GENETICAL STUDIES ON ECONOMICAL TRAITS OF SOME SQUASH HYBRIDS
(Cucurbita pepo, L.)

El-Sherbeny, G.A.R.; A.H. Abd El- Hadi; Soher E.A. El-Gendy

ABSTRACT

The present investigation aimed to study heterosis and nature of gene action controlling the economic traits of summer squash (Cucurbita pepo, L.) under two locations. The results showed that the mean squares due to locations (L), genotypes (G) and genotypes×locations interaction (G×L) were significant for all studied traits, indicating the differentially response of these traits from location to another. The results indicated that the majority of F_1 hybrids were significantly earlier and high yielding than their mid parents. In this respect, the crosses $(P_3×P_5)$, $(P_1×P_5)$ and $(P_2×P_5)$ showed the largest desirable heterotic estimates of -19.77%, -11.84% and -18.85% toward earliness for days to the first female flower (DIst FF), days to the first male flower (DIst MF) and days to the first picking (DIst P), respectively. Moreover, the cross combination $(P_4×P_5)$ exhibited the maximum heterotic values of 67.51%, 24.08%, 32.13%, 16.91% and 82.69% for number of fruit per plant (No.F/P), fruit length (Fl cm.), fruit diameter (FD cm.), fruit weight (FW gm.) and fruit yield per plant (FY/P kg), respectively. Estimates of general combining ability effects (g_i) of each parents indicated that P_1, P_3 and P_4 possessed more desirable additive genes to improve studied traits. The results showed that the crosses $(P_1×P_5)$, and $(P_3×P_4)$ revealed desirable SCA effects for vegetative traits. While, the crosses $(P_1×P_2)$, $(P_3×P_5)$ and $(P_4×P_5)$ were the most promising hybrids for all earliness traits. Concerning yield components, the crosses $(P_3×P_6)$, $(P_4×P_5)$ and $(P_4×P_6)$ exhibited significant SCA effects for increasing yield components. The results indicated that the magnitudes of non additive genetic variance $(\sigma^2 D)$ were larger than those of additive ones $(\sigma^2 A)$ for vegetative and earliness traits except for leaf area $(LA\ cm^2)$. In contrast, the ratio of $(\sigma^2 D/\sigma^2 A)^{1/2}$ for yield components was less than one except for number of fruit per plant (No. F/P), suggesting that additive genetic variance played the important role in the inheritance of these traits. Moreover, the magnitudes of $\sigma^2 A×L$ variance were less than those of $\sigma^2 D×L$ ones for all vegetative and earliness traits except for leaf area $(LA\ cm^2.)$, indicating that non additive gene action was more influenced by locations than additive one for these traits. On the other hand, the ratio of $(\sigma^2 D×L/\sigma^2 A×L)^{1/2}$ for yield components was lower than one except for number of fruit per plant (No. F/P), revealing that additive gene action interacts by locations more than non additive one for these traits. The values of narrow sense heritability for vegetative and earliness traits ranged from 11.56% to 38.51% for days to first male flower (DIst MF) and leaf area $(LA\ cm^2.)$, respectively. While, the estimates of narrow sense heritability ranged from 20.93% to 54.16% for number of fruits per plant (No.F/P) and fruit shape index (FSh I), respectively. According to the estimates of heterosis, nature of gene action and heritability, it could be concluded that improving of squash yield components would be possible through selection programs in segregated generations under more environments.

INTRODUCTION

Summer squash (Cucurbita pepo L.) is one of the most important vegetable crops in Egypt. Yield is the most important character of squash cultivars and hybrids. Thus, identification of a genotype with high yield potential and least seasonal fluctuation over a wide range of environ-mental is important in any breeding program. In this direction, Eberhart and Russell (1966) reported that an ideal genotype is that has the highest yield over a broad range of environments. Consequently, the effect of G×E interaction on heterosis and combining ability provides important information for improving economic traits in squash.

In this respect, different heterotic effects were obtained by many authors for economic traits in squash. Ghai et al (1998), El-Gendy (1999) and Abd El-Maksoud et al (2003) found desirable heterotic values over mid and better parents for earliness and vegetable traits. For yield components, Kasrawi (1994) observed high heterotic values versus mid and better parents over two seasons. Abd El-Hadi and El-Gendy (2004) reported highly significant heterosis values over mid and better parents for yield components at each location and combined data.

The role of GCA and SCA as well as their interactions with the environment were studied by several authors in the inheritance of summer squash. Korzeniewska and Niemirowicz (1993) obtained high GCA values for yield components over two seasons, while, significant SCA value was only noted for fruit

weight. Abd El-Hadi et al (2005) noticed that the estimates of GCA were larger than those of SCA for earliness and vegetative traits, reflecting the importance of additive gene action in the expression of these traits. Moreover, Samadia and Khandelwal (2002) found that the estimates of GCA, SCA, GCA × E and SCA × E were significant for earliness and yield components. In the same trend, Abd El-Hadi and El-Gendy (2004) and Abd El-Hadi et al (2004) stated that the estimates of GCA, SCA, GCA×L and SCA×L were important in the inheritance of earliness , vegetative traits and yield components, suggesting the importance of additive and non additive gene action at each location and combined data in the inheritance of these traits.

Therefore, the main target of this research was to study heterosis and the types of gene action controlling the inheritance of economical traits of summer squash under two locations.

