

GENETIC EVALUATION FOR SOME CHARACTERS IN SUMMER SQUASH (*Cucurbita pepo*, L.)

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ABSTRACT: *The experiments included in the present investigation were carried out during 2005 and 2006 seasons in Six squash (*Cucurbita pepo* L.) cultivars and breeding lines, viz., UR7-64 , UR33-A-4, Virginia Blanco, Alba , Ronde de Nice , Lungo di toscan, and breedig lines Esk₁ and Esk₂. On December under plastic house the crosses among these cultivars were made at suitable flowering stage in a diallel mating design excluding reciprocals, to produce the required F₁'s.*

All genotypes were evaluated in a field trials at Al-Dalgamoon village,, Kafr El-Zayat, El-Gharbia Governorate in the summer season of 2006, and obtained that general combining ability and specific combining ability were highly significant for all studied traits, except average seed weight which was insignificant.

Also indicated that the additive gene action was more important than non-additive gene action in the inheritance of most studied traits.

High heritability estimates in broad sense were detected for all studied traits, suggesting the importance of the genetic variance for inheritance of these traits. While, low estimates of heritability in narrow sense were observed for seed yield and in the other seed yield components.

Keywords: *Cucurbita pepo* L., General combining ability, Specific combining ability, Diallel, Heritability.

INTRODUCTION

Summer squash (*Cucurbita pepo* L) is one of the most important economic crops of the family Cucurbitaceae in Egypt. The constant and relatively high chromosome number ($2n = 40$) as well as the complex isozyme pattern suggest an allopolyploid origin for the genus (Singh, 1979) and (Kirkpatrick *et al*, 1985).

Unlike many vegetable crops cultivated in the United States, summer squash originated in the New World. It is found from the southern temperate zone of North America to the northern subtropical zone of South America. Squash was ranked the fourth crop among the world's most popular cucurbits (Robinson and Dicker-Walters 1997).

Many agronomic crops are grown for their seeds which are used for human consumption and animal feed. In contrast, the seeds of most horticultural crops are used mainly as reproductive material. Therefore, squash grown mainly for the consumption of their fruits, also furnish seeds that are used as a popular snack food and high quality oil source for reproduction (Paris, 2001).

The quality of edible squash seeds is determined mainly by seed size, with preference for large seeds, and by flavor and nutritional characteristics analyzed for the lipids and the proteins, as principle nutritive components (Mansour *et al.*, 1993).

The estimates of genetic variance and its components are of great importance as for the improvement of squash breeding programme.

If the estimates of genetic variance indicate that the additive genetic variance or general combining ability is the major importance the most effective breeding procedure will be the intra-population selection. While, hybrid program may be the appropriate choice if the non-additive or specific combining ability is the major component (Cocker ham, 1961).

The costs of hybrids production are very low when compared with that of the hybrid seed production from other vegetable crops (Metwally, 1985). (Metwally, 1985), El-Gendy (1999), Samadia and Khandelwal (2002) stated that both additive and non-additive genes played significant role in the inheritance of main stem length, number of leaves/plant and leaf area/plant and GCA : SCA. ratio was more than one.

The objectives of this study were: 1) Determining some genetic parameters controlling the economic traits in (*Cucurbita pepo*, L.) with focusing on seed yield and seed traits, 2) producing more superior hybrids of summer squash suitable for Egyptian conditions, 3) determining some useful genetic parameters such as general combining ability, specific combining ability, expected environmental variance, the mean degree of dominance, the ratio of dominant to recessive alleles and heritability.

MATERIALS AND METHODS

The experiments were carried out during 2005 and 2006 seasons to produce some promising hybrids of squash for seed production as well as to calculate some useful genetic parameters.

The genetic materials used in the present study included eight squash cultivars and breeding lines, viz., UR7-64 , UR33-A-4, Virginia Blanco, Alba , Ronde de Nice , Lungo di toscan, and breeding lines Esk₁ and Esk₂.

The eight cultivars were at a high degree of homozygosity since they were selfed for six successive generations to ensure the purity before initiating the study.

In 2005/2006 season, the parents were cultivated on December under plastic house, at flowering stage; crossing among these parents were made in a diallel mating design excluding reciprocals, to produce 28 F₁ crosses.

Genetic evaluation for some characters in summer squash.....

All the genotypes (8 parents and 28 F₁ crosses) were evaluated in trials at the Dalgamoon village, Kafr El-Zayat, El-Gharbia Governorate, Egypt in the summer season of 2006.

