

Journal of Plant Production

Journal homepage & Available online at: www.jpp.journals.ekb.eg

Production of Open Field New F₁ Hybrids Squash (*Cucurbita pepo* L.) under Egyptian Conditions

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ABSTRACT

This study was carried out in El-Gemmieza Agriculture Research Station, Agriculture Research Center, Horticulture Research Institute, El Gharbiah Governorate, Egypt, during two seasons 2020 and 2021. This study aimed to produce a new open field of F₁ squash hybrids under Egyptian conditions using 6 F₁ hybrids obtained from half diallel crosses. The results indicated that analysis of variance revealed highly significant for the mean squares of the parental lines for the studied traits. None of the F₁ hybrids had the highest values for all studied traits. Significant heterosis values versus mid and better parent were detected and showed highly significance for most studied traits. The values of SCA were larger than the corresponding values of GCA adverting pre-dominance of dominance gene effects with respect to most of studied traits. The best combiner parent was showed to have the significant positive magnitudes of GCA effects between P₁ and P₃ for most of studied traits. The best combinations for most of studied traits were observed in the following crosses; P₁ X P₃; P₁ X P₄ and P₃ X P₄, which had the highest values of SCA. Broad sense heritability was higher than their corresponding in narrow sense heritability for all traits. The results showed that the recorded magnitudes of heritability in broad sense ranged from 94.29 to 99.65 % for days to anthesis first female flower and number of leaves / plant, while heritability in narrow sense ranged from 8.20 to 50.10 % for plant length and average fruit weight respectively. From the previous results, it could be recommended that the integration of these parents in genetic enhancement of summer squash programme directing to increase yield and quality traits.

Keywords: Squash, heterosis, GCA and SCA, heritability, yield.



INTRODUCTION

Family gourd has varied around the world. A large number of genetic resources acclimatized to many various environmental and growing conditions can be found in different regions. Knowing the extant genetic variation between cucurbits is important to improve collection and conservation programme. Basic chromosomes number of the genus *Cucurbita pepo* is 20 ($2n = 40$) (Renner and Pandey, 2013). The availability of genetic resources facilitates was help to continuous efforts by vegetable breeders for improvement these traits in summer squash (Schaefer and Renner 2009; 2011). Therefore, vegetable breeders are working to create hybrids with higher yield, yield components and other desirable agronomic traits. As a result of the greater differences, summer squash shows many odds for the expansion of new and improved lines through hybridization of promise genes. *Cucurbits* breeders, utilizing the existing genetic variations to improvement the cucurbits genotypes in order to meet the needs of the growing population (Hussien, 2015). Genotype that owns a broad range of variation in economically important yield contributing characters has been used by the vegetable breeders to producing promise hybrids for the selection of optimal genotypes for every environmental condition. Several statistical factors such as hybrid vigour and gene action would be effective on increasing yield and its component. Fruit yield and their quality are considered to be complex quantitative traits because knowledge of factors responsible for high yield and its component has been opposite difficult (El - Sharkawy *et*

al., 2018). Hybrid vigour is the phenomenon by which hybrid, resulting from the crossing of two parental lines, is greater in vegetative growth, yield and quality than the means of these lines (Badr *et al.*, 2021). Recent studies have suggested the possibility of increasing the yield and quality through the production of new hybrids. Vegetable breeders should try development high yielding genotypes by crossing best general combiners for yield, quality and transgressive segregation should be selected from subsequent hybrids genotypes.

Also, diallel mating design is being used to regard specific and general combining ability of parents involved in crosses. With regard to, evaluation of genetic parameters, i.e. hybrid vigour, general and specific combining ability, allows inferences about the predominant gene effect. General combining ability is defined as a mean behavior of a parent in a series of hybrids, while specific combining ability indicates those cases where certain crosses are either poor or good than would be predicted as based on average mean behavior of other combinations (Sprague and Tatum, 1942). High values of general combining ability illustrated a greater proportion of additive genetic variance (Alabboud *et al.*, 2020). In the same time, specific combining ability referred to the good F₁ hybrid with high proportion of dominance gene effects (Esmaeili *et al.*, 2022). Diallel mating design supply useful genetic information, as general and specific combining ability, to devise devotes breeding and selection methods. Hussien (2015) witnessed that general combining ability effects for yield offers an important mean in selecting genotypes to

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DOI:10.21608/jpp.2022.164320.1173

develop high yielding hybrid combinations. Ene *et al.* (2019) and Selim (2019) noticed good specific combining ability effects were related with cross combination of parental lines, having at least one parent as a best general combiner for characters. In melon, Esmaeili *et al.* (2022) showed that the general combining ability effects (GCA) were significant for all parents in the studied characters. Also, the general combining ability effects was less than the specific combining ability effects (SCA) of yield/ plant, which indicates the additive and dominance actions of genes. The role of dominance effects of genes in controlling yield trait was greater than additive effects. In another study in melon, performed diallel analysis for yield and quality characters, reporting that number of fruits / plant, yield and its components were governed by additive and dominance gene actions. In the average fruit weight trait, the additive effect of genes played a major role (Barros *et al.*, 2011).

