04	0.01	0.02	0.66	0.62	0.64	0.29	0.63	0.46	418.8	2777	1598
Gen.	15	686.9^{**}	671.3^{**}	1355^{**}	76.8^{**}	61.8^{**}	137.1^{**}	300^{**}	279.6^{**}	578.2^{**}	143874^{**}	131871^{**}	27467^{**}
G ×Y	15	-	-	2.98	-	-	1.61	-	-	1.40	-	-	1075
Error	30	4.17	3.81	3.99	1.78	3.02	2.40	3.20	2.40	2.80	3208	1733	2470

Table 1: Cont.

S.V.	d.f	D.W./P.g			No.1stF.F.N.			D.1stF.F.			D.1stM.F.		
		Y_1	Y_2	Comb.	Y_1	Y_2	Comb.	Y_1	Y_2	Comb.	Y_1	Y_2	Comb.
Years	1	-	-	23.01	-	-	0.002	-	-	0.25	-	-	6.41
Rep.	2	14.65	28.31	21.48	0.001	0.002	0.002	2.28	0.35	1.3	0.20	1.71	0.96
Gen.	15	1147^{**}	1089^{**}	2217^{**}	0.06^{**}	0.05^{*}	0.11^{**}	44.7^{**}	45.6^{**}	89.6^{**}	14.2^{**}	13.2^{**}	25.7^{**}
G ×Y	15	-	-	18.68	-	-	0.002	-	-	0.69	-	-	1.59
Error	30	22.82	26.74	24.78	0.001	0.001	0.001	1.29	1.37	1.33	1.23	1.56	1.40

***,** Significant at 0.05 and 0.01 levels of probability, respectively.**

In the same time, the mean squares of genotypes by years interactions obtained from the combined data were insignificant for all studied traits.

The means of four parental varieties and their 12 $F_{1,1r}$ hybrids at two years and their com

bined data were calculated and the results are presented in Table 2. The results showed that there was no specific parent was superior or the best for all studied traits. It is also cleared that the parental variety P_1 was the highest parent for V.L.cm, No.L./P., F.W./P.g and D.W./P.g traits for the two years and from the combined data. While, the highest parent for L.A.cm^2 was P_2. On the other hand, the parental variety P_3 was the lowest parent for most studied traits. The differences between the means of the lowest and the highest parent were highly significant indicated the presence of genetic differences between these parental varieties.

In the same time, the results showed that there were no significant differences between the means of the F_1 hybrids and F_1 reciprocal hybrids for most studied traits. The results indicated that the highest F_1 hybrids for the V.L.cm was $P_1 \times P_3$ with the mean of 98.9 cm. from the combined data. Whereas, the highest F_1 reciprocal hybrid was $P_2 \times P_1$ with the mean of 70.5

cm. It was regarded that the means of F_1 hybrids calculated from the combined data ranged from 58.7 to 98.9; 27.8 to 40.1; 82.8 to 94.5; 889 to 1512 and 147.8 to 201.3 for V.L.cm, No.L./P., L.A.cm^2, F.W./P.g and D.W./P.g traits, respectively. In the same time, F_{1r} reciprocal hybrids ranged from 54.3 to 70.5; 26.8 to 35.7; 87.8 to 94.6; 860.6 to 1061 and 144.7 to 171.6 for the same above traits, respectively.

Concerning earliness traits, the result revealed that the means of the four parental varieties showed that the lowest (desirable) parent was P_2 for all earliness traits at the two years and from the combined data except for first year (Y_1) for D.1^{st}F.F. While, the highest parent for No.1^{st}F.F.N. was P_1 (undesirable) at the two years and from the combined data. On the other hand, the variety P_3 was the highest (undesirable) parent for D.1^{st}F.F. and D.1^{st}M.F, respectively at the two years and from the combined data.

The results also indicated that P_2 variety was the earliest variety for flowering followed by P_4. This finding could be confirmed by the means of days to first female flower, which ranged from 46.6 to 56.8 days from the combined data. Furthermore, days to first male flower ranged from 45.8 to 51.5 days from the combined data, indicating that P_3 was a very late variety, the variety P_2 followed by P_4 were early maturing varieties. In addition, the earlier F_1 hybrids and F_1 reciprocal hybrids were obtained when the included one or more of the earlier parents. For instance, the hybrid $P_2 \times P_4$ exhibited the lowest (desirable) number of nodes to the first female flower from combined data, while the hybrids $P_1 \times P_4$ and $P_2 \times P_3$ exhibited the highest (undesirable) means for number of nodes to the first female flower from the combined data. On the other hand, the F_{1r} reciprocal hybrid $P_2 \times P_1$ was the lowest (desirable) for combined data and the hybrid $P_4 \times P_3$ was the highest (undesirable) from combined data for the same trait.

The results of combined data also indicated that the latest F_1 hybrid for D.1^{st}F.F. was $P_3 \times P_4$ with the mean of 47.3 days. Whereas, the highest F_1 reciprocal hybrid for D.1^{st}F.F. was $P_3 \times P_1$ with the mean of 49.4 days. On the other hand, F_1 hybrid $P_1 \times P_2$ was the earlier (desirable) with the mean 43.0 days. While, F_1 reciprocal hybrid $P_4 \times P_2$ was the earlier (desirable) with the mean 40.9 days for the same trait. It could be also regarded that the means of F_1 hybrids for the combined data ranged from 3.66 to 3.83; 43.0 to 47.3 days and 43.8 to 45.6 days for No.1^{st}F.F.N, D.1^{st}F.F. and D.1^{st}M.F traits, respectively. In the same time, F_1 reciprocal hybrids ranged from 3.73 to 3.85; 40.9 to 49.4 days and 42.0 to 46.3 days for the same obvious traits, respectively.

Concerning the performances of F_1 and F_{1r} hybrids for vegetative and earliness traits, the results indicated that the magnitudes of the means of F_1 and F_{1r} hybrids were close to each other for most studied traits. In the same time, when the hybrids were compared with each other the results showed the presence of significant differences for many traits. It is also cleared that some F_1 and F_{1r} hybrids of studied traits exceeded the better parent. Therefore, it would be expected because there were quite heterosis values versus the mid-parents.

Table 2: The mean performances of four parental varieties, their F_1 and F_{1r} hybrids for vegetative and earliness traits for each year and the combined data.