The experimental design used was a randomized complete blocks with four replications, each replicate contained 36 plots (8 parents and 28 F₁), the plot area was 5 m².

Seeds of the 36 genotypes were sown on 15th March 2006, the distance between plants was 40 cm apart (one plant per hill). The cultural practices were done as followed by local growers.

After 90 days from sowing, 10 plants from each plot were taken to measure some seed characters, i.e, Seed yield/ plant, average seed weight, average seed length (cm), average seed width (cm), Embryo percentage, and Protein percentage according to A.O.A.C (1995).

Statistical procedure used in the present investigation was done according to the analysis of variance for the randomized complete block design as outlined by Cochran and Cox,(1957). Duncan's multiple range tests were used for the comparison among genotypes means (Duncan, 1955.)

In order to estimate the different genetic parameters in terms of additive and non-additive genetic variances, (Table 1) the F₁ hybrids were analyzed according to the analysis of the half-diallel crosses mating systems as outlined by Griffing, (1956) method 2 model II.

Table 1: The form of analysis of variance of the diallel crosses mating design.

S.O.V.	D.f.	M.S.	E.M.S.
GCA	P-1	Mg	$\sigma^2 e + \sigma^2 s + (p+2) \sigma^2 g$
SCA	P(P-1)/2	Ms	$\sigma^2 e + \sigma^2 s$
Error	(r-1) (g-1)	Me	$\sigma^2 e$

r : Number of replications.

g : Number of genotypes.

P : Number of parents.

Mg: Mean Square of (GCA)

Ms: Mean Square of (SCA)

Me: Mean Square of error.

$$\sigma^2 g = \frac{1}{P+2} (Mg - Ms)$$

$$\sigma^2 A = 2\sigma^2 gca$$

$$\sigma^2 s = Ms - Me$$

$$\sigma^2 D = \sigma^2 sca$$

$$\sigma^2 e = Me$$

$$\sigma^2 e = \sigma^2 e$$

Hayman's approach

Estimation of genetic variance components:

The genetic parameters D, F, H₁, H₂, h² and E were calculated using Hayman (1954) formula, where:

1- The expected environmental variance which is the same as the observed one.

2- Additive genetic variance (D) = VoLo – E

3- Variation due to dominant effect of the genes,

$$(E) = ((Error S.S. + Rep.s.s.) / d.f.) / r$$

$$(H) = VoLo - 4WoLo + 4V_1L_1 - (3P-2) E/P.$$

4- Dominance variance adjusted for symmetric positive and negative gene distribution among parents, (H₂) = 4V₁L₁ - 4VoL₁ - 2E or = H₁ [1-(U-V)²]

When : H₁ = H₂ both gene frequencies are equal.

5- Dominance variance overall heterozygous loci

$$(h)^2 = 4(ML_1 - Ml_0)^2 - 4(P-1) E/P^2.$$

6- (F): is the covariance of additive and dominance gene effects which determines gene symmetry. When F is not significantly differed from zero, asymmetric gene distribution exists. Significant and positive refers to majority of dominant genes, while significant and negative value of F indicates the majority of recessive genes.

$$(F) = 2VoLo - 4WoLo_1 - 2(P-2) E/P.$$

Test of significance among parameters was made using the standard error estimation technique suggested by Hayman (1954).

Estimates of genetic ratios

The estimates of genetic variance were used to calculate the following components and ratios :

(H₁ /D)^{1/2} = the mean degree of dominance, when less than one expresses partial dominance, equal to one expresses complete dominance and greater than one expresses over- dominance.

(H₂/4H₁) = the proportion of genes with positive and negative effects in the parents. When positive and negative alleles are unequally among the parents, the ratio is lesser than its maximum value 0.25 and U= V = 0.50 at all loci, where U and V are the frequencies of positive and negative alleles in the parents, respectively.

(K_D/K_R) = (4DH₁)^{1/2} + F/ (4DH₁)^{1/2} - F = the proportion of both dominance and recessive genes in the parents.

h²/H₂ = the number of gene groups, which control the character and exhibit dominance.