Heritability coefficients play a predictive part in breeding programme and understand that the breeding magnitudes of individuals are derivative from suitable analyses. It is the breeding magnitude, which detects how many of the phenotype would pass to the next generations. There is a direct relation among heritability and response to selection, which is pointing to as genetic advance. Heritability in broad and narrow sense determines combined for genetic progress are usually more available than heritability determines alone in determining the gain under selection. In addition, understanding genetic progress in conjunction with heritability is quite beneficial. A large heritability trait doesn't always imply a great genetic progress, in addition should be accompanied with substantial genetic progress. The expected genetic progress expressed as a percentage of the average illustrates the method of gene activation in the manifestation of a characteristic, which aids in the selection of a favorable breeding approach (Abo Sedera *et al.*, 2016). Recently, Esmaeili *et al.* (2022) noticed that high narrow sense heritability for the number of fruit / plant and total yield / plant, designated low environmental effect for characters and the important role of additive effects. Hence, the preparation of superior crosses using breeding programs based on progeny tests will be effective in improving the characters. The study was carried out using a diallel mating design between four genotypes of *Cucurbita pepo* L. to production of open field new F₁ hybrids squash (*Cucurbita pepo* L.) under Egyptian conditions.

MATERIALS AND METHODS

For this study, four *Cucurbita* genotypes beside the check variety (Sama hybrid) were used as the experimental material under field conditions in El-Gemmieza Agriculture Research Station, Agriculture Research Center, Horticulture Research Institute, El Gharbiah Governorate, Egypt, during two growing seasons 2020 and 2021. The field is located at Latitudes 30° 43' and 31° 47' Longitudes.

Plant material: the advance experimental line (P₁), (P₂), (P₃) and (P₄), these inbred lines segregated from open pollinated variety *Cucurbita pepo* L., landraces plants and commercial hybrids were collected from Some places from Egypt beside commercial check hybrid variety name Sama hybrid were used as parental lines for half a diallel mating design. The F₁ seeds from the 6 crosses were produced manually by hand pollination, ten seeds from each inbred line and their 6 F₁

hybrids were planted and grown to maturity. Fertilizer application and other agronomic activities were performed as recommended by El- Gemmieza Agriculture Research Station for squash production, using the Randomized Complete Block Design (RCBD), with three replications and ten plants per replication to estimate 11 treatments (four inbred lines + six F₁ hybrids + check hybrid (Sama hybrid)). Each plot was 5 meter in length and 1meter width. Thus, the dimension of each of the experimental fields (plot area) was 5 m²; the plants were spaced 0.30 m apart among plants within the same row. In the second year (2021), the seeds of both 6 hybrids and four parents beside the commercial check hybrid were planted. Observations were calculated on three randomly selected plants without border effect in all genotypes and chick hybrid variety. Observation was calculated on plant basis for all traits.

Traits estimated: Data were recorded for plant length (P.L. cm), number of leaves per plant (No.L./P.), days to anthesis first female flower (D.F.F.F. days). Fruit from plants in each replicates were randomly harvested for the traits measurement: number of fruits per plant (No. F. / P), early yield per plant (E.Y./ P.kg), fruit length (F.L. cm), average fruit weight (A. F. W. g); number of fruits per plot (No.F./Pt.) and total yield per plot (T.Y. / Pt. kg).

Data analysis: the analysis of variance for studied traits under the study was performed using the Co- Stat Statistical Software. The diallel crossed were analyses suggested by Griffings (1956), model I, method II.

The heterosis determination with respect to parent's mean was carried out using the formula $(F_1 - M.P) / M.P \times 100$, where F₁: first generation.

The heterosis determination with respect to best parents (B. P) mean was carried out using $B.P \% = (F_1 - B.P) / B. P \times 100$ formula.

Heterosis over the commercial check hybrid (C.H.) % = $(F_1 - C.H.) / C.H. \times 100$ formula

The t – test was used to estimate whether F₁ hybrids averages were statistically significant for M. P and B. P means as coined Fehr, 1987.

The general and specific combining ability were tested using the t – test Cochran and Cox (1950).

The relationship *GCA* / *SCA* was analyzed as indicative of the contribution of the additive (σ^2A) and dominance (non – additive) (σ^2D) actions for studied traits. σ^2A and σ^2D were recorded agreement Matzinger and Kempthorne (1956): $\sigma^2D = \sigma^2s$, $\sigma^2A = 2 \sigma^2g$.

Estimates of broad-sense ($h^2_{b,s}$) and narrow-sense ($h^2_{n,s}$) heritability were recorded according to the following equations:

$$h^2_{b,s} \% = \{ \sigma^2A + \sigma^2D / \sigma^2A + \sigma^2D + \sigma^2E \} \times 100.$$

$$h^2_{n,s} \% = \{ \sigma^2A / \sigma^2A + \sigma^2D + \sigma^2E \} \times 100.$$

RESULTS AND DISCUSSION

Variations play a major role in vegetable breeding, therefore mean squares and genetic parameter evaluates of 11 genotypes (four parents + six F₁ hybrids + check hybrid (Sama hybrid) accessions in the 2020 and 2021 seasons are showed in Table 1. Analysis of variance revealed the mean squares for the accessions were significantly or high significant for all genotypes for plant length; number of leaves / plant; days to anthesis first female flower; number of fruits / plant; early yield / plant; fruit length; average fruit weight;

number of fruits / plot and total yield / plot. Significant differences were noticed between crosses and lines, the observed genetic variability between the accessions were mostly contributed by the aforementioned traits which reported by El-Tahawey *et al.* (2015); Marxmathi *et al.* (2018) and Abd El-Hadi *et al.* (2020). Wide genetic variations between the accessions are required for effective selection

program (Abed *et al.*, 2020). Part of the genetic variance to its components could be made during the analysis of the partial diallel mating design. The obtained results were in agreement with Hussien (2015); Hussien and Hamed (2015); Mohamed (2016); Othman (2016); Restrepo (2018); Gad Allah (2019) and Badr *et al.* (2021).