MATERIALS AND METHODS

Six different squash varieties (Cucurbita pepo L.) represented a wide range of variability in their economic traits, were used in this study. These varieties were: Eskandrani (P_1, Egypt), Giado (P_2, Italy), Zucchino mezza lung bianco (P_3, Germany), Zucchino 544- 00S (P_4, Italy), White Bush Scallop (P_5, U.S.A.) and Zucchino nano Verde di Millano (P_6, Italy).

[1] Agric. Bot. Dept. (Genetics), Sohag Fac. of Agric., South Valley Univ., Sohag, Egypt
[2] Dept. of Genetics,Fac. of Agric., Mans. Univ., Mansoura, Egypt
[3] Horticultural Res. Inst., Vegetable Research Station (Mansoura) ARC, Egypt

In the summer season of 2003, the six parental genotypes were crossed according to a half diallel mating design to produce 15 F_1 hybrids. In addition, the six parental genotypes were also self pollinated to obtain more seeds from each one.

In the summer season of 2004, seeds of the six parents and their 15 F_1 hybrids were evaluated in a field trial experiment at two locations. These locations were: Sohag Faculty of Agriculture Farm, South Valley University (L_1) and Mansoura Faculty of Agriculture Farm, Mansoura University (L_2).

In each experiment, 21 genotypes included six parents and their 15 F_1 hybrids were grown in a randomized complete block design with three replications. Each replicate contains 21 plots. Each plot was one ridge 5.0 m. long and 1.0 m. wide. Hills were spaced at 0.5 m. apart. All agricultural practices were applied as recommended for squash production.

Data were recorded for the following vegetative, earliness and yield traits: vein length (VL cm.), number of leaves per plant (No.L/P), leaf area (LA cm^2), days to the first female flower (D1st FF), days to the first male flower (D1st MF), days to the first picking (D1st P), number of fruit per plant (No.F/P), fruit length (Fl cm.), fruit diameter (FD cm.), fruit shape index (FSh I), fruit weight (FW gm.) and fruit yield per plant (FY/P kg).

Analyses of variances were carried out separately at two locations. The homogeneity of experimental error was tested for each trait at the two locations. It was found to be non-significant. Therefore, combined data over the two locations were subjected to the combined analysis of variance in order to test the significance of the differences among the 21 genotypes including six parental genotypes

and their 15 F_1 hybrids according to Cochran and Cox (1957).

The sum squares of genotypes and genotypes by locations interaction was partitioned according to Griffing's (1956) method 2 into sources of variations due to GCA, SCA, GCA × L and SCA × L. The variances of GCA (σ^2g) and SCA (σ^2s) as well as their interactions with locations (σ^2gxL and σ^2sxL) were obtained on the basis of the expected mean squares for all studied straits. Additive (σ^2A), non-additive (σ^2D), additive by locations ($\sigma^2 AxL$) and non additive by locations (σ^2DxL) genetic variances were estimated according to Matzinger and Kempthorne (1956) as follows:-

$$\sigma^2A = 2\sigma^2g$$
$$\sigma^2D = \sigma^2s$$
$$\sigma^2A \times L = 2\sigma^2g \times L$$
$$\sigma^2D \times L = \sigma^2s \times L$$

Estimates of heritability in broad and narrow sense were calculated according to the following equations:

$$h^2_b\% = [(\sigma^2A + \sigma^2D) / (\sigma^2A + \sigma^2D + \sigma^2A \times L + \sigma^2D \times L + \sigma^2e)] \times 100$$

$$h^2_n\% = [(\sigma^2A) / (\sigma^2A + \sigma^2D + \sigma^2A \times L + \sigma^2D \times L + \sigma^2e)] \times 100$$

RESULTS AND DISCUSSION

Genotypic variations

Analysis of variance and mean squares (Table 1) were estimated from the combined data over two locations for earliness, vegetative traits and yield components. Mean squares due to locations were highly significant for all studied traits, indicating the differentially response of these

Table 1: Analysis of variance and mean squares of the six parents and their hybrids for all studied traits obtained over two locations.

S.V	DF	VLcm	No.L/P	LA cm^2	D1st FF	D1st MF	D1st P
Locations	1	82.61**	59.15**	166.47**	40.84**	33.87**	42.40**
Reps/L	4	24.54	15.10	38.19	12.68	10.54	20.34
Genotypes	20	1104.6**	139.50**	356.34**	81.52**	24.43**	87.50**
G×L	20	173.73**	25.65**	69.46**	26.69**	9.77**	24.11**
Error	80	6.83	5.94	6.18	3.37	3.81	3.22

Table 1: Cont.

S.V	DF	No.F/P	Flcm.	FDcm.	FshI	FWgm.	FY/Pkg
Locations	1	57.11**	24.82*	14.23**	16.55**	45.61**	38.47**
Reps/L	4	13.66	6.14	4.45	5.32	24.12	17.25
Genotypes	20	80.31**	62.34**	46.52**	53.76**	368.65**	214.16**
G×L	20	19.44**	12.32**	9.84**	11.12**	42.38**	36.86**
Error	80	3.68	3.44	3.06	3.15	6.57	6.24

**Significant at 1% level of probability.

traits from location to another. Mean squares of genotypes were highly significant for all studied traits, reflecting the genetic diversity among them. Moreover, highly significant mean squares of genotypes × locations interaction (G × L) were noticed for all studied traits, suggesting that these genotypes seemed to be inconstant from location to another. These results are in harmony with those previously obtained by Korzeniewska and Niemirowicz (1993), Samadia and Khandelwal (2002), Abd El-Maksoud et al (2003) and Abd El-Hadi et al (2005).