Heritability estimates in both broad and narrow senses for all traits studied were obtained as described by (Mather and Jinks, 1982) as follows:

$$\text{Heritability in broad senses (h}_b\text{)} = \frac{1/2D + 1/2H_1 - 1/4H_2 - 1/2F}{1/2D + 1/2H_1 - 1/4H_2 - 1/2F + E} \times 100$$

$$\text{Heritability in narrow senses (h}_n\text{)} = \frac{1/2D + 1/2H_1 - 1/2H_2 - 1/2F}{1/2D + 1/2H_1 - 1/4H_2 - 1/2F + E} \times 100$$

RESULTS AND DISCUSSION

1-Combining ability:

a) Seed yield/plant (g)

Data presented in Table (2) show that both GCA and SCA mean squares were highly significant, indicating that both additive and non-additive genetic variances were important for inheritance of this trait. The ratio between GCA and SCA mean squares was more than one (1.384) indicating that the additive genetic variances played the major role in the inheritance of this trait. This is in agreement with Metwally *et al*, (1988) on squash who stated that both additive and non-additive genetic effects were important for seed yield and most other related traits.

The Esk₂ and Ronde de Nice parents showed the maximum values of GCA effects viz., 8.90 ± 1.165 and 4.64 ± 1.165 , respectively. The statistical analysis clearly indicate that these values were positive and highly significant in comparison with the other parents. It could be suggested that these two parents could be considered as good combiners for seed yield. The other parents which had negative values of GCA effects considered as poor combiners .

Regarding SCA effects, fourteen crosses had significant or highly significant positive values ranging from 17.59 ± 3.106 in cross Alba x Esk₁ to 6.59 ± 3.106 in cross UR33-A-4 x Ronde de Nice as shown in Table (3). These F₁ combinations could be considered the best ones in this trait.

Table 2 : Mean squares for general combining ability (GCA) and specific combining ability (SCA) for studied seed yield and its components traits of squash plants grown in the summer season of 2006.

protein%	Embryo weight %	seed width (mm)	seed length (mm)	seed weight (g)	seed yield/plant (g)	d.f	S.O.V
17.01**	17.654**	1.546**	5.782**	0.015	341.825**	7	G.C.A
8.00**	10.058**	0.470**	0.781**	0.005	246.935**	28	S.C.A
0.00	0.002	0.003	0.003	0.012	15.501	105	error
2.127	1.755	3.290	7.399	3.290	1.384		G.C.A/S.C.A

b) average seed weight (g)

Data presented in Table (2) indicate that both GCA and SCA mean squares were not significant , indicating that this trait greatly affected by the environmental conditions.

Data presented in Table (3) show that none of the parents gave significant positive GCA values. Regarding SCA effects, one cross (UR33-A-4 x Lungo di toscan) had significant positive value of 0.11 ± 0.087 .

Table 3: Estimates of general and specific combining ability effects for the studied seed yield and its components in the parents and F₁ crosses of squash plants grown in the summer season of 2006.