Table 1. Analysis of variance and mean squares of all genotypes for all studied traits in squash.

S.O.V.	d.f	P.L. (cm)	No. L./ P	D.F.F.F. days	No.F./ P.	E.Y./P. (kg)	F. L. (cm)	A. F.W. (g)	No. F./ Pt	T.Y./Pt (kg)
Replication	2	2.03	4.63	0.30	21.43	1.30	0.43	1.90	15.70	1.30
Genotypes	9	454.70**	336.28**	12.39**	572.67**	20.99**	5.54**	1441.41**	5174.46**	298.93**
Error	18	5.26	1.67	0.60	8.47	0.74	0.29	26.20	44.55	2.89

P.L. (cm): plant length, No. L / P: number of leaves per plant, D. F. F. F. (days): days to anthesis first female flower, No. F. /P.: number of fruits per plant, E.Y.P.(kg): early yield per plant, F.L. (cm): fruit length, A. F. W. (g): average fruit weight, No. F. /Pt: number of fruits per plot and T.Y/Pt: Total yield per plot. **: significant at 0.01 levels of probability.

Mean performance of parental lines and F₁ hybrids:

The mean performances of all parents and their F₁ hybrids for aforementioned traits are listed in Table 2. The obtained results in reported that significant differences between the evaluated 11 genotypes for all the nine traits during 2020 and 2021. The results revealed that the obtained mean magnitudes illustrated that there was no single parent exceeded all the other parents for traits. Results showed that the parent P₄ was the lowest parent for all traits expect for plant length (cm), while the parental line P₁ showed the lowest values for plant length (cm). In the same table, P₁ was the largest parent for all studied traits expects for plant length and number of leaves / plant traits, also, P₂ and P₃ showed appeared to be the highest magnitude for plant length and number of leaves / plant traits, respectively. In the same table, the results recorded that the highest F₁ hybrids P₁ x P₃ for number of leaves /plant, days to anthesis first female flower,

number of fruits / plant and early yield / plant traits. In addition, the combination of P₁ x P₂ showed the highest means for average fruit weight, number of fruits /plot and total yield per plot traits, respectively. The results recorded that the means of F₁ hybrids ranged for plant length (35.67 to 62.67 cm); number of leaves/plant (33.33 to 55.33); days to anthesis first female flower (25.67 to 20.33 days); number of fruits / plant (76.00 to 99); early yield / plant (7.345 to 14.405 kg); fruit length (12.83 to 16.33 cm); average fruit weight (96.67 to 153.33 g); number of fruits / plot (275.67 to 333.33) and total yield / plot (28.85 to 51.10 kg). The obtained data indicated that the values of the means of the F₁ crosses were close to each other traits. These results were accordance to Marie *et al.* (2012), Hatem *et al.* (2013), Othman (2016), El-Sharkawy *et al.* (2018), El - Shoura *et al.* (2018) and Badami *et al.* (2020).

Table 2. Means of the four parental lines, their F₁ hybrid combinations and commercial check hybrid for all studied traits of summer squash.

Traits. Genotypes	P.L. (cm)	No. L./ P	D.F.F.F. days	No.F./ P.	E.Y./P. (kg)	F. L. (cm)	A.F.W. (g)	No. F. / Pt.	T.Y./Pt (kg)
Parents									
P ₁	30.67	31.67	20.67	68.00	9.025	15.00	132.67	247.33	32.815
P ₂	41.33	26.33	23.00	65.33	8.062	13.33	123.33	232.33	28.658
P ₃	37.33	32.33	23.33	65.33	8.319	13.33	127.33	233.33	29.717
P ₄	31.67	24.33	26.00	55.00	5.670	12.67	86.67	209.33	18.127
F ₁ hybrids									
P ₁ x P ₂	61.67	38.67	23.67	86.00	11.123	15.17	153.33	333.33	51.100
P ₁ x P ₃	59.67	55.33	20.33	99.33	14.405	15.33	150.00	317.33	47.600
P ₁ x P ₄	47.33	53.00	25.67	84.33	11.988	16.33	148.33	279.00	41.368
P ₂ x P ₃	41.67	36.33	21.33	88.33	11.930	13.67	135.00	309.00	41.727
P ₂ x P ₄	62.67	46.00	25.33	76.00	7.345	12.83	96.67	298.33	28.850
P ₃ x P ₄	35.67	33.33	22.67	88.00	11.17	14.67	126.67	275.67	34.925
Sama hybrid	56.67	41.00	19.00	75.00	10.008	15.67	133.33	240.00	32.03
LSD at 5 %	3.933	2.22	0.72	4.99	1.48	0.92	8.78	11.45	2.92
LSD at 1 %	5.388	3.04	0.99	6.84	2.02	1.26	12.03	15.69	3.99

P.L. (cm): plant length, No. L / P: number of leaves per plant, D. F. F. F. (days): days to anthesis first female flower, No. F. /P.: number of fruits per plant, E.Y.P.(kg): early yield per plant, F.L. (cm): fruit length, A. F. W. (g): average fruit weight, No. F. /Pt.: number of fruits per plot and T.Y/Pt.: Total yield per plot. **: significant at 0.01 levels of probability.