Estimates of heterosis

The amounts of heterosis versus mid parents over the two locations for all studied traits are shown in Table2. Concerning vegetative traits, all F_1 hybrids exhibited significant positive heterosis values except (P_2xP_4) and (P_3xP_6) crosses in the cases of number of leaves per plant (No. L/P) and leaf area (LA cm^2). The cross combination (P_1xP_5) revealed the maximum values of heterosis of 66.41%, 64.62% and 31.21% for vein length (VL cm), number of leaves per plant (No. L/P) and leaf area (LA cm^2), respectively. Regarding to earliness traits, all F_1 hybrids were significantly flowered earlier than their mid parents except (P_3xP_6) and (P_4xP_6) for these traits. The crosses (P_3xP_5), (P_1xP_5) and (P_2xP_5) showed the largest desirable heterotic estimates of -19.77%, -11.84% and -18.85% toward earliness for days to the first female flower (D1st FF), days to the first male flower (D1st MF) and days to the first picking (D1st P), respectively.

As for yield components, highly significant useful heterotic values for number of fruits per plant (No.F/P), fruit length (Fl cm.) and fruit yield per plant (FY/P kg) were detected in all F_1 hybrids. While, 12, 7 and 11 out of the15 crosses exhibited highly significant positive heterosis values for fruit diameter (FD cm.), fruit shape index (Fsh I) and fruit weight (FW gm.). The cross combination (P_4xP_5) exhibited the maximum heterotic values of 67.51%, 24.08%, 32.13%, 16.91% and 82.69% for number of fruit per plant (No.F/P), fruit length (Fl cm.), fruit diameter (FD cm.), fruit weight (FW gm.) and fruit yield per plant (FY/P kg), respectively. However, the largest estimate of heterosis for fruit shape index (8.98%) was obtained in the cross combination (P_1xP_3).

In general, the results indicated that the majority of F_1 hybrids were significantly earlier and high yielding than their mid parents, suggesting the superiority of these hybrids and the important role of non additive gene action in the expression of studied traits in this set of materials. These results confirm the previous findings of Kash and El-Diasty (1989), Abd El- Hadi (1995), Gabr (2003), Abd El-Hadi and El-Gendy (2004) and Abd El-Hadi et al (2004, 2005).

Combining ability analysis

Combining ability analysis of variance of the six varieties and their F_1 hybrids for studied traits over two locations are found in Table 3. General (GCA) and specific (SCA) combining ability were highly significant for all studied traits over the two locations, confirming the important role of all types of gene action in the expression of these traits. Significant variance of genotype × location interaction was partitioned into its components (GCA×L and SCA×L). The results showed that GCA×L interaction was highly significant for earliness, vegetative traits and yield components. While, SCA×L interaction was significant for all studied traits except for fruit diameter. These results indicate that the magnitude of all types of gene action fluctuated from location to another. Therefore, selection under more environments would be effective for these traits. Similar results were recorded by El-Adl et al (1996), El-Gendy (1999), Samadia and Khandelwal (2002) and Sadek (2003). On the other hand, Khalaf Allah et al (2001) reported that mean squares of SCA were more important than those of GCA for most studied traits.

GCA effects (g$_i$)

Estimates of general combining ability effects (g$_i$) of each parent over the two locations for all studied traits are presented in Table 4. The results showed that P_1 was the best general combiner for vegetative traits, fruit length (FL cm.), fruit diameter (FD cm.) fruit shape index (Fsh I) and fruit yield per plant (FY/P kg.). While, P_3 and P_4 were found to be the excellent general combiner for earliness traits as days to the first female flower (D1st FF), days to the first male flower (D1st MF) and days to the first picking (D1st P). Moreover, the same parents (P_3 and P_4) were considered to be good general combiners for yield components except for fruit diameter (FD cm.) and fruit weight (FW gm.). Whereas, the parents P_2, P_5 and P_6 were the poorest general combiners for vegetative traits, earliness and the majority of yield components. However, P_5 was only the best general combiner for fruit diameter (FD cm.) and fruit weight (FW gm.). It could be concluded that P_1, P_3 and P_4 possessed more desirable additive genes and could be utilized in a squash breeding to improve studied traits.

SCA effects (S$_{ij}$)

Estimates of specific combining ability effects (S$_{ij}$) of each hybrid for studied traits over two locations are given in Table 5. The results showed that the crosses (P_1xP_5), which resulted from one good and one poor general combiners and (P_3xP_4) involving two poor general combiners revealed desirable SCA effects for vein length (VL cm.), number of leaves per plant (No. L/P) and leaf area (LA cm^2). The crosses (P_1xP_2), (P_3xP_5) and (P_4xP_5), resulting from two types of cross combinations (poor × poor) and (good × poor) general combiners, were the most promising hybrids for all earliness traits. While, the crosses (P_1xP_6), (P_2xP_4) and (P_2xP_5) revealed desirable SCA effects only for days to first female flower (D1st FF) and days to the first picking (D1st P).