Genotype	seed yield/plant (g)	average seed weight (g)	Seed length (mm)	seed width (mm)	Embryo %	Protein %
GCA effects (gi)						
1-UR7-64	1.17	-0.07*	-1.12**	-0.73**	-0.51**	2.73**
2-UR33-A-4	1.93	0.02	-0.69**	0.17	-2.77**	-0.85**
3-Virginia Blanco	1.11	0.02	0.38*	0.19	1.20**	-0.33**
4-Alba	-9.94**	-0.03	-0.29*	-0.26	0.86**	0.82**
5-Ronde de Nice	4.64**	0.05	1.31**	0.52**	0.20**	-0.62**
6-Lungo di toscan	-5.14**	0.03	0.03	0.27	-0.63**	0.32**
7-Esk1	-2.66*	-0.03	-0.19	-0.26	1.31**	-0.65**
8-Esk2	8.90**	0.01	0.58**	0.09	0.34**	-1.42**
SCA effects (sij)						
1x2	-9.66**	0.04	1.49**	0.39	-0.37**	1.68**
1x3	16.84**	0.04	0.16	0.36	-3.41**	5.14**
1x4	17.56**	0.01	0.34	0.06	-3.38**	-4.82**
1x5	15.01**	0.00	0.24	0.04	-2.77**	-8.75**
1x6	13.61**	0.05	0.76*	0.54	5.41**	5.66**
1x7	1.16	0.01	-0.51	0.06	1.15**	-0.84**
1x8	2.77	-0.05	-0.29	-0.54	0.84**	-0.92**
2x3	15.17**	-0.18*	-0.01	-1.79**	1.60**	-0.63**
2x4	5.55	0.04	0.91*	0.41	0.36**	-0.96**
2x5	6.59*	0.06	0.56	0.64	0.94**	1.63**
2x6	12.47**	0.11*	0.09	1.14**	-7.98**	-2.51**
2x7	-0.61	0.04	-0.19	0.41	5.11**	-1.29**
2x8	-0.12	-0.07	0.54	-0.69	-4.00**	-0.94**
3x4	-4.90	0.09	0.34	0.89*	-2.16**	-1.43**
3x5	-7.41*	0.04	-0.01	0.36	0.40**	0.47**
3x6	-2.54	-0.09	-0.24	-0.89*	1.76**	-2.60**
3x7	-5.01	-0.04	-0.01	-0.36	-0.18**	-1.63**
3x8	16.28**	0.00	-0.04	0.04	0.09**	0.82**
4x5	10.47**	0.06	1.66**	0.56	3.19**	1.49**
4x6	5.11	0.03	0.19	0.31	-6.23**	1.32**
4x7	17.59**	-0.04	-0.09	-0.41	0.96**	-0.24**
4x8	7.53*	0.00	0.64	-0.01	1.07**	2.91**
5x6	13.36**	-0.07	0.09	-0.71	0.43**	0.14**
5x7	17.08**	0.03	0.06	0.31	-2.26**	2.71**
5x8	-6.57*	0.02	-0.21	0.21	0.51**	-1.79**
6x7	8.11**	0.08	1.34**	0.81*	1.62**	-0.59**
6x8	-3.45	0.05	0.56	0.46	2.59**	0.19**
7x8	1.22	0.05	0.79*	0.49	-3.05**	0.56**
S.E (GCA)	1.165	0.032	0.157	0.158	0.012	0.004
S.E (SCA)	3.106	0.087	0.417	0.421	0.032	0.010

*, ** significant at 0.05 and 0.01 levels of probability, respectively

Genetic evaluation for some characters in summer squash.....

c) Seed length (mm)

Data presented in Table (2) show that both GCA and SCA mean squares were highly significant, indicating that both additive and non-additive genetic variances were important for inheritance of this trait. The ratio between GCA and SCA mean squares was more than one (7.399) indicating that the additive genetic variances played the major role in the inheritance of this trait.

Data presented in Table (3) show that only Ronde de Nice, Esk₂ and Virginia Blanco parents reflected highly significant with positive values of GCA effects (1.31 ± 0.157 , 0.58 ± 0.157 and 0.38 ± 0.157), respectively. Therefore, these three parents could be considered as good combiners for breeding to high seed length, the other parents which had negative values of SCA effects were poor combiners.

Regarding SCA effects, six crosses had significant or highly significant positive values ranging from 1.66 ± 0.417 in the cross Alba x Ronde de Nice to 0.76 ± 0.417 in the cross UR7-64 x Lungo di toscan.

d) Seed width (mm)

Both GCA and SCA mean squares were highly significant, as shown in Table (2), indicating that both additive and non-additive genetic variances were important for inheritance of this trait. The GCA and SCA mean squares ratio was more than one (3.290) indicating that the additive genetic variances played the major role in the inheritance of this trait.

Data presented in Table (3) show that the Ronde de Nice cv. reflected in highly significant positive values of GCA effects with a value of 0.52 ± 0.158 . It could be suggested that these parent could be considered as good combiner for seed width, the other parents which had negative values were poor combiners.

Regarding SCA effects, three crosses had significant or highly significant positive values ranging from 1.14 ± 0.421 in cross UR33-A-4 x Lungo di toscan to 0.81 ± 0.421 in cross Lungo di toscan x Esk₁. Indicating that these crosses are the best in this respect.

e) Embryo percentage

Data presented in Table (2) show that both GCA and SCA mean squares were highly significant, indicating that both additive and non-additive genetic variances were important for inheritance of this trait . The ratio between GCA and SCA mean squares was more than one (1.755) indicating that the additive genetic variances played the major role in the inheritance of this trait.

Data presented in Table (3) show that the parents Esk₁, Virginia Blanco, Alba, Esk₂, and Ronde de Nice cultivars reflected highly significant positive GCA values effects and the parent Esk₁ could be considered as the best

combiners for seed embryo%, the other parents which had negative values were poor combiners.

