

# GENERAL PERFORMANCE, COMBINING ABILITIES, AND HERITABILITY OF YIELD AND YIELD COMPONENT TRAITS IN PUMPKIN (*Cucurbita moschata* Poir.) AT DIFFERENT CONDITIONS

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## Abstract

Complete diallel cross  $4 \times 4$  of pumpkin was evaluated with their parents for evaluate the genetic behavior of yield and yield component traits at two locations in Egypt. Four different pumpkin varieties belong to the species (*Cucurbita moschata* Poir.) were selected to use in this study. The parents Bugle Pumpkin and Long Island Cheese Pumpkin gave good combinations with the other parental lines to produce the highest  $F_1$  hybrid and the two hybrids (Bugle Pumpkin  $\times$  Long Island Cheese Pumpkin) and (Long Island Cheese Pumpkin  $\times$  Bugle Pumpkin) appeared the highest values in most studied traits.

The present investigation included the estimation of general combining ability, specific combining ability, genetic parameters and heritability in both broad and narrow senses. The estimation of genetic parameters showed that the additive genetic variance was very important for the most studied traits. The results showed that both additive and non-additive genetic gene were positive for all studied yield and yield component traits except additive genetic variance for fruit diameter (F.D.cm), weight of fruit (W.F.g), flesh thickness (F.T.cm) and seeds weight (S.W.gm). In addition, the estimates of heritability in broad sense were larger in magnitudes than their corresponding values in narrow sense. Heritability in broad sense ranged from 99.224 to 99.762% for fruit length (F.L.cm) and fruit diameter (F.D.cm) for the combined data. In the same time, the highest value of  $h^2_n$  were 57.196% for the combined data for fruit shape index (F.Sh.I.) trait.

**Keywords:** Pumpkin, diallel, combining abilities, genetic parameters and heritability.

## Introduction

The family of Cucurbitaceae is one of the most important botanical families for human including favorable and common vegetable crops. Pumpkin ( $n=20$ ) has a wide range of variability in shape and color it was a member of Cucurbitaceae family as well as squash, cucumber and melons. Most of them are vines. Pumpkin breeding involves the hybridization.

The gab of this study, it would be very useful to study the magnitudes of variation in nature of gene action among some selected varieties of pumpkin which are used in this study.

The manifestations of nature of gene action, genetic parameters and heritability were studied in pumpkin by many authors among them ([5], [17], [10], [1] and [9]).

[5] determined the heritability of some characters related to fruit yield and quality in *Cucurbita moschata*, using a  $7 \times 7$  half-diallel cross. Heritability was the highest for beta carotene (98.6%), followed by those for seed size index (SI; length  $\times$  breadth; 89.5%) and fruit weight (82.9%).

Nine agronomic characters in pumpkin were studied by [17] in diallel crosses of ten lines. Specific combining ability variance exceeded that of GCA in all characters, except vine length. The results concluded that the superior performance of hybrids with high SCA was due to epistasis effects. The cross S93  $\times$  Cm12 had the greatest SCA for yield/plant and the second greatest SCA for fruit number/plant and fruit weight. In another study, [10] studied GCA and SCA in *Cucurbita maxima* hybrids. They recorded high GCA estimates for all yield component traits while significant SCA was noted for fruits yield only.

[1] investigated the hybridization on pumpkin (*Cucurbita moschata*) and cleared the narrow sense heritability estimates were 29.36 and 38.81% for fruit weight and fruit shape index, respectively. They also added that the broad sense heritability estimates were 62.66 and 67.16% for the same traits, respectively. [7] in melon found that additive gene effects were most important with respect to average weight per fruit and yield, while genetic dominance effects were also important yield. Nahavand and Tashkandi as parents had significant positive general combining ability effects for yield and acceptable yield. [3] in summer squash found high heritability estimates in broad sense were detected for all studied yield traits. Heritability in narrow sense were obtained for total yield as number or weight of fruits/plot and all fruit traits, while the estimates in narrow sense were low for weight of fruits/plot. [6] found additive and non-additive gene effects were important in the expression of parthenocarpy and resistance to PRSV-W in summer squash. [9] found in *Cucurbita moschata* a high heritability coupled with high genetic advance found in parents and hybrids for number of fruits per plant, individual fruit weight and fruit yield suggested that improvement would be effective through phenotypic selection. [14], in ridge gourd [*Luffa acutangula* (Roxb.) L.] studied 28 genotypes, including 7 parental lines and 21 crosses, GCA and SCA for yield and antioxidants indicate the existence of abundant genetic variation. The cross combinations with superior per se performance coupled with high SCA estimates and having at least one hermaphrodite parent would be useful for concentrating desirable alleles to improve the antioxidants and yield simultaneously. Recently, [15] in butternut squash studied the predominance of

additive gene action over the dominance type for the traits under study suggested that a recurrent selection program could serve as a strategy to increase the frequencies of genes that promote the expression of traits associated with seed production and starch content in butternut squash.