Table 2: Estimates of heterosis relative to mid parents for all studied traits from the combined data over two locations

Crosses	VLcm	No.L/P	LA cm^2	D1st FF	D1st MF	D1st P
$P_1 \times P_2$	34.24**	37.50**	6.46**	-19.33**	-6.57**	-15.62**
$P_1 \times P_3$	13.25**	31.24**	10.73**	-9.92**	-3.64**	-8.54**
$P_1 \times P_4$	26.19**	23.19**	8.61**	-14.51**	-2.96*	-11.08**
$P_1 \times P_5$	66.41**	64.62**	31.21**	-12.56**	-11.84**	-13.35**
$P_1 \times P_6$	35.56**	31.09**	3.23	-13.21**	-2.89*	-11.72**
$P_2 \times P_3$	14.28**	18.41**	13.16**	-12.08**	-2.75*	-9.84**
$P_2 \times P_4$	18.72**	3.24	-0.97	-15.30**	-2.90*	-12.51**
$P_2 \times P_5$	42.28**	15.45**	3.18	-17.63**	-8.61**	-18.85**
$P_2 \times P_6$	37.15**	29.87**	1.26	-4.34**	-4.47**	-3.52**
$P_3 \times P_4$	19.64**	24.35**	15.47**	-8.68**	-2.86*	-6.96**
$P_3 \times P_5$	21.47**	3.48*	21.90**	-19.77**	-6.87**	-18.25**
$P_3 \times P_6$	2.84	-2.19	3.35	2.31	1.28	2.60
$P_4 \times P_5$	42.73**	11.80**	12.32**	-16.81**	-9.58**	-15.61**
$P_4 \times P_6$	20.32**	17.74**	3.87*	2.26	2.65	1.56
$P_5 \times P_6$	28.61**	16.49**	16.71**	-8.60**	-6.74**	-9.73**
LSD 5%	3.63	3.37	3.45	2.55	2.70	2.49
1%	4.77	4.44	4.54	3.35	3.56	3.28

Table 2: Cont.

Crosses	No.F/P	Flcm.	FDcm.	FshI	FWgm.	FY/Pkg.
$P_1 \times P_2$	32.18**	6.61**	7.87**	-3.32**	2.39	30.86**
$P_1 \times P_3$	26.43**	7.43**	1.92	8.98**	1.85	17.63**
$P_1 \times P_4$	35.61**	2.97*	-1.86	2.11	1.65	35.07**
$P_1 \times P_5$	58.56**	2.86*	28.74**	-30.45**	10.41**	71.18**
$P_1 \times P_6$	31.44**	7.47**	-2.85*	4.40**	2.46	36.71**
$P_2 \times P_3$	30.92**	8.12**	7.95**	3.17*	3.59*	34.42**
$P_2 \times P_4$	49.68**	9.74**	12.61**	-2.72*	4.83**	55.45**
$P_2 \times P_5$	65.46**	10.34**	29.53**	-33.68**	10.49**	79.60**
$P_2 \times P_6$	33.74**	14.45**	13.74**	2.66*	7.50**	37.15**
$P_3 \times P_4$	31.52**	8.48**	4.18**	6.76**	6.18**	35.27**
$P_3 \times P_5$	63.77**	9.25**	31.33**	-31.47**	10.22**	72.43**
$P_3 \times P_6$	30.47**	12.77**	13.79**	3.98**	12.63**	31.33**
$P_4 \times P_5$	67.51**	24.08**	32.13**	-28.84**	16.91**	82.69**
$P_4 \times P_6$	24.40**	16.94**	14.48**	5.41**	14.24**	38.28**
$P_5 \times P_6$	45.64**	15.52**	29.63**	-30.78**	14.55**	64.34**
LSD 5%	2.66	2.57	2.43	2.45	3.55	3.47
1%	3.51	3.38	3.20	3.23	4.67	4.57

*,**Significant at 5% and 1% levels of probability, respectively.

Concerning yield components, the crosses ($P_3 \times P_6$), ($P_4 \times P_5$) and ($P_4 \times P_6$) exhibited significant SCA effects for increasing all yield traits. These crosses involved at least one of its parents which is good general combiner for most yield components. However, the crosses ($P_1 \times P_5$) and ($P_2 \times P_5$), which resulted from two types of cross combinations (poor × poor) and (good × poor) general combiners, showed significant SCA effects for most yield components as, number of fruit per plant (No. F/P), fruit diameter (FD cm.), fruit weight (FW gm.) and fruit yield per plant (FY/P kg.).

It is interesting to noticed that the best cross combinations were obtained from (good × good), (good × poor) and (poor × poor) general combiners. Therefore, it is not necessary that parents having estimates of GCA effects would also give high estimates of SCA effects in their respective cross combinations. It could be also observed that the promising crosses which exhibited desirable SCA effects showed as previously mentioned high heterosis values for studied traits, suggesting the important role of non- additive gene action in the inheritance of these traits.

Table 3: Combining ability analysis of variance for all studied traits from the combined data over two locations

S.V	DF	VLcm	No.L/P	LA cm²	D1ˢᵗ FF	D1ˢᵗ MF	D1ˢᵗ P
GCA	5	705.2**	74.85**	316.15**	31.97**	13.32**	48.72**
SCA	15	255.87**	37.05**	52.99**	25.57**	6.42**	22.69**
GCA × L	5	123.84**	15.34**	56.52**	11.36**	4.48**	13.22**
SCA × L	15	35.93**	6.29**	12.03**	8.08**	2.85*	6.29**
Error	80	2.28	1.98	2.06	1.12	1.27	1.07

Table 3: Cont.