Heterosis:

Significant difference between means performance of each cross and its mid parents, which is an indicator for heterosis were estimated with respect all studied traits. Furthermore, types of heterosis estimates for plant length, number of leaves /plant, days to anthesis first female flower, number of fruits / plant, early yield / plant, fruit length, average fruit weight, number of fruits / plot and total yield / plot traits, respectively are presented in Table 3. Generally, heterosis mid parent estimates was higher than their

corresponding heterosis best parent estimates. Both positive and negative mid parents and best parents' heterosis were recorded for aforementioned traits. The obtained data illustrated the magnitudes of heterosis (hybrid vigour) over mid parents from six F₁ hybrids varied from 3.39% (P₃X P₄) to 75.5 % (P₁ X P₃) for plant length; 7.65 % (P₃ X P₄) to 89.29% (P₁ X P₄) for number of leaves / plant; - 8.11 % (P₃ X P₄) to 9.98 % (P₁ X P₄) for days to anthesis of first female flower (day); 26.31 % (P₂ X P₄) to 48.99 % (P₁ X P₃) for number of fruits / plant; 6.91 % (P₂ X P₄) to 66.15 % (P₁ X

P₃) for early yield per plant; - 1.31 % (P₂ X P₄) to 17.99 % (P₁ X P₄) for fruit length; -7.93 % (P₂ X P₄) to 35.25 % (P₁ X P₄) for average fruit weight; 22.19 % (P₁ X P₄) to 38.99 % (P₁ X P₂) for number of fruits / plot and 23.34 % (P₂ X P₄) to 66.23 % (P₁ X P₂) for total yield / plot. In the same table, the obtained results revealed that the magnitudes of heterosis over best parents from six F₁ hybrids ranged from - 4.45% (P₃ x P₄) to 59.85 (P₁ x P₃) for plant length; 3.09 % (P₃ X P₄) to 74.71% (P₂ X P₄) for number of leaves / plant; - 7.26 % (P₂ X P₃) to 24.19 % (P₁ X P₄) for days to anthesis of first female flower (day); 16.33 % (P₂ X P₄) to 46.07 % (P₁ X P₃) for number of fruits / plant; -11.71 % (P₂ X P₄) to 59.61 % (P₁ X P₃) for early yield /plant; -3.75 % (P₂ X P₄) to 10.05 % (P₃ X P₄) for fruit length; - 21.62% (P₂ X P₄) to 15.57 % (P₁ X P₂) for average fruit weight; 12.80 % (P₁ X P₄) to 34.77 % (P₁ X P₂) for number of fruits / plot and 0.67 % (P₂ X P₄) to 55.72 % (P₁ X P₂) for total yield / plot. Positive heterosis of total yield / plot might be the reflection of heterosis of number of fruits / plot while the negative heterosis was recorded from negative heterosis of days to anthesis of first female flower (day). The obtained results suggested the successive way to improve total yield per plot (T.Y./Pt.) of F₁ cross through average fruit weight (A.F.W.g) and number of fruits / plot (N.F./Pt). Esmaili *et al.* (2022) found that positive heterosis on these traits in many F₁ hybrids of melon. None of crosses exhibited high heterosis for traits, nevertheless largely significant and

favorable level of heterosis percentage versus mid parents (M.P) and best parents (B.P) was recorded in F₁ crosses for the variant traits in squash (Abd El-Hadi *et al.*, 2020). In addition, Saha *et al.*(2018) reported that a higher magnitude of heterosis was noticed for the number of fruits /plant, average fruit weight and total yield / plant in muskmelon. The obtained data showed that preponderance of non-additive (dominance) genetic variability in the expression of the nine traits under this study which displays best scope for the exploitation of heterosis in enhancing the productivity of squash plant. The obtained results in this study on the aforementioned traits were also given by Bayoumy *et al.* (2014), El - Sharkawy *et al.* (2018); Ene *et al.* (2019) and Selim (2019). The maximum significant desirable heterosis values versus mid-parent were 3.39 (P₃ X P₄), 89.29 (P₁ X P₄), -8.11 (P₃ X P₄), 48.99 (P₁ X P₃), 66.15 (P₁ X P₃), -1.31 (P₂ X P₄), 35.25 (P₁ X P₄), 38.99 (P₁ X P₂) and 66.23 (P₁ X P₂) for plant length, number of leaves / plant, days to anthesis first female flower, number of fruits / plant, early yield / plant, fruit length, average fruit weight, number of fruits / plot and total yield / plot traits respectively. Also, the heterosis versus better parent were recorded the following values-4.45 (P₃ X P₄), 74.71(P₂ X P₄), -7.26(P₂ X P₃), 46.07 (P₁ X P₃), 59.61 (P₁ X P₃), -3.75 (P₂ X P₄), 15.57 (P₁ X P₂), 34.77 (P₁ X P₂) and 55.72 (P₁ X P₂) for aforementioned traits.