The main objectives of the present investigation included the estimation of general combining ability (GCA) and specific combining ability (SCA), genetic parameters and heritability in both broad and narrow senses.

It is hoped that the obtained results from the study reported herein would throw some more light on the potentiality of the studied cultivars in producing superior hybrids and facilitate for the various genetics parameters involved in determining the general performance of pumpkin hybrid cultivar.

## Materials and Methods

### Genetic materials

Four different genetic parental varieties from different countries including were Butternut Pumpkin ( $P_1$ ) from Egypt; Queensland Blue Pumpkin ( $P_2$ ) from USA; Bugle Pumpkin ( $P_3$ ) from India and Long Island Cheese Pumpkin ( $P_4$ ) from Pakistan were used in (Table 1). All this experiment possible combinations 12  $F_1$  hybrids were made through diallel crosses mating design. The produced hybrids and their symbols are shown in Table 2.

**Table 1 Names, genetic resources and characteristics of four pumpkin genotypes parental**

Genotypes	Symbol	Source	Skin color	Fruit flesh color	Fruit size
Butternut Pumpkin	$P_1$	Egypt	Light Copper	Light yellow	Small (< 2kg)
Queensland Blue Pumpkin	$P_2$	USA	Green	Light yellow	Medium (2-4kg)
Bugle Pumpkin	$P_3$	India	Dark Copper	Deep Orange	Large (> 4kg)
Long Island Cheese Pumpkin	$P_4$	Pakistan	Light Orange	Deep Orange	Large (> 4kg)

**Table 2 Diallel crosses among four parental lines from different genetic resources, the produced 12 hybrids and their symbols**

F <sub>1</sub> hybrids			
No.	Symbol	Female	Male
1	$P_1 \times P_2$	Butternut Pumpkin	Queensland Blue Pumpkin
2	$P_1 \times P_3$	Butternut Pumpkin	Bugle Pumpkin
3	$P_1 \times P_4$	Butternut Pumpkin	Long Island Cheese Pumpkin
4	$P_2 \times P_3$	Queensland Blue Pumpkin	Bugle Pumpkin
5	$P_2 \times P_4$	Queensland Blue Pumpkin	Long Island Cheese Pumpkin
6	$P_3 \times P_4$	Bugle Pumpkin	Long Island Cheese Pumpkin
F <sub>1r</sub> reciprocal hybrids			
7	$P_2 \times P_1$	Queensland Blue Pumpkin	Butternut Pumpkin
8	$P_3 \times P_1$	Bugle Pumpkin	Butternut Pumpkin
9	$P_4 \times P_1$	Long Island Cheese Pumpkin	Butternut Pumpkin
10	$P_3 \times P_2$	Bugle Pumpkin	Queensland Blue Pumpkin
11	$P_4 \times P_2$	Long Island Cheese Pumpkin	Queensland Blue Pumpkin
12	$P_4 \times P_3$	Long Island Cheese Pumpkin	Bugle Pumpkin

### Experimental design:-

In the summer season 2014, the four parental varieties were crossed to produce 12  $F_1$  hybrids and also self-pollinated to obtain enough seeds from each variety. The number of plants in each genotype 30 plants with the total plants in population are 480 plants in each condition. The all genetic populations are evaluated in a field trial at two locations in private farms: Alkatba (Menofia government) and Alosyrat in (Sohag government) at the summer season 2015. Land preparation, fertilizer applications and other field practices for pumpkin crop were done according to the recommendations of the Egyptian Ministry of Agriculture.

The experimental was designed by Randomized Complete Blocks Design (RCBD) with three replications at the two locations.

At the end of the summer season 2015 after 90 days of germination when the all fruits ripening we harvesting the yield fruits in the two conditions. Data were recorded for nine traits: fruit length (F.L.cm); fruit diameter (F.D.cm); fruit shape index (F.Sh.I.); total soluble solid% (T.S.S%); flesh thickness (F.T.cm), weight of fruit (W.F.g); seeds weight (S.W.gm); number of fruits per plant (No.F./P.) and total yield per plant (T.Y./P.kg).