S.V	DF	No.F/P	Flcm.	FDcm.	Fshl	FWgm.	F Y/Plg
GCA	5	51.04**	61.10**	50.22**	58.14**	333.09**	200.12**
SCA	15	18.68**	7.35**	4.00**	4.55**	52.82**	28.47**
GCA × L	5	9.90**	9.08**	7.68**	8.66**	34.44**	29.10**
SCA × L	15	5.34**	2.46*	1.81	2.06*	7.35**	6.68**
Error	80	1.23	1.15	1.02	1.05	2.19	2.08

*,**Significant at 5% and 1% levels of probability, respectively.

Table 4: Estimates of general combining ability effects (gi) of each parent for all studied traits from the combined data over two locations.

Parents	VLcm	No.L/P	LA cm²	D1ˢᵗ FF	D1ˢᵗ MF	D1ˢᵗ P
P₁	10.86**	4.31**	4.42**	-0.28	0.54	-0.44
P₂	-1.76**	0.46	0.74	0.39	1.21**	0.62
P₃	-0.74	0.54	1.96**	-2.47**	-1.74**	-2.72**
P₄	-4.14**	-0.97	4.82**	-1.12**	-0.98**	-01.13**
P₅	-3.81**	-3.78**	-8.35**	2.51**	1.63**	2.69**
P₆	-0.41	-0.56	-3.54**	0.97**	-0.66	0.98**
SE(gi)	0.49	0.45	0.46	0.34	0.36	0.33

Table 4: Cont.

Parents	No.F/P	Flcm.	FDcm.	Fshl	FWgm.	FY/Plg.
P₁	0.64	1.21**	1.12**	1.52**	-0.97*	1.34**
P₂	0.91*	0.96**	-1.24**	1.15**	-2.16**	0.82
P₃	1.49**	1.26**	-0.89**	1.22**	-2.13**	1.51**
P₄	0.96**	0.99**	-1.38**	1.54**	-0.87	1.29**
P₅	-2.61**	-5.31**	4.14**	-6.58**	7.49**	-2.79**
P₆	-1.39**	0.89**	-1.75**	1.1 6**	-1.36**	-2.17**
SE(gi)	0.36	0.34	0.32	0.33	0.48	0.46

*,**Significant at 5% and 1% levels of probability, respectively.

Table 5: Estimates of specific combining ability effects (Sᵢⱼ) of each cross for all studied traits from the combined data over two locations.

Crosses	VLcm	No.L/P	LA cm²	D1ˢᵗ FF	D1ˢᵗ MF	D1ˢᵗ P
P₁ × P₂	3.87**	3.74**	0.68	-3.82**	-2.94**	-4.26**
P₁ × P₃	-1.61	3.62**	2.71*	-0.94	0.78	-0.78
P₁ × P₄	2.01	0.76	0.48	-2.67**	0.69	-2.65**
P₁ × P₅	19.26**	7.98**	11.83**	-0.96	-2.89**	-1.42
P₁ × P₆	7.47**	2.52*	-2.21	-3.81**	0.48	-3.91**
P₂ × P₃	2.24	2.38**	4.63**	-1.32	0.93	-1.37
P₂ × P₄	-0.63	-2.57**	-2.25	-2.78**	0.75	-2.84**
P₂ × P₅	4.86**	0.34	-3.12*	-4.77**	-1.99*	-4.64**
P₂ × P₆	8.68**	3.96**	0.38	0.68	-1.28	1.11
P₃ × P₄	5.69**	3.78**	6.14**	-0.63	-0.51	-0.61
P₃ × P₅	0.47	-2.66**	4.46**	-4.93**	-2.66**	-4.99**
P₃ × P₆	-3.98**	-3.67**	-2.42	2.32*	0.85	2.52**
P₄ × P₅	4.21**	0.33	1.34	-3.88**	-2.94**	-4.24**
P₄ × P₆	2.88*	2.46*	0.83	2.91**	1.92	2.32**
P₅ × P₆	-1.31	0.77	4.47**	-1.68	-1.55	-1.28
SE(Sij)	1.34	1.25	1.27	0.94	0.99	0.92

*,**Significant at 5% and 1% levels of probability, respectively.

Table 5: Cont.

Crosses	No.F/P	Flcm.	FDcm.	Fshl	FWgm.	FY/Pkg.
$P_1 \times P_2$	1.23	1.96*	1.01	-0.96	0.63	2.52*
$P_1 \times P_3$	0.81	2.72**	-2.41**	2.61**	-0.78	-1.13
$P_1 \times P_4$	1.94*	-2.68*	-2.52**	1.92*	-2.74*	2.63*
$P_1 \times P_5$	3.36**	-2.90**	1.85**	-2.60**	4.52**	3.14**
$P_1 \times P_6$	2.54**	0.87	-2.68**	1.85*	-2.82*	2.74*
$P_2 \times P_3$	1.62	2.86**	-0.57	1.98*	0.51	2.66*
$P_2 \times P_4$	3.89**	2.65**	1.86*	-0.64	-0.47	2.74*
$P_2 \times P_5$	3.53**	0.56	2.36**	-3.31**	3.42**	3.54**
$P_2 \times P_6$	1.98*	2.73**	0.59	2.52**	1.61	2.81*
$P_3 \times P_4$	0.88	1.66	-1.77*	1.80*	0.79	2.55*
$P_3 \times P_5$	3.61**	0.49	3.52**	-2.48**	1.54	3.15**
$P_3 \times P_6$	2.69**	3.11**	1.99*	2.11*	4.56**	2.76*
$P_4 \times P_5$	3.36**	2.99**	3.12**	2.76**	6.25**	3.41**
$P_4 \times P_6$	2.74**	3.63**	2.42**	2.35**	6.29**	3.19**
$P_5 \times P_6$	1.23	0.67	2.37**	-2.62**	5.18**	2.80**
SE(Sij)	0.98	0.95	0.89	0.91	1.31	1.28