Genotypes	V.L.cm			No.L./P.			L.A.cm^2			F.W./P.g		
	Y_1	Y_2	Comb.	Y_1	Y_2	Comb.	Y_1	Y_2	Comb.	Y_1	Y_2	Comb.
P_1	67.1^{H}	69.1^{H}	68.1^{H}	27.1^{H}	27.8^{H}	27.5^{H}	79.4	80.3	79.9	957.3^{H}	970.5^{H}	963.9^{H}
P_2	46.8	47.8	47.3	26.7	27.3	27.0	81.4^{H}	82.6^{H}	82.0^{H}	800.6	853.9	827.3
P_3	34.4^{L}	35.4^{L}	34.9^{L}	19.9^{L}	20.5^{L}	20.2^{L}	54.6^{L}	55.5^{L}	55.0^{L}	483.8^{L}	530.8^{L}	507.3^{L}
P_4	55.9	54.9	55.4	26.9	26.2	26.6	77.1	75.8	76.4	960.4	954.0	957.2
$P_1 \times P_2$	76.4	78.0	77.2	33.8	34.3	34.0	90.7	91.9	91.3	1034	1104	1069
$P_1 \times P_3$	99.7^{H}	98.1^{H}	98.9^{H}	41.1^{H}	39.0^{H}	40.1^{H}	95.6^{H}	93.3^{H}	94.5^{H}	1517^{H}	1507^{H}	1512^{H}
$P_1 \times P_4$	86.5	86.7	86.6	35.5	36.0	35.7	82.7^{L}	82.9^{L}	82.8^{L}	1301	1317	1309
$P_2 \times P_3$	58.8^{L}	58.7^{L}	58.7^{L}	29.1	28.7	28.9	87.9	87.5	87.7	893.9^{L}	884.1^{L}	889.0^{L}
$P_2 \times P_4$	68.7	66.4	67.5	32.8	31.0	31.9	92.4	92.1	92.3	1111	1094	1102
$P_3 \times P_4$	61.1	62.5	61.8	27.6^{L}	28.0^{L}	27.8^{L}	84.8	85.4	85.1	977.4	987.2	982.3
$P_2 \times P_1$	70.1^{H}	70.8^{H}	70.5^{H}	30.9	31.1	31.0	92.1	91.8	92.0	1064^{H}	1057^{H}	1061^{H}
$P_3 \times P_1$	54.9^{L}	53.7^{L}	54.3^{L}	25.9^{L}	27.7	26.8^{L}	94.9^{H}	94.3^{H}	94.6^{H}	850.7^{L}	870.5^{L}	860.6^{L}
$P_4 \times P_1$	67.4	69.3	68.4	36.2^{H}	35.2^{H}	35.7^{H}	92.4	91.7	92.1	1014	1007	1011
$P_3 \times P_2$	60.9	62.4	61.7	26.9	27.9	27.4	87.8^{L}	88.1	88.0	967.3	963.9	965.6
$P_4 \times P_2$	66.8	67.0	66.9	30.9	31.8	31.4	91.9	92.2	92.0	997.3	987.3	992.3
$P_4 \times P_3$	56.9	55.2	56.1	27.7	27.3^{L}	27.5	88.2	87.5^{L}	87.8^{L}	977.2	967.3	972.3
L.S.D.$_{0.05}$	3.40	3.25	3.26	2.22	2.89	2.53	2.98	2.58	2.73	94.34	69.33	81.16
L.S.D.$_{0.01}$	4.59	4.38	4.34	3.00	3.90	3.36	4.02	3.48	3.63	127.2	93.46	107.9

Table 2: Cont.

Genotypes	D.W./P.g			No.1st F.F.N.			D. 1st F.F.			D.1st M.F.		
	Y_1	Y_2	Comb.	Y_1	Y_2	Comb.	Y_1	Y_2	Comb.	Y_1	Y_2	Comb.
P_1	153.9^{H}	156.1^{H}	155.0^{H}	4.22^{H}	4.21^{H}	4.22^{H}	52.1	51.5	51.8	47.3	46.7	47.0
P_2	145.4	146.0	145.7	3.96^{L}	3.97^{L}	3.97^{L}	46.4	46.8^{L}	46.6^{L}	45.4^{L}	46.1^{L}	45.8^{L}
P_3	114.1^{L}	115.5^{L}	114.8^{L}	3.98	3.99	3.99	57.2^{H}	56.3^{H}	56.8^{H}	51.8^{H}	51.3^{H}	51.5^{H}
P_4	153.6	152.1	152.9	4.03	4.01	4.02	46.1^{L}	47.4	46.8	45.4^{L}	46.3	45.9
$P_1 \times P_2$	166.1	165.5	165.8	3.72	3.75	3.73	43.4^{L}	42.6^{L}	43.0^{L}	43.8^{L}	44.1	43.9
$P_1 \times P_3$	199.9^{H}	202.8^{H}	201.3^{H}	3.75	3.74	3.75	46.7	46.5	46.6	44.4	44.8	44.6
$P_1 \times P_4$	190.8	187.5	189.2	3.82	3.84^{H}	3.83^{H}	44.1	43.5	43.8	45.2	45.9^{H}	45.6^{H}
$P_2 \times P_3$	148.9^{L}	146.7^{L}	147.8^{L}	3.84^{H}	3.83	3.83^{H}	43.5	43.6	43.6	43.5^{H}	44.1	43.8^{L}
$P_2 \times P_4$	165.5	166.9	166.2	3.64^{L}	3.68^{L}	3.66^{L}	44.9	45.3	45.1	44.4	43.6^{L}	44.0
$P_3 \times P_4$	153.2	153.9	153.5	3.81	3.83	3.82	47.1^{H}	47.6^{H}	47.3^{H}	45.2	45.3	45.3
$P_2 \times P_1$	170.6^{H}	172.7^{H}	171.6^{H}	3.72^{L}	3.75^{L}	3.73^{L}	43.4	43.3	43.4	44.2	43.7	44.0
$P_3 \times P_1$	139.7^{L}	149.8^{L}	144.7^{L}	3.83	3.81	3.82	49.3	49.4	49.4	46.1^{H}	46.5^{H}	46.3^{H}
$P_4 \times P_1$	158.8	159.5	159.2	3.79	3.82	3.80	47.3	47.6	47.5	45.2	45.5	45.4
$P_3 \times P_2$	153.1	156.8	155.0	3.81	3.84^{H}	3.83	44.9	43.7	44.3	44.2	46.0	45.1
$P_4 \times P_2$	152.3	155.1	153.7	3.73	3.76	3.74	41.3^{L}	40.4^{L}	40.9^{L}	41.4^{L}	42.5^{L}	42.0^{L}
$P_4 \times P_3$	159.4	153.8	156.6	3.87^{H}	3.83	3.85^{H}	48.3	48.9	48.6	45.1	45.5	45.3
L.S.D.$_{0.05}$	7.95	8.61	8.13	0.05	0.05	0.05	1.89	1.94	1.88	1.85	2.08	1.93
L.S.D.$_{0.01}$	10.72	11.61	10.81	0.07	0.07	0.07	2.55	2.62	2.50	2.49	2.80	2.57

H= The highest value L= The lowest value

Heterosis versus the mid-parents ($H_{M.P.}$%) were estimated for vegetative and earliness traits and the results are presented in Table 3. The result cleared the presence of heterosis versus the mid-parents for most vegetative traits over two years and their combined data. All hybrids exhibited highly significant and positive values for V.L.cm, No.L./P. and L.A.cm^2. The results also revealed that heterotic effects for F_1 hybrids for the combined data ranged from 31.5 to 92.1% for V.L.cm; 18.9 to 68.1% for No.L./P; 6.0 to 40.0% for L.A.cm^2; 19.4 to 105.6% for F.W./P.g and 10.3 to 49.3% for D.W./P.g. In the same time, the results revealed that heterotic effects for F_{1r} hybrids ranged from 5.4 to 49.9%; 12.4 to 32.3%; 13.6 to 40.2%; 5.2 to 44.7% and 3.0 to 19.0% for V.L.cm, No.L./P., L.A.cm^2, F.W./P.g and D.W./P.g, respectively.

The results also showed the presence of heterosis relative to mid-parents for earliness traits over two years and the combined data. All hybrids showed negative highly significant and desirable heterotic values for No.1stF.F.N, D.1stF.F. and D.1stM.F. toward earliness, except the F_1 hybrid $P_1 \times P_4$ was insignificant for Y_2 and only significant for combined data for D.1stM.F. trait.

Heterosis versus the better parent ($H_{B.P.}$%) was estimated for vegetative and earliness traits and the results are presented in Table 4. The result indicated that all hybrids showed positive and highly significant heterosis values for L.A.cm^2 for the two years and the combined data except for $P_1 \times P_4$ in Y_2. While, all hybrids were insignificant for F.W./P.g. At the same time, most hybrids were highly significant for V.L.cm and No.L./P. While, most hybrids were insignificant for D.W./P.g for the two years and their combined data.