Regarding SCA effects, seventeen crosses had significant or highly significant positive effects these values ranging from 5.41 ± 0.032 in cross UR7-64 x Lungo di toscan to 0.09 ± 0.032 in cross Virginia Blanco x Esk₂. These crossed could be considered as the best combination for this trait.

f) Protein percentage

Both GCA and SCA mean squares were highly significant, indicating that both additive and non-additive genetic variances were important for inheritance of this trait. The GCA/SCA mean squares ratio was more than one (2.127), indicating that the additive genetic variances played the major role in the inheritance of this trait (Table, 2).

Data presented in Table (3) show that UR7-64, Alba and Lungo di toscan cultivars reflected highly significant positive values of GCA effects with a value of 2.73 ± 0.004 , 0.82 ± 0.004 and 0.32 ± 0.004 respectively, so it could be suggested that these three parents could be considered as good combiners for breeding to high protein percentage.

Regarding SCA effects, thirteen crosses had highly significant positive values ranging from 5.14 ± 0.010 in cross UR7-64 x Virginia Blanco to 0.19 ± 0.010 in cross Lungo di toscan x Esk₂.

2-Genetic parameters

The additive genetic variance (D) was highly significant. As shown in Table (4) Also, the dominance genetic variances (H_1) and (H_2) were highly significant. It is clear that both additive and dominance genetic variances were important in the inheritance of seed yield of summer squash crop. Comparing between the magnitude of additive and dominance values, it could be concluded that the dominance effects for this trait were more important than the additive ones. Therefore, producing superior hybrids of summer squash for seed production is the best way to maximized seed yield. These results are in agreement with those of Metwally *et al*, (1988).

The (F) value was highly significant and positive. This indicate that the dominance genes were more frequent in the parental lines and the majority is for the dominant genes.

The (h^2) value was highly significant and positive for seed yield (Table 4). This indicate that dominance variance over all the heterozygous loci is important in the inheritance of this character.

The mean degree of dominance ($(H_1/D)^{1/2}$) exceeded the unity, indicating over dominance for seed yield. The proportion of genes with positive and negative effects ($H_2/4H_1$) in the parent was nearly to one quarter, indicating that the positive and negative alleles controlled seed yield had nearly equal distributed among the parents. The ratio of dominant to recessive genes (K_D/K_R) was found to be greater than unity.

Genetic evaluation for some characters in summer squash.....

This confirm the existence of more dominant genes than recessive ones in the parents.

The additive genetic variance (D) was highly significant for average seed length. However, it was significant for average seed width. The additive genetic variances (D) at the remaining seed yield components, i.e; average seed weight, embryo percent to the whole seed and protein percentage in the seeds were not significant (Table 4).

The dominance genetic variances (H_1) and (H_2) were significant or highly significant for average seed weight, length, embryo percentage and protein percentage in the seeds. However, it was insignificant for average seed width. Comparing between the magnitude of additive and dominance values for seed yield components, it could be concluded that each of additive and dominance effects were important in the inheritance of average seed length. However, the additive effect plays the major role in the inheritance of average seed width. While, dominance effects plays the major role in the inheritance of average seed weight, embryo percentage and protein percentage in the seeds.

The (F) value was highly significant and positive for average seed length, indicating that the dominance genes were more frequent in the parental lines and the majority is for the dominant genes. On the other hand, the (F) values were insignificant for the rest seed yield components. The insignificant values of (F) for these traits might indicate that there is a symmetric gene distribution or the equality in the relative frequencies of dominant and recessive genes in the parents.

The (h^2) values were significant or highly significant and positive for average seed weight, length and width. This indicates that dominance variance over all the heterozygous loci is important in the inheritance of these traits. However, (h^2) parameter was insignificant for both embryo percentage and protein percentage. This indicates that dominance variance over all the heterozygous loci is not important in the inheritance of these two traits.

The average degree of dominance $(H_1/D)^{1/2}$ was found to be greater than unity for average seed weight, embryo percentage and protein percentage in the seeds, indicating over dominance. However, the mean degree of dominance $(H_1/D)^{1/2}$ did not exceed the unity and showed complete dominance for average seed length.

Values of $(H_2/4H_1)$ were not close enough from one quarter proportion in all seed yield components under study, indicating unequal distribution between the positive and negative alleles among the parents.

Estimates of the ratio of dominant to recessive alleles in the parents (K_D/K_R) were found to be more than unity for all seed yield components, confirming the existence of more dominant genes than recessive ones in the parents.