*,**Significant at 5% and 1% levels of probability, respectively.

Nature of gene action

Estimates of all types of gene action for all studied traits obtained from the combined data obtained over two locations are shown in Table 6. The results indicated that the magnitudes of non additive genetic variance ($\sigma^2 D$) were larger than those of additive ones ($\sigma^2 A$) for vegetative and earliness traits except for leaf area (LA cm^2). This finding could be emphasized by the ratio of $(\sigma^2 D/ \sigma^2 A)^{1/2}$ which was more than one for all vegetative and earliness traits except for leaf area (LA $cm.^2$), reflecting that non additive gene action was more pronounced in the inheritance of these traits. However, Abd El-Hadi et al (2005) noticed that additive genetic variances were important than those of non additive ones in the expression of vegetative and earliness traits. In contrast, the ratio of $(\sigma^2 D/ \sigma^2 A)^{1/2}$ for yield components was less than one except for number of fruits per plant (No. F/P), indicating that additive genetic variance played the important role in the inheritance of these traits. Similar results were obtained by El-Gendy (1999) and Sadek (2003).

Concerning the interactions, the magnitudes of $\sigma^2 AxL$ variance were less than those of $\sigma^2 DxL$ ones for all vegetative and earliness traits except for leaf area (LA $cm.^2$), verifying by the ratio of $(\sigma^2 DxL/ \sigma^2 AxL)^{1/2}$ which was more than one. This finding indicates that non additive gene action was more influenced by locations than additive one for these traits. On the other hand, the ratio of $(\sigma^2 DxL/ \sigma^2 AxL)^{1/2}$ for yield components was lower than one except for number of fruits per plant (No. F/P), suggesting that additive gene action interacts by locations more than non additive one for these traits.

Table 6: Estimates of genetic parameters for all studied traits from the combined data over two locations.

Genetic Parameters	VLcm	No.L/P	LA cm^2	D1stFF	D1stMF	D1stP
$\sigma^2 A$	45.18	3.59	27.33	6.24	0.66	2.39
$\sigma^2 D$	109.97	15.38	20.48	8.75	1.79	8.20
$\sigma^2 AxL$	21.98	2.26	11.12	0.82	0.41	1.73
$\sigma^2 DxL$	33.65	4.31	9.97	6.96	1.58	5.22
$\sigma^2 e$	2.28	1.98	2.06	1.12	1.27	1.07
$(\sigma^2 D / \sigma^2 A)^{1/2}$	2.43	4.28	0.75	1.40	2.71	3.43
$(\sigma^2 DxL / \sigma^2 AxL)^{1/2}$	1.53	1.91	0.89	8.48	3.85	3.02
$h^2_b\%$	72.82	68.93	67.38	62.74	42.91	56.90
$h^2_n\%$	21.21	13.04	38.51	26.12	11.56	12.84

Table 6: Cont.

Genetic Parameters	No.F/P	Flcm.	FDcm.	FshI	FWgm.	FY/Pkg
$\sigma^2 A$	3.48	5.89	5.02	5.86	31.65	18.65
$\sigma^2 D$	6.67	2.46	1.10	1.25	22.74	10.89
$\sigma^2 AxL$	1.14	1.66	1.47	1.65	6.77	5.61
$\sigma^2 DxL$	4.11	1.31	0.79	1.01	5.16	4.60
$\sigma^2 e$	1.23	1.15	1.02	1.05	2.19	2.08
$(\sigma^2 D / \sigma^2 A)^{1/2}$	1.92	0.42	0.22	021	0.72	0.58
$(\sigma^2 DxL / \sigma^2 AxL)^{1/2}$	3.61	0.79	0.54	0.61	0.76	0.82
$h^2_b\%$	61.03	66.96	65.11	65.71	79.39	70.62
$h^2_n\%$	20.93	47.23	53.40	54.16	46.20	44.59

Estimates of heritability

Estimates of broad and narrow sense heritability for all studied traits from the combined data obtained over two locations are found in Table 6. The results showed that the estimates of broad sense heritability ($h^2_b\%$) were larger than those of narrow sense heritability ($h^2_n\%$) for vegetative and earliness traits. The values of broad sense heritability for vegetative and earliness traits ranged from 42.91% to 72.82% for days to first male flower (D1st MF) and vein length (VLcm), respectively. While, the values of narrow sense heritability for the same traits ranged from 11.56% to 38.51% for days to first male flower (D1st MF) and leaf area (LA cm.^{2}), respectively. This finding reflects the presence of considerable heterosis values and suggested that non additive gene effects played the major role in the inheritance of these traits. These results were in agreement with those obtained by Khalaf Allah et al (2001) and El-Shimi et al (2003).