Table 3. Estimations of heterosis percentage based on mid parents, better parent and over check hybrid of variables for F₁ hybrids of squash.

Traits. Genotypes	P.L. (cm)		No. L/P		D.F.F.F. (days)		No. F./P		E. Y./P.(kg)		F.L.(cm)		A.F.W.(g)		No. F./Pt.		T.Y./ Pt.(kg)	
	M.P	B.P	M.P	B.P	M.P	B.P	M.P	B.P	M.P	B.P	M.P	B.P	M.P	B.P	M.P	B.P	M.P	B.P
P ₁ x P ₂	71.31	49.21	33.34	22.10	8.38	14.51	28.99	26.47	30.25	23.25	7.06	1.33	19.79	15.57	38.99	34.77	66.23	55.72
Sama hybrid	8.82		-5.68		24.58		14.67		11.14		-3.19		15.00		38.89		59.54	
P ₁ x P ₃	75.50	59.85	72.91	71.14	-7.59	-1.64	48.99	46.07	66.15	59.61	8.19	2.20	15.38	13.06	32.04	28.30	52.22	45.06
Sama hybrid	5.29		34.95		7.00		32.44		43.93		-2.17		12.50		32.22		48.61	
P ₁ x P ₄	51.84	49.45	89.29	67.35	9.98	24.19	37.12	24.01	63.10	32.83	17.99	8.87	35.25	11.80	22.19	12.80	62.42	26.06
Sama hybrid	-16.48		29.27		35.11		12.44		19.78		4.21		11.25		16.25		29.15	
P ₂ x P ₃	5.95	0.82	23.87	12.37	-7.94	-7.26	35.21	35.21	45.67	43.41	2.55	2.55	7.72	6.02	32.71	32.43	42.95	27.16
Sama hybrid	-26.47		-11.39		12.26		17.77		19.20		-12.76		1.25		28.75		30.27	
P ₂ x P ₄	71.70	51.63	81.60	74.71	3.39	10.13	26.31	16.33	6.91	-11.71	-1.31	-3.75	-7.93	-21.62	35.00	28.29	23.34	0.67
Sama hybrid	10.59		12.20		33.32		1.33		-26.61		-18.12		-27.50		24.30		-9.93	
P ₃ x P ₄	3.39	-4.45	17.65	3.09	-8.11	-2.83	46.25	34.70	59.80	34.27	12.85	10.05	18.38	-0.52	24.55	18.15	46.01	17.53
Sama hybrid	-37.06		-18.71		19.31		17.33		11.61		-6.28		-5.00		14.86		9.04	
LSD at 5 %	3.40	3.93	1.94	2.21	1.15	1.32	4.44	5.13	1.27	1.47	0.80	0.92	7.60	8.78	9.91	11.44	2.52	2.91
LSD at 1 %	4.66	5.38	2.62	3.03	1.57	1.82	6.09	7.03	1.75	2.02	1.09	1.26	10.41	12.02	13.58	15.68	3.45	3.99

P.L. (cm): plant length, No. L / P: number of leaves per plant, No. F. / P.: number of fruits per plant, E.Y.P. (kg): early yield per plant, F.L. (cm): fruit length, A. F. W. (g): average fruit weight, No. F. /Pt: number of fruits per plot and T.Y/Pt.: total yield per plot.

Combining abilities analyses:

Analysis of variance and mean square for combining abilities of studied traits are listed in Table 5. The obtained data exhibited that the analysis of variance for general and specific combining ability effects were highly significant between crosses for aforementioned traits, indicating a wide range of variability between the genotypes. The obtained results indicate both specific and general combining ability played the greater role in determining the inheritance of the studied characters, showing that the highest part of the total genetic variation correlated with traits were a result of dominance gene effect. In this respect, many authors among them Selim (2019) and Esmaili *et al.* (2022) obtained similar results indicating the importance of GCA and SCA variances. Values of mean squares of general combining ability were higher than those of specific combining ability

for studied traits expect for plant length, number of leaves, number of fruits / plant and number of fruits / plot, respectively, it referred that the predominance of the additive gene action. Furthermore, Abd El-Hadi *et al.* (2014) and El- Sharkawy *et al.* (2018) found that the values of general combining ability were greater than those of specific combining ability for studies traits and indicating the importance of GCA variances in squash. Ene *et al.* (2019) in cucumber, observed that GCA was greater than SCA for yield and its components, suggesting that additive gene effect was most importance than dominance (non-additive) genetic variance one. Significant effects of GCA and SCA obtained in this study on the aforementioned studied traits were also reported by Bayoumy *et al.* (2014), Hussien (2015), Selim (2019) and Badami *et al.* (2020). GCA / SCA ratio is higher than one for studied traits

excluding plant length, number of leaves / plant, days to anthesis first female flower and number of fruits /plot, revealing the predominance of dominance gene effect in the

inheritance of aforementioned trait. This result agreement with Abd El-Hadi *et al.* (2020) and Esmaeili *et al.* (2022).

Table 5. The combining abilities analysis and the mean squares of F₁ hybrids for all studied traits of squash.