These results revealed that heterotic effects ($H_{B.P.}$%) for F_1 and their F_{1r} hybrids from the combined data showed that 10,11,12,0 and 4 hybrids from the 12 had positive significant values for V.L.cm, No.L./P, L.A.cm^2, F.W./P.g and D.W./P.g, respectively. The results cleared the presence of heterosis percentage of the 12 hybrids relative to better parent for earliness traits at two years and from the combined data. All hybrids showed highly significant and (desirable) negative heterotic values for No.1stF.F.N. for the two years and their combined data. Similarly, 10 and 6 hybrids showed highly significant and (desirable) negative heterotic values for D.1stF.F. and for D.1stM.F. from the combined data, respectively.

The analysis of variances for combining ability of the four varieties and their hybrids for vegetative and earliness traits for the two years and their combined data are shown in Table 5. The combined data revealed that the mean squares due to hybrids were highly significant for all studied traits except for F.W./P.g. which was significant. While, the mean squares due to general combining ability were significant and highly significant for all studied traits except for No.1stF.F.N. and D.1stM.F were insignificant for the two years.

Table 3: Heterosis relative to mid-parents ($H_{M.P.}$%) for vegetative and earliness traits for each year and the combined data over the two years.

Hybrids	V.L.cm			No.L./P.			L.A.cm^2			F.W./P.g		
	Y_1	Y_2	Comb.	Y_1	Y_2	Comb.	Y_1	Y_2	Comb.	Y_1	Y_2	Comb.
$P_1 \times P_2$	34.1**	33.4**	33.8**	25.8**	24.4**	25.1**	12.8**	12.8**	12.8**	16.8^{L}	21.9	19.4^{L}
$P_1 \times P_3$	96.5**^{H}	87.8**^{H}	92.1**^{H}	74.8**^{H}	61.6**^{H}	68.1**^{H}	42.7**^{H}	37.5**^{H}	40.0**^{H}	108.6*^{H}	102.6**^{H}	105.6**^{H}
$P_1 \times P_4$	40.7**	39.9**	40.3**	31.5**	33.2**	32.3**	5.7**^{L}	6.3**^{L}	6.0**^{L}	34.7	37.9	36.3
$P_2 \times P_3$	44.7**	41.0**	42.8**	24.7**	20.1**	22.4**	29.3**	26.7**	28.0**	39.2	27.7	33.2
$P_2 \times P_4$	33.7**^{L}	29.3**^{L}	31.5**^{L}	22.5**	16.2**^{L}	19.3**	16.6**	16.4**	16.5**	26.1	21.0^{L}	23.5
$P_3 \times P_4$	35.3**	38.4**	36.8**	17.8**^{L}	19.9**	18.9**^{L}	28.8**	30.2**	29.5**	35.4	33.0	34.2
$P_2 \times P_1$	23.1**	21.2**	22.2**	14.9**	12.9**^{L}	13.9**	14.6**^{L}	12.7**^{L}	13.6**^{L}	20.1	16.7	18.4
$P_3 \times P_1$	8.2**^{L}	2.7^{L}	5.4**^{L}	10.2**^{L}	14.6**	12.4**^{L}	41.7**^{H}	38.8**^{H}	40.2**^{H}	17.0	17.0	17.0
$P_4 \times P_1$	9.6**	11.9**	10.7**	34.2**^{H}	30.4**^{H}	32.3**^{H}	18.1**	17.5**	17.8**	5.0^{L}	5.4^{L}	5.2^{L}
$P_3 \times P_2$	49.9**^{H}	49.9**^{H}	49.9**^{H}	15.6**	16.8**	16.2**	29.1**	27.7**	28.4**	50.6^{H}	39.2^{H}	44.7^{H}
$P_4 \times P_2$	30.1**	30.5**	30.3**	15.4**	19.2**	17.3**	15.9**	16.4**	16.2**	13.3	9.2	11.2
$P_4 \times P_3$	26.0**	22.3**	24.2**	18.3**	16.9**	17.6**	33.9**	33.3**	33.6**	35.3	30.3	32.8
L.S.D.$_{0.05}$	2.95	2.82	2.82	1.92	2.51	2.19	2.58	2.23	2.37	81.7	60.04	70.29
L.S.D.$_{0.01}$	3.97	3.80	3.76	2.59	3.38	2.91	3.48	3.01	3.15	110.1	80.94	93.48

Table 3: Cont.

Hybrids	D.W./P.g			N.1stF.F.N.			D.1stF.F.			D.1stM.F.		
	Y_1	Y_2	Comb.	Y_1	Y_2	Comb.	Y_1	Y_2	Comb.	Y_1	Y_2	Comb.
$P_1 \times P_2$	10.8**^{L}	9.7*^{L}	10.3**^{L}	-9.1**^{L}	-8.4**	-8.8**^{L}	-11.9**	-13.3**	-12.6**	-5.5**	-5.1**	-5.3**
$P_1 \times P_3$	49.2**^{H}	49.3**^{H}	49.3**^{H}	-8.5**	-8.7**^{L}	-8.6**	-14.5**	-13.7**	-14.1**	-10.3**	-8.6**	-9.4**
$P_1 \times P_4$	24.7**	21.1**	22.9**	-7.3**	-6.4**	-6.9**	-10.1**	-12.1**	-11.1**	-2.5**	-1.2^{H}	-1.8*^{H}
$P_2 \times P_3$	14.5**	12.5**	13.5**	-3.4**^{H}	-3.9**^{H}	-3.6**^{H}	-16.0**^{L}	-15.5**^{L}	-15.7**^{L}	-10.5**^{L}	-9.4**^{L}	-10.0**^{L}
$P_2 \times P_4$	11.1**	11.6**	11.3**	-8.9**	-7.7**	-8.3**	-2.8**^{H}	-3.9**^{H}	-3.4**^{H}	-2.2**^{H}	-5.7**	-4.0**
$P_3 \times P_4$	15.1**	14.4**	14.7**	-4.8**	-4.3**	-4.5**	-8.8**	-8.3**	-8.5**	-7.1**	-7.1**	-7.1**
$P_2 \times P_1$	13.8**	14.5**	14.1**	-9.0**^{L}	-8.4**^{L}	-8.7**^{L}	-11.9**	-11.8**	-11.9**	-4.6**	-5.9**	-5.2**
$P_3 \times P_1$	4.3	10.3**	7.3*	-6.7**	-7.0**	-6.9**	-9.7**	-8.4**	-9.1**	-6.8**	-5.1**	-6.0**
$P_4 \times P_1$	3.8	3.0^{L}	3.4	-8.2**	-7.1**	-7.6**	-3.5**^{H}	-3.8**^{H}	-3.7**^{H}	-2.6**^{H}	-2.1*^{H}	-2.3**^{H}
$P_3 \times P_2$	17.8**	20.2**^{H}	19.0**^{H}	-4.0**	-3.4**^{H}	-3.7**^{H}	-13.3**^{L}	-15.2**^{L}	-14.2**^{L}	-9.1**^{L}	-5.5**	-7.3**
$P_4 \times P_2$	2.2^{L}	3.7	3.0^{L}	-6.6**	-5.8**	-6.2**	-10.6**	-14.2**	-12.4**	-8.8**	-8.0**^{L}	-8.4**^{L}
$P_4 \times P_3$	19.8**^{H}	14.3**	17.0**	-3.5**^{H}	-4.2**	-3.8**	-6.5**	-5.8**	-6.1**	-7.1**	-6.7**	-6.9**
L.S.D.$_{0.05}$	6.89	7.46	7.04	0.05	0.05	0.05	1.64	1.68	1.62	1.60	1.80	1.67
L.S.D.$_{0.01}$	9.29	10.06	9.36	0.06	0.06	0.06	2.21	2.27	2.16	2.16	2.43	2.23

*,** Significant and highly significant at 0.05 and 0.01 probability levels, respectively .
H= The highest value L= The lowest value

Table 4: Heterosis relative to better parent ($H_{B.P.}$%) for vegetative and earliness traits for each year and the combined data over the two years.