High heritability estimates in broad sense were detected for all studied traits, suggesting the importance of the genetic variance in the inheritance of these traits. While, low estimates of heritability in narrow sense were observed for the seed yield and in the other seed yield components.

Table (4): The estimates of genetic components of variation and their portions for Seed yield and it's components.

Parameter	Seed yield /plant (g)	Average seed weight (g)	Seed length (mm)	Seed width (mm)	Embryo%	protein%
D	287.71** ± 46.685	0.014± 0.013	3.532 ** ± 0.214	0.961** ± 0.294	6.849 ± 6.205	9.63 ± 7.097
F	249.37** ± 55.151	0.003± 0.016	2.116 ** ± 0.253	0.741* ± 0.347	3.020 ± 7.330	6.26 ± 8.384
H ₁	710.09** ± 107.320	0.103** ± 0.030	2.979 ** ± 0.492	1.991* ± 0.675	41.451** ± 14.264	33.94* ± 16.315
H ₂	641.00** ± 93.370	0.090** ± 0.026	2.241** ± 0.428	1.601* ± 0.587	37.345** ± 12.410	30.53* ± 14.195
E	15.35 ± 15.562	0.012** ± 0.004	0.003** ± 0.071	0.003** ± 0.098	0.002 ± 2.068	0.00** ± 2.366
h ²	2228.13** ± 62.619	0.171** ± 0.018	4.581 ** ± 0.287	0.907* ± 0.394	9.755 ± 8.323	0.82 ± 9.520
(H ₁ /D) ^{1/2}	1.57	2.695	0.918	1.439	2.460	1.88
H ₂ /4H ₁	0.23	0.220	0.188	0.201	0.225	0.22
K _D /K _R	1.76	1.080	1.968	1.732	1.197	1.42
h ² (n.s)	0.23	0.255	0.656	0.430	0.298	0.31
h ² (b.s)	0.93	0.741	0.998	0.996	1.000	1.000

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

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Genetic evaluation for some characters in summer squash.....

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تقدير بعض الثوابت الوراثية لبعض صفات قرع الكوسة

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الملخص العربي

استخدم في هذه الدراسة ثمانية أصناف وسلالات من قرع الكوسة تتبع النوع

Cucurbita pepo L. وهذه الأصناف هي

UR7-64, UR33-A-4, Virginia Blanco, Alba, Ronde de Nice, Lungo di toscan, Inbred line (1) from Eskandranii cultivar, and Inbred line (2) from Eskandranii cultivar

وتم زراعة الآباء في موسم ٢٠٠٥ و إجراء التهجينات فيما بينها في اتجاه واحد فقط وذلك للحصول على بذور الجيل الأول الهجين اللازمة للدراسة (تحت الصوبة البلاستيكية) تم تقسيم هذه التراكيب الوراثية (٣٦) تركيباً وراثياً هي عبارة عن الثمانية آباء مع الـ ٢٨ هجين المتحصل عليها في تجربة حقلية بقرية الدلجمون مركز كفر الزيات في الموسم الصيفي لعام ٢٠٠٦ مصممة بطريقة القطاعات الكاملة العشوائية. تم تسجيل القياسات على ستة صفات هي: كمية محصول البذرة/ نبات متوسط وزن البذرة ، طول البذرة، عرض البذرة، نسبة وزن الجنين الى وزن البذرة، ونسبة البروتين بالبذرة. وتم حساب المتوسطات لكل صفة على حدة ولكل تركيب وراثي وتم تحليل النتائج بالطرق الاحصائية المناسبة - واجريت القياسات الوراثية او البيومترية المطلوبة. ويمكن تلخيص أهم النتائج في الآتي: كانت قيم القدرة العامة والقدرة الخاصة على التآلف عالية المعنوية لمعظم الصفات تحت الدراسة إلا أن قيم القدرة العامة و القدرة الخاصة على التآلف كانت غير معنوية لصفة وزن البذرة. وأوضحت قيم القدرة العامة والخاصة على التآلف أهمية الفعل المضيف للجنين عن الفعل غير المضيف في توريث معظم الصفات التي درست. ويشير ذلك الى فعالية الانتخاب في تحسين هذه الصفات.

كانت قيم درجة التوريث بمعناها الواسع مرتفعة في جميع الصفات المدروسة، بينما كانت قيم درجة التوريث بمعناها الضيق مرتفعة في صفات محصول البذور ومكوناته. ويعنى ذلك إمكانية تحسين الصفات التي درست عن طريق التحسين الوراثي.