Traits. S.V	df	P.L. (cm)	No.L./ P.	D.F.F.F. days	No.F./ P	E.Y./P. (kg)	F.L. (cm)	A.F.W (g)	No. F. / Pt.	T.Y./Pt. (kg)
GCA	3	56.55**	41.91**	7.97**	87.64**	7.00**	2.49**	873.30**	769.09**	118.87**
SCA	6	199.08**	147.19**	2.21**	242.52**	6.99**	1.03**	284.06**	2202.68**	90.03**
GCA:SCA		0.28	0.28	3.61	0.36	1.00	2.42	3.07	0.35	1.32
Error	18	1.75	0.577	0.20	2.824	0.247	0.095	8.73	14.85	0.96

P.L. (cm): plant length, No. L / P: number of leaves per plant, D. F. F. F. (days): days to anthesis first female flower, No. F./P.: number of fruits per plant, E.Y.P. (kg): early yield per plant, F.L. (cm): fruit length, A. F. W. (g): average fruit weight, No. F. /Pt: number of fruits per plot and T.Y/Pt: Total yield per plot. **: significant at 0.01 levels of probability.

General combining ability effects:

Estimates of GCA effects of each parental line for traits listed in Table 6. GCA effects (*gi*) were positive and significant for the parent (P₄) for all characters. However, the parent (P₁) was best general combiner for studied traits. While, the parent (P₂) was good general combiner for plant length (cm) and number of fruits /plot traits. On the other hand, the parent (P₃) was good general combiner for number of fruits / plant, early yield / plant, average fruit weight (g) and

total yield / plot traits. Also, parent (P₄) was best general combiner for days to anthesis first female flower trait. In general, the obtained results exhibited the parent (P₁) was the good general combiners for all traits under the study. It could be proposed that these genotypes own favorable genes to improve F₁ crosses for traits under this study. This is in accordance to (Al – Ballat, 2008; Hatem *et al.*, 2014; Ene *et al.*, 2019; Esmaeili *et al.*, 2022).

Table 6. Estimation of GCA and SCA effects of parents and their F₁ hybrids for all studied traits of squash.

Traits. Genotypes	P. L. (cm)	No.L/ P.	No. F./ P	D.F.F.F. days	E.Y./P. (kg)	F.L. (cm)	A.F.W (g)	No. F. / Pt.	T.Y./Pt. (kg)
GCA									
P ₁	0.86*	3.62**	2.97**	-0.832**	1.01**	0.94**	12.84**	9.47**	4.71**
P ₂	3.97**	-2.50**	-1.14**	0.055	-0.50**	-0.47**	-1.39	6.31**	0.26
P ₃	-2.20*	0.17	3.08**	-0.835**	0.77**	-0.14	4.39**	0.20	1.04**
P ₄	-2.64**	-1.28**	-4.92**	1.612**	-1.28**	-0.33**	-15.83**	-15.97**	-6.01**
SE(<i>gi</i>)	0.468	0.264	0.594	0.158	0.176	0.109	1.01	1.362	0.347
SE(<i>gi – gj</i>)	0.764	0.431	0.970	0.258	0.287	0.178	1.71	2.225	0.567
SCA									
P ₁ x P ₂	11.87**	-0.18	6.60**	1.25**	0.71**	0.47**	13.88**	44.06**	10.64**
P ₁ x P ₃	16.04**	13.83**	15.71**	-1.20**	2.73**	0.30**	4.78**	34.17**	6.36**
P ₁ x P ₄	4.14**	12.93**	8.71**	1.69**	2.36**	1.49**	23.33**	12.00**	7.18**
P ₂ x P ₃	-5.07**	0.93*	8.82**	-1.09**	1.76**	0.05	4.00**	29.00**	4.94**
P ₂ x P ₄	16.37**	12.05**	4.49**	0.47*	-0.78**	-0.60**	-14.11**	34.50**	0.89
P ₃ x P ₄	-3.46**	-3.29**	12.27**	-1.30**	1.75**	0.91**	10.11**	17.95**	4.41**
SE (<i>sii</i>)	1.133	0.639	1.439	0.383	0.423	0.264	2.53	3.300	0.840
SE (<i>sij</i>)	0.837	0.472	1.063	0.283	0.314	0.195	1.87	2.437	0.621

P.L. (cm): plant length, No. L / P: number of leaves per plant, D. F. F. F. (days): days to anthesis first female flower, No. F./P.: number of fruits per plant, E.Y.P. (kg): early yield per plant, F.L. (cm): fruit length, A. F. W. (g): average fruit weight, No. F. /Pt: number of fruits per plot and T.Y/Pt: Total yield per plot. GCA= general combining ability, SCA= specific combining ability * and ** Significant differences at 0.05 and 0.01 levels of probabilities.