With regard to yield components, the broad sense heritability estimates were close to their corresponding narrow sense heritability for most of these traits. The results revealed that the lowest value of broad sense heritability was 61.03% for number of fruits per plant (No. F/P), while, the largest estimate was 79.39% for fruit weight (FW gm.). The estimates of narrow sense heritability ranged from 20.93% to 54.16% for number of fruits per plant (No.F/P) and fruit shape index (Fsh I), respectively. These results which were verified by the ratio of $(\sigma^2 D / \sigma^2 A)^{1/2}$ ensure the predominance of additive genetic variance in the inheritance of these traits except number of fruits per plant which appeared to be controlled by non additive gene action. Therefore, improving of squash yield components in this set of genetic materials could be possible through selection programs in segregated generations. Similar results were obtained by Samadia and Khandelwal (2002), Sadek (2003), Abd El-Hadi and El-Gendy (2004) and Abd El-Hadi et al (2004).

In conclusion, according to mean squares of genotypes × locations interaction (G × L), the studied genotypes seemed to be inconstant from location to another. It could be also observed that the promising crosses which exhibited desirable SCA effects showed high heterosis values for studied traits. The estimates of additive × location ($\sigma^2 AxL$) variance and non additive

× location ($\sigma^2 DxL$) variances showed that the magnitude of all types of gene action fluctuated from location to another. Therefore, selection program in segregated generations would be effective under more environments for improvement of squash economic traits.

REFERENCES

Abd El-Hadi, A. H. (1995): Nature of gene action and the performances of the hybrids among the new developed inbred lines of agoor (*Cucumis melo var. chate*, L.). Ph.D. Thesis, Fac. of Agric., Mansoura Univ.

Abd El-Hadi, A. H., A. M. El-Adl, M. S. Hamada and M. A. Abdein (2005): Manifestation of heterosis and genetic parameters associated with it for some vegetative and earliness traits in squash. J. Agric. Sci. Mansoura Univ., 30 (3): 1363 – 1379.

Abd El-Hadi, A. H and Soher. E. A. El-Gendy (2004): Effect of genotypes by locations interactions on economical traits in squash. J. Agric. Sci. Mansoura Univ., 29 (10): 5667 – 5687.

Abd El-Hadi, A. H., M. M. Zaghloul and A. H. Gabr (2004): Nature of gene action, heterosis and inbreeding depression of yield and yield component traits in squash (*Cucurbita pepo L*). Zagazig J. Agric. Res., 31 (6): 2707 – 2725.

Abd El-Maksoud, M. M., A. M. El-Adl, M. S. Hamada and M. S. Sadek (2003): Inheritance of some economical traits in squash (*Cucurbita pepo L*). J. Agric. Sci., Mansoura Univ., 28 (6): 4463 – 4474.

Cochran, W.G. and G.M. Cox (1957): Experimental designs. 2nd ed., John Wily Sons, New York, U. S. A.

Eberhart, S.A. and W.A. Russell (1966): Stability parameters for comparing varieties. Crop Sci., 6: 36 – 40.

El-Adl, A.M.; Z.A. Kosba; Z.M. El-Diasty and A. H. Abd El-Hadi (1996): Types of gene action associated with the performances of hybrids among newly developed inbred lines of agoor (*Cucumis melo var. chate*, L.). J. Agric. Sci., Mansoura Univ., 21 (8): 2821 – 2835.

El-Gendy, Soher, E. A. (1999): Estimates of genetic parameters in some squash hybrids through two mating designs. Ph. D. Thesis, Fac. Of Agric., Mansoura Univ.

El-Shimi, A.S.; S.A. Mohamedein and A.H. M. El-Fouly (2003): Inheritance of some economical traits in melon (*Cucumis melo, L.*). J. Agric. Sci., Mansoura Univ., 28 (6): 4907 – 4918.

Gabr, A.H. (2003): Nature of gene action and performances of hybrids in squash (*Cucurbita pepo, L.*). M. Sc. Thesis, Fac. of Agric., Mansoura Univ.

Ghai, T. R.; S. Jaswinder; S. K. Arora and J. Singh (1998): Heterosis studies for earliness and yield in summer squash (*Cucurbita pepo, L.*). Punjab Vegetable Grower, 33: 35 – 40.

Griffing, B. (1956): Concept of general and specific combining ability in relation to diallel crosses systems. Aust. J. Biol. Sci., 9: 463 – 493.

Kash, Kawther S. and Z. M. El-Diasty (1989): The importance of additive and non additive genetic variance estimated from diallel and factorial mating designs in squash (*Cucurbita pepo, L.*). I- Heterosis and types of gene action associated with it. J. Agric. Sci., Mansoura Univ., 14 (1): 222 - 232.

Kasrawi, M. A. (1994): Heterosis and reciprocal differences for quantitative traits in summer squash (*Cucurbita pepo L*). J. of Genetics & Breeding, 48 (4): 399 – 403.

Khalaf Allah, A.M.; M. N. Feleafel and G. A. El-Sharkawy (2001): The genetic behavior of some important characters of summer squash (*Cucurbita pepo, L.*) using a diallel cross system among seven inbred lines of "Eskandrani" cultivar. Minufyia J. Agric. Res. 26 (1): 143 – 155.