Hybrids	V.L.cm			No.L./P.			L.A.cm^2			F.W./P.g		
	Y_1	Y_2	Comb.	Y_1	Y_2	Comb.	Y_1	Y_2	Comb.	Y_1	Y_2	Comb.
$P_1 \times P_2$	13.8**	12.9**^{L}	13.3**	24.7**	23.3**	23.8**	11.4**	11.3**	11.3**	6.5	15.3	10.9
$P_1 \times P_3$	48.6**^{H}	42.0**^{H}	45.3**^{H}	51.5**^{H}	40.4**^{H}	45.6**^{H}	20.4**^{H}	16.2**^{H}	18.2**^{H}	56.3^{H}	57.4^{H}	56.9^{H}
$P_1 \times P_4$	29.0**	25.5**	27.2**	31.0**	29.4**	29.9**	4.2**^{L}	3.3*^{L}	3.7**^{L}	34.0	37.6	35.8
$P_2 \times P_3$	25.6**	22.7**	24.1**	8.9**	5.0**^{L}	6.9**	8.0**	5.9**	7.0**	11.6	3.5^{L}	7.5
$P_2 \times P_4$	22.8**	20.9**	21.9**	22.1**	13.7**	18.3**	13.5**	11.5**	12.5**	15.6	14.7	15.2
$P_3 \times P_4$	9.2**^{L}	13.8**	11.5**^{L}	2.6*^{L}	6.7**	4.4**^{L}	10.0**	12.7**	11.4**	1.8^{L}	3.5^{L}	2.6^{L}
$P_2 \times P_1$	4.5*	2.5	3.5*	13.9**	11.9**	12.7**	13.1**	11.1**	12.1**	9.6	10.4	10.0
$P_3 \times P_1$	-18.2**^{L}	-22.3**^{L}	-20.3**^{L}	-4.4**^{L}	-0.5^{L}	-2.6*^{L}	19.5**^{H}	17.4**^{H}	18.4**^{H}	-12.3^{L}	-9.1^{L}	-10.7^{L}
$P_4 \times P_1$	0.45	0.34	0.39	33.7**^{H}	26.6**^{H}	29.9**^{H}	16.4**	14.2**	15.2**	4.5	5.2	4.8
$P_3 \times P_2$	30.1**^{H}	30.5**^{H}	30.3**^{H}	0.87	2.1	1.5	7.8**^{L}	6.7**^{L}	7.3**^{L}	20.8^{H}	12.9^{H}	16.7^{H}
$P_4 \times P_2$	19.6**	22.0**	20.8**	15.0**	16.6**	16.2**	12.9**	11.6**	12.2**	3.8	3.5	3.7
$P_4 \times P_3$	1.8	0.61	1.20	3.1**	4.1**	3.4**	14.4**	15.4**	15.0**	1.8	1.4	1.6
L.S.D.$_{0.05}$	3.40	3.25	3.26	2.22	2.89	2.53	2.98	2.58	2.73	94.3	69.3	81.2
L.S.D.$_{0.01}$	4.59	4.38	4.34	3.00	3.90	3.36	4.02	3.48	3.63	127.2	93.5	107.9

Table 4: Cont.

Hybrids	D.W./P.g			N.1stF.F.N.			D.1stF.F.			D.1stM.F.		
	Y_1	Y_2	Comb.	Y_1	Y_2	Comb.	Y_1	Y_2	Comb.	Y_1	Y_2	Comb.
$P_1 \times P_2$	7.9	6.0	7.0	-6.1**	-5.6**	-6.0**	-6.5**	-9.0**	-7.8**	-3.5**	-4.4**	-4.1**
$P_1 \times P_3$	29.9**^{H}	29.9**^{H}	29.9**^{H}	-5.7**	-6.3**	-6.1**	-10.3**^{L}	-9.6**^{L}	-10.0**^{L}	-6.1**^{L}	-4.1**	-5.1**^{L}
$P_1 \times P_4$	24.0**	20.1**	22.0**	-5.1**	-4.2**	-4.6**	-4.3**	-8.2**	-6.4**	-0.4^{H}	-0.8^{H}	-0.7^{H}
$P_2 \times P_3$	2.1	0.85	1.5	-3.1**^{H}	-3.6**^{H}	-3.5**^{H}	-6.2**	-6.9**	-6.5**	-4.3**	-4.3**	-4.4**
$P_2 \times P_4$	8.8*	8.6*	8.7*	-8.2**^{L}	-7.2**^{L}	-7.8**^{L}	-2.5*	-3.3**	-3.2**	-2.2*	-5.5**^{L}	-4.0**
$P_3 \times P_4$	0.70^{L}	0.20^{L}	0.40^{L}	-4.2**	-4.1**	-4.3**	2.1*^{H}	0.4^{H}	1.1^{H}	-0.5	-2.1*	-1.4
$P_2 \times P_1$	10.8**^{H}	10.6*^{H}	10.7*^{H}	-6.1**^{L}	-5.6**^{L}	-6.0**^{L}	-6.5**	-7.4**	-7.0**	-2.6**	-5.2**	-4.0**
$P_3 \times P_1$	-9.2*^{L}	-4.1^{L}	-6.6^{L}	-3.9**	-4.5**	-4.3**	-5.3**	-4.1**	-4.7**	-2.5**	-0.5	-1.5
$P_4 \times P_1$	3.2	2.2	2.7	-6.0**	-4.8**	-5.4**	2.7**	0.4	1.4	-0.5^{H}	-1.7	-1.2^{H}
$P_3 \times P_2$	5.0	7.8	6.4	-3.8**	-3.2**^{H}	-3.6**^{H}	-3.2**	-6.6**	-4.9**	-2.7**	-0.1^{H}	-1.5
$P_4 \times P_2$	0.15	1.0	0.53	-5.9**	-5.4**	-5.8**	-10.3**^{L}	-13.6**^{L}	-12.3**^{L}	-8.7**^{L}	-7.8**^{L}	-8.4**^{L}
$P_4 \times P_3$	4.8	0.15	2.4	-2.8**^{H}	-4.0**	-3.6**^{H}	4.8**^{H}	3.2**^{H}	3.8**^{H}	-0.6	-1.7	-1.3
L.S.D.$_{0.05}$	7.95	8.61	8.13	0.05	0.05	0.05	1.89	1.94	1.88	1.85	2.08	1.93
L.S.D.$_{0.01}$	10.7	11.6	10.8	0.07	0.07	0.07	2.55	2.62	2.50	2.49	2.80	2.57

***,** Significant and highly significant at 0.05 and 0.01 probability levels, respectively .**
H= The highest value L= The lowest value

Genetic parameters, including additive (٢نA), dominance (٢نD), reciprocal effect (٢نr),additive variance × year (٢نA × Y), non-additive genetic variances × year (٢نD × Y) and reciprocal effect × year (٢نr × Y) in addition to heritability in broad (h^2_b%) and narrow (h^2_n%) senses for vegetative traits and the obtained results are presented in Table 6.The results from the two years and the combined data illustrated that the magnitudes of δ٢A were larger in magnitudes than corresponding values of δ٢D for V.L.cm, F.W./P.g. and D.W./P.g traits. On the other hand, the magnitudes of δ٢D were larger for No.L./P. and L.A.cm^2. The results also indicated that the magnitudes of ٢نA × Y were larger than those of ٢نD × Y for all studied traits except L.A.cm^2 trait. It could be emphasized on the important of ٢نA and ٢نD for the inheritance of the studied traits. The obtained results of ٢نA and ٢نD could explain the presence of heterosis could be due to ٢نD and ٢نA × A epistasis. The results also cleared the presence of ٢نr for all studied traits. All of genetic parameters played an important role in the inheritance of all studied traits. Similar results were obtained by values of heritability in narrow sense.