Specific combining ability effects (S_{ij}):-

The data in the same table showed that mean performances of the most crosses, which were fluctuated between their parental lines for studied traits. The obtained results revealed that there was no specific parental line, which was superior for all studied traits. Estimates of specific combining ability revealed F₁ hybrid P₁ X P₃ had the largest positive estimated values of SCA for number of leaves /plant, number of fruits / plant and early yield / plant, while F₁ hybrid P₃ X P₄ and F₁ hybrid P₁ X P₃ reflected earliness of flowering, since they showed the highest suitable negative estimates for days to anthesis first female flower and early yield per plant, respectively. Whereas, F₁ hybrid P₁ x P₄ had the highest positive estimated values of SCA for fruit length (1.49) and fruit weight (23.33), The cross P₁X P₂ and P₁ X P₄ had the highest significant positive estimated magnitudes of SCA for number of fruits /plot and total yield /plot traits. It was recorded that the good cross combination in terms of SCA effects always involved one or both high general combiners

as parents. Most hybrids with high SCA effects included at least one of large general combining parents. However, the poor general combiner sometimes gave best cross combinations when they were crossed with highly general combiners. So, it is not essential that parents having evaluates of highly general combining ability effects (*gi*) would too gave high estimates of specific combining ability effects in their specific cross combination. Therefore, the obtained results propose the greater role of dominance gene effect in the inheritance of traits. Hatem (2009) in watermelon proposed that when parent with high GCA cross and other with low GCA, the poor parent could throw up favorable transgressive segregation giving rise to favorable population. This is only enabled if the additive genetic variance present in the best general combiner and the complementary epistasis effects show in the crosses act in a complementary method to maximize favorable plant attributes which could be exploited for farther breeding. Also, the results are in accordance to Esmaeili *et al.* (2022) they obtained hybrids of melon with

high SCA effects from parents having either high × low or high × high general combining ability effects. Hence, it cannot be generalized that the parental lines with high GCA effects could only produce best hybrids. These findings agreement with Aravindakumar *et al.* (2005); Hatem *et al.* (2014); Selim (2019) and Badami *et al.* (2020).

Types of gene effect and heritability:-

Estimates of the types of gene action and heritability are shown in Table 7. The types of gene effects (genetic parameters) were significantly, suggesting the magnitudes of both additive (σ^2A) and dominance (σ^2D) effects in the estimation of aforementioned traits. Obtained results revealed the non-additive genetic variance (σ^2D) and additive (σ^2A) were positive and large in magnitudes for traits. In addition, magnitudes of σ^2D were positive and larger than those of σ^2A for all traits expect for days to anthesis of first female flower, fruit weight and total yield per plot. The obtained results indicate that the dominance effects σ^2D play greater part in the manifestation of studied traits, meanwhile, additive effects σ^2A had a great part. The non-additive effects (σ^2D) showed higher than the additive effects (σ^2A) for studied traits excluding for days to anthesis of first female flower and average fruit weight, indicated that non-additive variance mainly controlled in these traits. With these respect, the obtained results inquiring the predominance of σ^2D in the inheritance of these aforementioned traits. Therefore, hybridization would be successful method for improving these traits. While, the other traits were controlled by additive variance. Therefore, selection would be successful method in improving days to anthesis of first female flower and fruit weight. Abd El-Hadi *et al.* (2020) reported that the σ^2D were the most major source of genetic variability. Degree of dominance which was larger than the one for traits expect for days to anthesis of first female flower (0.88) and fruit weight (0.98). Bayoumy *et al.* (2014) reported that additive variance played a greater role in the inheritance of these traits. These results reflected the over - dominance gene effect in the inheritance of traits, exhibiting the important role of dominance in genetic control of these traits. On the other side, degree of dominance was lower than one indicate that the partial dominance and the additive genetic effect played the

greater role in the inheritance of studied traits. These results were in accordance to Jat *et al.* (2017); Saha *et al.* (2018) and Ene *et al.* (2019).

Selim (2019) noticed that the characteristics that have a heritability of over 60% and controlled by additive effects, can play a major role in vegetable breeding programs. In addition, selection of favorable breeding methods for good exploitation of the potential of various agronomic traits in a plant depends on the type of gene action and heritability. The obtained results reported that the selection may be more efficient for improving characters of genotypes at early generations in melon. The results in agreement with those obtained by Abd El-Hadi and El-Gendy (2004), Saha *et al.* (2018) and Abd El-Hadi *et al.*(2020). With respect to broad sense heritability $h^2_{b.s.}\%$ and narrow sense heritability $h^2_{n.s.}\%$, the obtained results listed in Table 7 exhibited very high broad sense heritability (94%) and low heritability in narrow sense (8%). In addition, the estimates of heritability in broad sense ($h^2_{b.s.}\%$) showed larger in values than their corresponding estimates in narrow sense for traits. Low magnitude of the narrow sense heritability evaluates indicates the high involvement of the dominance gene action on the expression of this traits. Large heritability indicates few effect of the environment of the studied traits. Evaluates of $h^2_{n.s.}$ was found to be relatively moderate for average fruit weight (50.10) which reflecting the important role of additive gene actions in the inheritance of such trait. On the other hand, it was showed low heritability in narrow sense values of P.L. (8.40 %), No. L. / P.(8.56 %), D.F.F.F. (36.95 %), No. F./P. (10.44 %), E.Y./P. (24.35 %), F.L. (43.77 %), No. F. /Pt (10.24 %) and T.Y./Pt (9.64 %). The obtained results indicating the predominant of dominance gene action in the inheritance of these traits. However, magnitudes of the $h^2_{b.s}$ ranged from 94.29 to 99.65 % for days to anthesis first female flower and number of leaves / plant, respectively. On the other side, the magnitudes of heritability in narrow sense percentage $h^2_{n.s.}\%$ ranged from 8.40 to 50.10 % for plant length and average fruit weight, consequently. In this respect, many authors among them Saha *et al.* (2018), Ene (2019) and Abd El-Hadi *et al.* (2020).