Korzeniewska, A. and K. Niemirowicz (1993): Combining ability and heterosis effect in winter squash. Genetica Polonica, 34 (3): 259 – 272.

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

Sadek, Mariam S.S. (2003): Inheritance of some economical traits in squash (*Cucurbita pepo L*). M. Sc. Thesis, Fac. of Agric., Mansoura Univ.

Samadia, D.K. and R.C. Khandelwal (2002): Combining ability in bottle gourd. Indian J. Hort., 59(4): 402 – 405.

الملخص العربى

دراسات وراثية على الصفات الاقتصادية لبعض هجن قرع الكوسة

جلال أحمد رزق الشربينى¹، أشرف حسين عبد الهادى²، سهير السيد عبده الجندى³

¹ قسم النبات الزراعي (وراثة) – كلية الزراعة بسوهاج – جامعة جنوب الوادي-مصر
² قسم الوراثة – كلية الزراعة – جامعة المنصورة – مصر.
³ معهد بحوث البساتين – محطة بحوث الخضر بالمنصورة – مركز البحوث الزراعية – مصر.

تم إجراء هذا البحث لدراسة قوة الهجين وفعل الجيني المتحكم في وراثة الصفات الاقتصادية في قرع الكوسة في موقعين مختلفين هما: مزرعة كلية الزراعة بسوهاج (ل₁)- جامعة جنوب الوادي، مزرعة كلية الزراعة (ل₂)- جامعة المنصورد. أستخدم في هذا البحث ستة أصناف مختلفة من قرع الكوسة وذلك باستخدام نظام التهجين النصف دائري للحصول على خمسة عشر هجن جيل أول.
ويمكن تلخيص أهم النتائج فيما يلي:

- أوضحت النتائج وجود اختلافات معنوية بين المواقع، التراكيب الوراثية، والتفاعل بين التراكيب الوراثية والموقع مما يدل على اختلاف سلوك التراكيب الوراثية من موقع لآخر.

- أعطت معظم الهجن قوة هجين عالية بالنسبة لمتوسط الأبوين لكل الصفات المدروسة، وأظهرت الهجن (P₃×P₂)، (P₅×P₁)، (P₅×P₃) أعلى قوة هجين لصفات التزهير. بينما أظهر الهجين (P₅×P₄) أعلى قوة هجين لصفات المحصول.

- أظهرت الآباء P₁,P₃,P₄ قدرة عامة عالية على التآلف لكل الصفات المدروسة.

- أظهرت الهجن (P₃×P₄)، (P₁×P₃)، (P₁×P₂)، (P₃×P₅)، (P₄×P₅) قدرة خاصة عالية على التآلف لصفات الخضرية، بينما أعطت الهجن (P₃×P₄)، (P₄×P₆)، (P₄×P₅)، (P₃×P₆) قدرة خاصة عالية على التآلف لصفات التزهير. بينما أظهرت الهجن (P₄×P₆) قدرة خاصة عالية على التآلف لصفات المحصول.

- كانت قيم التباين الوراثي غير المضيف (σ²D) أعلى من قيم التباين الوراثي المضيف (σ²A) لصفات التزهير وكذلك الصفات الخضرية فيما عدا صفة مساحة سطح الورقة. بينما كانت قيم التباين الوراثي المضيف (σ²A) أعلى من قيم التباين الوراثي غير المضيف (σ²D) لصفات مكونات المحصول فيما عدا صفة عدد الثمار للنبات الواحد.

- أوضحت أن قيم التفاعل بين التباين الوراثي غير المضيف والموقع (σ²DxL) أعلى من قيم التفاعل بين التباين المضيف والموقع (σ²AxL) للصفات الخضرية والتزهير فيما عدا صفة مساحة سطح الورقة. وهذا يدل على أن التباين الوراثي غير المضيف أكثر تأثرا بالبيئة عن التباين الوراثي المضيف لهذه الصفات. وعلى العكس من ذلك كانت قيم التفاعل بين التباين المضيف والموقع (σ²AxL) أعلى من قيم التفاعل بين التباين الوراثي غير المضيف والموقع (σ²DxL) لمكونات المحصول، مما يدل على أن التباين الوراثي المضيف أكثر تأثرا بالبيئة عن التباين الوراثي غير المضيف لمكونات المحصول.

- كانت قيم معامل التوريث في المدى الواسع أعلى من مثيلاتها في المدى الضيق. وتتراوح قيم معامل التوريث في المدى الضيق في الصفات الخضرية والتزهير من ١١,٥٦% إلى ٣٨,٥١% لصفات عدد الأيام حتى ظهور أول زهرة مذكرة، مساحة سطح الورقة على الترتيب. بينما تتراوح قيم معامل التوريث في المدى الضيق لصفات مكونات المحصول من ٢٠,٩٣% إلى ٥٤,١٦% لصفات عدد الثمار في النبات، ودليل شكل الثمرة على الترتيب.

- من خلال النتائج المتحصل عليها لقوة الهجين وطبيعة الفعل الجيني ومعامل التوريث، يمكن تحسين الصفات الاقتصادية في قرع الكوسة بالانتخاب في الأجيال الانعزالية المتقدمة للهجن المتفوقة تحت ظروف بيئية مختلفة.