The results also illustrated the importance of reciprocal variances (٢نr), which was larger than both additive and dominance genetic variances,except for L.A.cm^2.This result indicated that these traits not only controlled by nuclear genetic factors,but also the cytoplasmic genetic factors which play an important role in the inheritance of these traits.The same trend was also observed for vegetative traits as presented in the same table for earliness traits.Thus,both additive (٢نA),non-additive genetic variances including dominance (٢نD) contributed to the inheritance of No.1stF.F.N, D.1stF.F. and D.1stM.F.traits.The dominance (٢نD) genetic variance was larger than the corresponding values of additive genetic variance (٢نA) for No.1stF.F.N trait. This suggests that dominance genetic variance played the major role in the genetic expression of earliness traits. On the other hand, the magnitudes of ٢نA were larger for D.1stF.F. and D.1stM.F. This suggests that additive genetic variance played the major role in the genetic expression of these traits. Furthermore, the reciprocal effect variance (٢نr) were positive for all studied earliness traits, indicating that cytoplasmic factors have their role in the expression of these traits in addition to nuclear genes.

The values of heritability in broad (h^2_b%) and narrow (h^2_n%) senses were also estimated and the results are cleared in the same Table.

Concerning heritability values from the combined data. The results indicated that the magnitudes of the values in broad sense (h^2_b%) were always larger than their corresponding narrow sense (h^2_n%) for all studied traits. The values of heritability in broad sense ranged from 24.71% to 82.01% for No.L./P. and L.A.cm^2 traits, respectively. In the same time, the highest value of h^2_n% was 74.24% for D.1stF.F. These obtained values of heritability indicated the possibility of improving these studied traits through selection programs in the segregated generations.

The results also cleared that GCA mean squares were important than that SCA mean squares for all studied traits except for L.A.cm^2 and No.1stF.F.N. This finding cleared that additive genetic variances were more important in the inheritance of these traits. This was emphasized by the ratio of GCA/SCA exceed one. Meanwhile, the SCA mean square or non-additive genetic variances were more important than GCA mean squares for L.A.cm^2.

The reciprocal effect variance was significant for combined data for all studied traits except for D.W./P.g, No.1stF.F.N. and D.1stM.F. While, the interactions of GCA by years (GCA × Y), SCA by years (SCA × Y) and rec. by years (Rec.×Y) were insignificant for all studied traits. The interaction between crosses by years were only significant for D.1stF.F.

Positive or negative GCA effects (g_i) estimates could indicate that a given inbred is better or poorer than the average of the group involved with it in the complete diallel crosses mating system.

The general combining ability effects (g_i) of four parents for vegetative and earliness traits of the two years and their combined data are given in Table 7.The results revealed that the P_1 for GCA effects showed (desirable) positive and highly significant values for V.L.cm, No.L./P., F.W./P.g and D.W./P.g. While, it only significant for L.A.cm^2. On the other hand, the GCA effects showed highly significant and positive (desirable) for the parent P_2 for L.A.cm^2 for the two years and their combined data. These results indicated that the parents P_3 and P_4 having negative (undesirable) and significant GCA for V.L.cm, No.L./P. and D.W./P.g.

These results indicated that the parents P_2 and P_1 were the best combiner for L.A.cm^2. In the same time, the two parents P_1 and P_2 were the best combiner for No.L./P. Meanwhile, the GCA effects were significant and positive for most studied traits. The parent P_1 was the best combiner for V.L.cm, No.L./P., F.W./P.g and D.W./P.g. The results for the two years and their combined analysis revealed that the GCA effects showed (desirable) negative and highly significant values to the parent P_2 for all earliness traits, No.1stF.F.N, D.1stF.F. and D.1stM.F. toward earliness. Meanwhile, the GCA effects were found to be significant and positive (undesirable) for the parent P_3 for all studied earliness traits.

Estimates of specific combining ability effects (s_{ij}) of 12 hybrids for vegetative and earliness traits for two years and their combined data are presented in Table 8. The results showed that the F_1 hybrids $P_1 \times P_3$ and $P_2 \times P_4$ showed highly significant positive (desirable) of SCA effects for V.L.cm for combined data. While, the F_1 hybrids $P_1 \times P_2$ and $P_3 \times P_4$ showed highly significant and negative (undesirable) of SCA effects for combined data for the same trait.The F_1 hybrid $P_1 \times P_3$ gave the highest value for V.L.cm 2.90 for the combined data. On the other hand, F_{1r} hybrids $P_2 \times P_1$, $P_3 \times P_1$, $P_4 \times P_1$ and $P_4 \times P_3$ showed highly significant positive (desirable) of SCA effects for V.L.cm for combined data. While, the F_{1r} hybrid $P_3 \times P_2$ showed highly significant negative (undesirable) of SCA effects for combined data for the same trait. The F_{1r} hybrid $P_3 \times P_1$ showed the highest value 22.3 for the combined data for the same trait.

For No.L./P.,the F_1 hybrid $P_2 \times P_4$ gave the highest significant value 1.02 for the combined data. While, the F_{1r} hybrid $P_3 \times P_1$ showed the highest value 6.63 for combined data for the same trait. For L.A.cm^2 the F_1 hybrid $P_1 \times P_3$ cleared the highest value 3.37 for the combined data. While, the F_{1r} hybrid $P_4 \times P_2$ gave the highest value 0.11 for the combined data for the same trait. For F.W./P.g the F_1 hybrid $P_1 \times P_3$ cleared the highest value 56.4 for combined data. While, the F_{1r} hybrid $P_3 \times P_1$ gave the highest value 131 for combined data for the same trait. For D.W./P.g the F_1 hybrid $P_1 \times P_3$ gave the highest value 2.75 for combined data. While, the F_{1r} hybrid $P_3 \times P_1$ gave the highest value 28.3 for the combined data for the same trait.

Table 5: Analysis of combining abilities and mean squares of F_1 hybrids for vegetative and earliness traits.

S.V.	d.f.	V.L.cm			No.L./P.			L.A.cm^2			F.W./P.g		
		Y_1	Y_2	Comb.	Y_1	Y_2	Comb.	Y_1	Y_2	Comb.	Y_1	Y_2	Comb.
Crosses	11	515.8**	510**	1023**	61.42**	44.95**	104.4**	45.55**	36.97**	81.36**	100906**	100179**	200226**
G.C.A.	3	135.9**	146**	281.7**	8.80*	9.78*	18.2*	19.24*	16.14*	34.84**	18145*	23569**	41453**
S.C.A.	2	42.2*	21.6	61.2*	7.67	5.59	13.2	39.73*	31.08*	70.4*	11851	8469	20091
R.E.	6	233.2**	231**	463.7**	30.6**	20.7**	50.3**	4.98	4.17*	8.84*	48642**	46613**	94937**
C × Y	11	--	--	3.19	--	--	1.93	--	--	1.16	--	--	859
G.C.A. × Y	3	--	--	0.29	--	--	0.38	--	--	0.55	--	--	260.7
S.C.A. × Y	2	--	--	2.60	--	--	0.10	--	--	0.41	--	--	229.6
R.E. × Y	6	--	--	0.94	--	--	0.96	--	--	0.30	--	--	318.1
Pooled Error	22/44	1.90	1.73	1.81	0.81	1.37	1.09	1.45	1.09	1.27	1458	787.6	1123
G.C.A./ S.C.A.	--	3.22	6.76	4.60	1.15	1.75	1.38	0.48	0.52	0.49	1.53	2.78	2.06
G.C.A.× Y/S.C.A.× Y	--	--	--	0.11	--	--	3.80	--	--	1.34	--	--	1.14

Table 5: Cont.