Table 7. Estimation of genetic components and heritability for all studied traits.

Traits	P.L.	No.L/	No. F./	D.F.F.F.	E.Y./P.	F.L	A.F.W.	No.F./	T.Y./ Pt.
Genetic components	(cm)	P	P	days	(kg)	(cm)	(g)	Pt.	(kg)
σ^2A	18.26	13.78	28.27	2.59	2.25	0.80	288.19	251.42	9.61
σ^2D	197.33	146.63	239.69	2.01	6.75	0.93	278.33	2187.83	89.07
σ^2A / σ^2D	0.09	0.09	0.12	1.29	0.33	0.86	1.04	0.11	0.11
σ^2E	1.75	0.56	2.824	0.20	0.25	0.10	8.73	14.851	0.963
D. d	3.29	3.26	2.91	0.88	1.73	1.08	0.98	2.95	3.04
$h^2_{b.s.}\%$	99.19	99.65	98.96	94.29	97.33	94.79	98.48	99.39	99.03
$h^2_{n.s.}\%$	8.40	8.56	10.44	36.95	24.35	43.77	50.10	10.24	9.64

P.L. (cm): plant length, No. L / P: number of leaves per plant, D. F. F. F. (days): days to anthesis first female flower, No. F. /P.: number of fruits per plant, E.Y.P. (kg): early yield per plant, F.L. (cm): fruit length, A. F. W. (g): average fruit weight, No. F. /Pt.: number of fruits per plot and T.Y./Pt.: Total yield per plot.

CONCLUSION

The present study illustrated that heterosis breeding is the good possible breeding strategy for improvement fruit yield and its contributing traits in summer squash. In addition, the obtained results recorded that partial to over-dominance effects are involved in the inheritance of yield and other economically traits. P₁ and P₃ were noticed to be most promising because they produced the maximum of high-

yielding hybrids with favorable traits when crossed either between them or with other parents. None of the F₁ hybrids had the highest values for all studied traits, the highest F₁ hybrids P₁ X P₃ for number of leaves / plant, days to anthesis first female flower, number of fruits / plant and early yield per plant traits. While F₁ cross P₁ X P₂ showed the highest means for fruit weight, number of fruits / plot and total yield / plot traits, respectively. The inbred lines P₁, and P₃ had good

horticultural traits. They were the good and promising inbred lines. Furthermore, the highest SCA values were obtained by the following combinations; P₁ XP₃; P₁ X P₄ and P₃ X P₄ for most traits, which are the best and promising F₁ crosses. Heritability in broad sense ($h^2_{b.s.}\%$) were larger than their corresponding in narrow sense ($h^2_{n.s.}\%$) for all traits. So, it recommended that the vegetable breeder could be used these F₁ cross to improvement these traits in squash.

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إنتاج هجن جديدة من الكوسة للحقل المفتوح تحت الظروف المصرية

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الملخص

الهدف من هذه الدراسة هو إنتاج هجن جديدة وواحدة من الكوسة للحقل المفتوح تحت الظروف المصرية ، حيث تم التهجين بين أربعة سلالات من الكوسة عن طريق إستخدام نظام التزاوج النصف دائري لإنتاج ستة هجن وقد تم تقييم الآباء و الستة هجن والهجين التجارى (سما) فى تصميم قطاعات كاملة العشوائية فى ثلاث مكررات بمحطة البحوث الزراعية بالجميزة - معهد بحوث البساتين - مركز البحوث الزراعية وقد أشارت النتائج الى : لم يظهر أى هجين تفوق كامل فى قوة الهجين لجميع الصفات، ولكن وجد أن الهجين $P_1 \times P_2$ و $P_1 \times P_4$ قد أعطى أعلى قوة هجين لصفة المحصول الكلى سواء المحسوبة عن طريق متوسط الأبوين أو أحسن الآباء. وجدت إختلافات معنوية لكلاً من تباين القدرة العامة والخاصة على التآلف لكل الصفات. كذلك أشارت النتائج إلى أن الآباء P_1 ، P_3 كانت لهما قدرة عامة عالية على الخلط لصفة المحصول المبكر ومتوسط وزن الثمرة والمحصول الكلى. كان للهجين $(P_1 \times P_2)$ قدرة خاصة على الخلط لصفى عدد الثمار للقطعة التجريبية و المحصول الكلى، بينما كان للهجين $(P_1 \times P_4)$ قدرة خاصة على الخلط لصفة متوسط وزن الثمرة و الهجين $(P_3 \times P_4)$ قدرة خاصة على الخلط لصفة عدد الأيام حتى تفتح أول زهرة مؤنثة. كذلك أشارت النتائج إلى أن التباين الغير إضافى كان أعلى من التباين الإضافى لجميع الصفات ماعدا صفى عدد الأيام حتى تفتح أول زهرة مؤنثة ومتوسط وزن الثمرة. أن قيم معامل التوريث فى المدى الواسع كانت أكبر من نظيرتها فى المدى الضيق. لذلك أوصت النتائج المتحصل عليها على إدخال هذه الآباء فى برامج تربية الكوسة لزيادة المحصول والجودة فى الكوسة.