S.V.	d.f.	D.W./P.g			No.1st F.F.N.			D.1st F.F.			D.1st M.F.		
		Y_1	Y_2	Comb.	Y_1	Y_2	Comb.	Y_1	Y_2	Comb.	Y_1	Y_2	Comb.
Crosses	11	895.9**	820.3**	1691.2**	0.013**	0.008**	0.019**	17.04**	23.14**	39.69**	4.22**	7.63**	10.04**
G.C.A.	3	195.2*	278.8*	468.4**	0.009	0.004	0.012*	14.49*	19.24**	33.4**	2.35	5.59	7.36*
S.C.A.	2	38.6	62.01	48.29	0.006	0.006	0.012*	0.45	1.15	1.49	0.26	1.75	1.25
R.E.	6	448.6**	341.3**	783.2**	0.002	0.001	0.003*	3.02*	4.14*	7.06**	1.32	1.29	2.04
C × Y	11	--	--	25.1	--	--	0.001	--	--	0.49	--	--	1.81*
G.C.A. × Y	3	--	--	5.65	--	--	0.0008	--	--	0.34	--	--	0.58
S.C.A. × Y	2	--	--	17.6	--	--	0.0001	--	--	0.11	--	--	0.76
R.E. × Y	6	--	--	6.63	--	--	0.0001	--	--	0.10	--	--	0.56
Pooled Error	22/44	10.4	12.2	11.3	0.0006	0.0007	0.0006	0.59	0.62	0.60	0.56	0.71	0.63
G.C.A./ S.C.A.	--	5.06	4.50	9.70	1.5	0.7	1.0	32.2	16.7	22.4	9.04	3.19	5.89
G.C.A.×Y/S.C.A.×Y	--	--	--	0.32	--	--	8.00	--	--	3.09	--	--	0.76

***,** Significant at 0.05 and 0.01 levels of probability, respectively .**

The F_1 hybrids $P_1 \times P_3$ and $P_2 \times P_4$ showed highly significant negative (desirable) of SCA effects for No.1stF.F.N. from combined data. While, the F_{1r} hybrid $P_4 \times P_2$ was significant and negative (desirable) of SCA effects for combined data for the same trait. This value was -0.044 for the combined data for the same trait. For D.1stF.F. the F_1 hybrids $P_1 \times P_4$ and $P_2 \times P_3$ showed the highest negative values for combined data. While, the F_{1r} hybrid $P_3 \times P_2$ gave the highest negative value -1.95 from the combined data for the same trait. For D.1stM.F. the F_1 hybrids $P_1 \times P_3$ and $P_2 \times P_4$ gave the highest negative values for combined data. While, the F_1 reciprocal hybrid $P_3 \times P_1$ gave the highest negative value -1.18 for the combined data for the same trait.

Table 6: The relative magnitudes of different genetic parameters and heritability for vegetative and earliness traits for each year and the combined data over the two years.

Genetic parameters and heritability	V.L.cm			No.L./P.			L.A.cm^2			F.W./P.g		
	Y_1	Y_2	Comb.	Y_1	Y_2	Comb.	Y_1	Y_2	Comb.	Y_1	Y_2	Comb.
ن۲ A	46.8	62.2	55.6	0.56	2.1	1.18	-10.24	-7.48	-8.92	5197	7550	5332
ن۲ D	20.2	9.94	14.7	3.43	2.11	3.27	19.1	15.0	17.5	3148	3841	4965
ن۲ r	115.6	114.9	115.7	14.9	9.67	12.4	1.76	1.53	2.14	23592	22913	23655
ن۲ A × Y	--	--	0.57	--	--	0.07	--	--	-0.03	--	--	7.75
ن۲ D × Y	--	--	0.39	--	--	-0.49	--	--	0.43	--	--	-446.6
ن۲ r × Y	--	--	-0.44	--	--	-0.06	--	--	-0.49	--	--	-402.4
ن۲ E	1.89	1.73	1.81	0.81	1.37	1.09	1.45	1.09	1.27	1458	787.6	1122.8
H^2_b%	36.32	38.22	37.24	20.25	27.61	24.71	85.61	85.13	82.01	24.99	32.46	29.35
h^2_n%	25.37	32.95	29.45	2.84	13.77	6.55	0.00	0.00	0.00	15.56	21.52	15.20

Table 6: Cont.

Genetic parameters and heritability	D.W./P.g			No.1stF.F.N.			D.1stF.F.			D.1stM.F.		
	Y_1	Y_2	Comb.	Y_1	Y_2	Comb.	Y_1	Y_2	Comb.	Y_1	Y_2	Comb.
ن۲ A	95.7	108.4	108.0	0.0014	0.0014	0.0004	7.02	9.04	7.92	1.04	1.92	1.58
ن۲ D	3.26	24.9	7.68	0.0028	0.0028	0.0031	0.07	0.27	0.35	0.15	0.52	0.12
ن۲ r	219.1	164.5	194.1	0.0005	0.0002	0.0006	1.22	1.76	1.74	0.38	0.29	0.37
ن۲ A × Y	--	--	3.16	--	--	0.0002	--	--	0.058	--	--	0.05
ن۲ D × Y	--	--	2.98	--	--	-0.0003	--	--	-0.246	--	--	0.06
ن۲ r × Y	--	--	-2.32	--	--	-0.0003	--	--	-0.25	--	--	-0.04
ن۲ E	10.37	12.15	11.26	0.0006	0.0007	0.0006	0.59	0.62	0.60	0.56	0.71	0.63
h^2_b%	30.13	43.01	35.36	79.25	82.35	71.43	79.66	79.64	77.52	55.87	70.93	60.50
h^2_n%	29.14	34.97	33.01	26.42	27.45	8.16	78.88	77.33	74.24	48.83	55.81	56.23

Note: Negative values were considered equal to zero during the calculation of heritability in broad and narrow senses.

Table 7: General combining ability effects (g_i) of the four parents for vegetative and earliness traits from each year and from the combined data.

Parents	V.L.cm			No.L./P.			L.A.cm^2			F.W./P.g		
	Y_1	Y_2	Comb.	Y_1	Y_2	Comb.	Y_1	Y_2	Comb.	Y_1	Y_2	Comb.
P1	8.61**	8.83**	8.72**	1.21**	1.74**	1.48**	0.76*	0.75*	0.76*	95.4**	111.7**	103.5**
P2	-1.48**	-1.05*	-1.27**	1.13**	0.79*	0.96**	1.67**	1.96**	1.81**	-59.6**	-60.0**	-59.8**
P3	-3.84**	-4.22**	-4.03**	-0.41	-0.78*	-0.60	0.80*	0.07	0.43	-30.4*	-37.5**	-34.0**
P4	-3.30**	-3.55**	-3.43**	-1.93**	-1.75**	-1.84**	-3.23**	-2.78**	-3.00**	-5.42	-14.2	-9.79
L.S.D. $_{0.05}$	0.87	0.83	0.83	0.57	0.74	0.64	0.76	0.66	0.70	24.2	17.8	20.7
L.S.D. $_{0.01}$	1.19	1.13	1.11	0.77	1.00	0.86	1.03	0.90	0.92	32.9	24.1	27.7

Table 7: Cont.

Parents	D.W./P.g			No.1stF.F.N.			D.1stF.F.			D.1stM.F.		
	Y_1	Y_2	Comb.	Y_1	Y_2	Comb.	Y_1	Y_2	Comb.	Y_1	Y_2	Comb.
P1	10.2**	12.5**	11.3**	-0.002	-0.006	-0.004	-0.083	-0.533*	-0.308	0.396	0.921**	0.658**
P2	-4.13**	-4.71**	-4.42**	-0.058**	-0.038**	-0.048**	-2.075**	-2.108**	-2.092**	-0.971**	-1.687**	-1.329**
P3	-4.88**	-4.79**	-4.83**	0.056**	0.031**	0.044**	2.533**	3.084**	2.808**	0.788**	0.704*	0.746**
P4	-1.21	-2.96*	-2.08*	0.005	0.013	0.009	-0.375	-0.442	-0.408	-0.213	-0.062	-0.075
L.S.D. $_{0.05}$	2.04	2.21	2.07	0.015	0.016	0.015	0.49	0.50	0.48	0.47	0.53	0.49
L.S.D. $_{0.01}$	2.77	2.99	2.77	0.021	0.022	0.021	0.66	0.67	0.64	0.64	0.72	0.65

***,** Significant and highly significant at 0.05 and 0.01 probability levels, respectively.**

The degree of association among different traits of squash is of great importance. The coefficient of genotypic correlation provides a measure of the genotypic association between pairs of traits to identify the traits which could be used as indicator for improvement of other traits through the selection programs.

Table 8: Specific combining ability effects(s_{ij}) of the 12 hybrids for vegetative and earliness traits from the two years and their combined data.

Hybrids	V.L.cm			No.L./P.			L.A.cm^2			F.W./P.g		
	Y_1	Y_2	Comb.	Y_1	Y_2	Comb.	Y_1	Y_2	Comb.	Y_1	Y_2	Comb.
$P_1 \times P_2$	-2.90**	-2.42**	-2.66**	-1.54**	-1.34*	-1.43**	-1.16*	-0.70	-0.93	-45.5*	-33.2*	-39.3**
$P_1 \times P_3$	3.47**	2.20**	2.90**	1.10**	0.90	1.00*	3.61**	3.10**	3.37**	60.0**	52.9**	56.4**
$P_1 \times P_4$	-0.60	-0.21	-0.41	0.40	0.44	0.42	-2.40**	-2.30**	-2.35**	-14.4	-19.0	-16.7
$P_2 \times P_3$	-0.61	0.20	-0.20	0.39	0.42	0.40	-2.41**	-2.34**	-2.38**	-14.7	-19.2	-16.9
$P_2 \times P_4$	3.51**	2.23**	2.86**	1.14**	0.95	1.02*	3.57**	3.08**	3.33**	60.3**	52.2**	56.2**
$P_3 \times P_4$	-2.87**	-2.40**	-2.63**	-1.51**	-1.36*	-1.44**	-1.15*	-0.74	-0.95	-45.6*	-33.3*	-39.5**
$P_2 \times P_1$	3.12**	3.58**	3.35**	1.47*	1.58	1.53*	-0.72	0.07	-0.33	-15.0	23.3	4.17
$P_3 \times P_1$	22.4**	22.2**	22.3**	7.58**	5.68**	6.63**	0.33	-0.47	-0.07	133**	128**	131**
$P_4 \times P_1$	12.8**	12.2**	12.5**	4.28**	4.05**	4.17**	-2.53**	-2.60**	-2.57**	117**	107**	112**
$P_3 \times P_2$	-4.32**	-5.33**	-4.83**	-3.58**	-3.27**	-3.43**	-2.23*	-2.12**	-2.18**	-60.0*	-61.7**	-60.8*
$P_4 \times P_2$	0.92	-0.30	0.31	0.95	-0.40	0.28	0.25	-0.03	0.11	56.7*	53.3*	55. 0*
$P_4 \times P_3$	2.08*	3.63**	2.86**	-0.07	0.35	0.14	-1.68	-1.02	-1.35	0.00	10.0	5.00
L.S.D.(s_{ij}) $_{0.05}$	1.23	1.17	1.17	0.81	1.05	0.91	1.08	0.93	0.98	34.2	25.1	29.3
L.S.D.(s_{ij}) $_{0.01}$	1.67	1.59	1.57	1.00	1.42	1.22	1.46	1.27	1.32	46.4	34.1	39.1
L.S.D.(r_{ij}) $_{0.05}$	2.01	1.92	1.92	1.32	1.71	1.49	1.76	1.53	1.61	55.9	41.1	47.9
L.S.D.(r_{ij}) $_{0.01}$	2.73	2.61	2.56	1.79	2.33	1.99	2.39	2.07	2.15	75.9	55.8	64.0

Table 8: Cont.

Hybrids	D.W./P.g			No.1stF.F.N.			D.1stF.F.			D.1stM.F.		
	Y_1	Y_2	Comb.	Y_1	Y_2	Comb.	Y_1	Y_2	Comb.	Y_1	Y_2	Comb.
$P_1 \times P_2$	-0.83	-2.94	-1.89	0.003	0.001	0.002	0.164	0.408	0.286	0.180	-0.390	-0.105
$P_1 \times P_3$	1.11	4.47**	2.75	-0.041**	-0.043**	-0.042**	0.220	0.200	0.210	-0.289	-0.375	-0.332
$P_1 \times P_4$	-0.29	-1.50	-0.90	0.035**	0.040**	0.037**	-0.386	-0.608	-0.497	0.110	0.760*	0.434
$P_2 \times P_3$	-0.25	-1.53	-0.89	0.038**	0.039**	0.039**	-0.380	-0.610	-0.494	0.109	0.764*	0.436
$P_2 \times P_4$	1.08	4.50**	2.70	-0.049**	-0.045**	-0.047**	0.224	0.204	0.214	-0.295	-0.375	-0.335
$P_3 \times P_4$	-0.81	-2.92	-1.87	0.003	0.001	0.002	0.160	0.412	0.285	-0.183	-0.386	-0.285
$P_2 \times P_1$	-2.33	-3.50	-2.92	-0.002	0.00	-0.001	0.00	-0.367	-0.183	-0.20	0.184	-0.008
$P_3 \times P_1$	30.2**	26.5**	28.3**	-0.037*	-0.035	-0.036*	-1.30*	-1.42*	-1.36*	-0.85	-1.52*	-1.18*
$P_4 \times P_1$	18.8**	15.3**	17.1**	0.007	0.008	0.007	-0.384	-0.177	-0.25	0.517	-0.850	-0.167
$P_3 \times P_2$	-4.80*	-6.30*	-5.58*	0.025	0.005	0.015	-1.90**	-2.00**	-1.95**	-0.840	-0.717	-0.782
$P_4 \times P_2$	6.50**	5.80*	6.17*	-0.045*	-0.042*	-0.044*	1.80**	2.42**	2.11**	1.48*	0.534	1.01
$P_4 \times P_3$	-3.17	0.00	-1.58	-0.027	-0.008	-0.018	-0.617	-0.65	-0.633	0.017	-0.084	-0.033
L.S.D.(s_{ij}) $_{0.05}$	2.88	3.12	2.93	0.022	0.024	0.021	0.69	0.69	0.68	0.67	0.75	0.69
L.S.D.(s_{ij}) $_{0.01}$	3.91	4.24	3.92	0.031	0.032	0.031	0.93	0.94	0.90	0.91	1.02	0.93
L.S.D.(r_{ij}) $_{0.05}$	4.71	5.10	4.79	0.036	0.039	0.035	1.12	1.15	1.11	1.09	1.23	1.13
L.S.D.(r_{ij}) $_{0.01}$	6.30	6.65	6.41	0.049	0.053	0.047	1.53	1.56	1.48	1.49	1.67	1.52

***,** Significant and highly significant at 0.05 and 0.01 probability levels, respectively .**

The covariance analysis between pairs of all studied traits were made from the combined data over both years. Subsequently, genotypic (r_g) and phenotypic (r_{ph}) correlations were determined and the results are presented in Table 9. The results showed positive highly significant genotypic (r_g) and phenotypic (r_{ph}) correlations between V.L.cm and No.L./P., F.W./P.g and D.W./P.g. The coefficients were 0.93, 0.96 and 0.96 for genotypic correlation and 0.89, 0.93 and 0.91 for phenotypic correlation, respectively. At the same time, No.L./P. trait showed highly significant positive genotypic and phenotypic correlations with L.A.cm^2, F.W./P.g and D.W./P.g the coefficients were 0.68, 0.91 and 0.90 for genotypic correlation and 0.66, 0.87 and 0.86 for phenotypic correlation, respectively. On the other hand, L.A.cm^2 showed highly significant and positively genotypic correlation with F.W./P.g and D.W./P.g. The coefficients were 0.63 and 0.62, respectively. While, the same trait showed highly significant positive phenotypic correlation with F.W./P.g and the coefficient was 0.64. F.W./P.g showed highly significant positive genotypic and phenotypic correlations with D.W./P.g. The values coefficients were 0.99 for genotypic correlation and 0.96 for phenotypic correlation, respectively. Also, No.1stF.F.N showed highly significant positive genotypic correlation with D.1stF.F. and D.1stM.F. the coefficients were 0.63 and 0.62, respectively. D.1stF.F. showed highly significant positive genotypic correlation with D.1stM.F. the coefficient was 0.95.

In general, most pairs of studied traits exhibited negative genotypic and phenotypic correlation coefficients. However, the same pairs of traits showed significant positive genotypic and phenotypic correlation among them. These results indicated that the selection of one trait would improve the other correlated trait.

Table 9: Genotypic (above diagonal) and phenotypic (below diagonal) correlation for all pairs of vegetative and earliness traits.

Traits	V.L.cm	No.L./P.	L.A.cm^2	F.W./P.g	D.W./P.g	No.1stF.F.N.	D.1stF.F.	D.1stM.F.
V.L.cm		0.93**	0.59*	0.96**	0.96**	-0.41	-0.51*	-0.57*
No.L./P.	0.89**		0.68**	0.91**	0.90**	-0.56*	-0.57*	-0.66**
L.A.cm^2	0.60*	0.66**		0.63**	0.62**	-0.65**	-0.70**	-0.84**
F.W./P.g	0.93**	0.87**	0.64**		0.99**	-0.44	-0.54*	-0.60*
D.W./P.g	0.91**	0.86**	0.61*	0.96**		-0.43	-0.55*	-0.60*
No.1stF.F.N.	-0.35	-0.43	-0.55*	-0.36	-0.34		0.63**	0.62**
D.1stF.F.	-0.45	-0.46	-0.61*	-0.46	-0.47	0.51*		0.95**
D.1stM.F.	-0.42	-0.46	-0.57*	-0.43	-0.41	0.43	0.56*	

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مظهر قوة الهجين والقياسات الوراثية المرتبطة بها لبعض الصفات الخضرية والتبكير في قرع الكوسة

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تهدف هذه الدراسة إلى تقدير قيم قوة الهجين قياسا من متوسط الآباء و أفضل الآباء، وطبيعة فعل الجين، ومعامل التوريث في مداه الواسع والضيق ومعامل الارتباط الوراثي والمظهري لبعض الصفات الخضرية و التبكير في قرع الكوسة.

في هذه الدراسة تم استخدام أربع أصناف من قرع الكوسة كآباء وهى: Eskandrani(الأب الأول)، Zucchino mezza lung bianco(الأب الثاني)، White Bush Scallop (الأب الثالث)، Zucchino nano verde di Milano(لأب الرابع).

أظهرت الآباء مدا واسعا من التباينات والاختلافات لجميع الصفات محل الدراسة. في الموسم الصيفي ٢٠٠٢ تم زراعة بذور الأصناف الأربعة المستخدمة كآباء لإجراء كل التهجينات الممكنة (الهجن والهجن العكسية) بنظام التهجين الدوري الكامل كما أجريت عملية إخصاب ذاتي للأصناف المستخدمة كآباء. جميع التراكيب الوراثية الناتجة من السنة السابقة في هذه الدراسة تم تقييمها في تجربة حقلية في موسمي الصيف ٢٠٠٣ و٢٠٠٤ في تجربة قطاعات كاملة العشوائية من ثلاث مكررات بغرض تقييم جميع التراكيب الوراثية المتحصل عليها . وقد تم إجراء هذه التجربة في المزرعة البحثية بالبرامون محطة بحوث البساتين بالمنصورة.

وبعد إجراء التحليلات الإحصائية المناسبة يمكن تلخيص النتائج المتحصل عليها فيما يلي:

أشارت اختبارات المعنوية لجميع التراكيب الوراثية (١٦ تركيب وراثي) من البيانات المجمعة لكلا السنتين إلى وجود اختلافات عالية المعنوية بين التراكيب الوراثية محل الدراسة لجميع الصفات الخضرية وصفات التبكير وهذه النتائج من المتوقع الحصول عليها، حيث أن هذه التراكيب الوراثية المستخدمة في هذه الدراسة تختلف وتتباين من حيث صفات الآباء المختارة للبدء في هذا العمل.

أظهرت النتائج وجود اختلافات كبيرة بين هجن الجيل الأول والأول العكسي مع عدم تميز هجين معين بذاته لكل الصفات المدروسة، ولكن معظم التراكيب الوراثية للجيل الأول الهجين تميزت عن الآباء الداخلة في تكوينها، ولذا فإن الهجن قد فاقت الآباء في معظم الصفات محل الدراسة. القيم المحسوبة لقوة الهجين مقارنة بمتوسط الآباء تؤكد وجود قيم معنوية لقوة الهجين لجميع الصفات محل الدراسة عدا صفة الوزن الغض للنبات بالجرام. القيم المحسوبة لقوة الهجين مقارنة بأفضل الآباء أوضحت وجود قيم عالية المعنوية لمعظم الصفات محل الدراسة.

أظهرت النتائج تعاظم قيم كل من القدرة العامة على التآلف (GCA) والقدرة الخاصة على التآلف (SCA). وأوضحت النتائج أهمية القدرة العامة على التآلف لجميع الصفات التي تمت دراستها للجيل الأول الهجين، بينما كانت قيمة تأثير التهجين العكسي معنوية لمعظم الصفات المدروسة. كما تؤكد النتائج أن الفعل الجينى المضيف وغير المضيف لعبا الدور الأكبر في توريث هذه الصفات وكانت قيمة التباين الوراثي الراجع للإضافة أعلي من قيمة التباين الوراثي غير الإضافي لمعظم الصفات المدروسة والذي يشمل على تباين السيادة والأخير يحتوى ضمنيا على جزء من التباين الوراثي والذي يعزى إلى التفوق كما أنه لا يمكن تجاهل تأثير التهجين العكسي (العوامل السيتوبلازمية)، وكذلك تم تقدير معامل التوريث في مداه الواسع والضيق لجميع الصفات محل الدراسة وقيم معامل التوريث في مداه الواسع كانت أعلي منه في مداه الضيق لجميع الصفات محل الدراسة.

كما أظهرت النتائج وجود ارتباط معنوي بين معظم أزواج الصفات التي درست فقد كانت صفة طول الساق مرتبطة ارتباطا معنويا موجبا مع صفات عدد الأوراق على النبات والمساحة الورقية والوزن الغض والوزن الجاف وارتبطت صفة أول عقدة تحمل زهرة مؤنثة مع صفتي عدد الأيام حتى ظهور أول زهرة مذكرة وأول زهرة مؤنثة ، وبالتالي فالانتخاب إلى أي من هذه الصفات يؤدى إلى تحسين الصفات الأخرى المرتبطة بها.

ومن النتائج السابقة يمكن لمربى النبات أن يستخدم هذه المميزات لتصميم برنامج تربية مناسب من أجل إنتاج أصناف محسنة في الأجيال الانعزالية المتقدمة للهجن المتفوقة.