### Definitions of studied traits:-

The data were recorded on total 60 fruits to each genotype (30 fruits in each location) randomly as summarize as example chosen within 10 from each plot of the three replicates for the following yield and yield component traits: -

#### 1- Fruit length (F.L.cm): -

It was measured as average length of fruits in centimeters for the selected plants.

## 2- Fruit diameter (F.D.cm): -

It was expressed as the average diameter of fruits in centimeters for the selected plants.

## 3-Fruit shape index (F.Sh.I.): -

It was recorded as the ratio between length and diameter of a fruit.

$$\text{Shape index} = \frac{\text{Length of fruit}}{\text{Diameter of fruit}}$$

## 4-Total soluble solid (T.S.S%):

It was determined by Refract meter.

## 5- Flesh thickness (F.T.cm): -

It was measured as average length of flesh thickness fruits in centimeters for the selected fruits.

## 6- Weight of fruit (W.F.kg): -

This trait was determined as the average weight in kilograms of the harvested ripping fruit at the end of season.

## 7- Seeds weight (S.W.gm): -

It was measured from the total weight in grams of drying seeds into the harvested rips fruits.

## 8- Number of fruits per plant (No.F./P.): -

This trait was obtained by calculating the total number of fruits, which harvested per plant at the end season.

## 9- Total yield per plant (T.Y./P.kg):-

It was measured from the total weight in kilograms of harvested rips fruits per plant at the end of harvesting season.

### Statistical analyses:-

The significance of differences among genetic means for all studied traits were tested according to F-test. The analysis of variances and the expectations of mean squares were made according to [16].

The analysis of variance of diallel crosses were made to obtain the estimates of GCA, SCA and reciprocal effect (r). The procedures of these analyses were described by [8] method I.

The estimates of GCA variance ( $\delta^2_g$ ) and SCA variance ( $\delta^2_s$ ) could be expressed in terms of genetic variances according to ([11] and [4]) with the assumption that there was no epistasis into additive and non-additive variances.

## Results and Discussion

### - Analysis of variance:-

Combined analysis of variance was made for all studied genetic materials (4 parents, 12 F<sub>1</sub> hybrids) in the two locations and mean squares for all studied traits for all genotypes are presented in **Table 3**.

The results cleared that the estimated values of mean squares due to the genotypes (G) appeared highly significance and much higher in magnitude, in all studied traits, than those of the interaction genotype  $\times$  locations (G $\times$ L). Such a result means that the detected differences due to genotypes were so pronounced compared with locations, reflecting the relatively high stability of the various genotypes over locations and suggesting that the superior genotypes can be selected and recommended for growers. The partition of the genetic variation to its components could be made through the analysis of complete diallel crosses. In addition, the interaction between genotypes and locations (G $\times$ L) were not significant for all studied traits with one exception of S.W.gm trait appearing significant.

Thus, the partition of the genetic variation to its components could be made through the analysis of complete diallel crosses. Similar results were obtained by ([13], [2], [12], [7] and [15]).

**Table 3 Combined analysis of variance and mean squares of the two locations for all studied traits of the evaluated 16 genotypes**

S.O.V.	d.f.	Yield and yield component traits								
		F.L.(cm)	F.D.(cm)	F.Sh.I.	T.S.S.(%)	F.T.(cm)	W.F.(kg)	S.W.(gm)	No.F./P.	T.Y./P.(kg)
Locations	1	0.127	0.009	0.003	0.025	0.253	0.059	3.476	0.568	0.127
Replication	4	0.318	0.036	0.023	0.009	4.262	2.482	28.213	1.389	3.351
Genotypes	15	49.02**	10.59**	11.02**	16.851**	45.36**	119.282**	82.953**	24.845**	79.141**
G $\times$ L	15	0.085	0.027	0.018	0.029	0.513	7.043	56.445*	2.123	8.137
Error	60	0.096	0.054	0.039	0.026	0.582	9.826	28.878	1.447	10.735

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

- **The mean performance of all genotypes:**

General performances of the studied 16 genotypes (4 parents and 12 F<sub>1</sub> hybrids in two directions) for the different nine traits are presented

in **Table 4**. The data cleared that the parent P<sub>4</sub> has the highest mean values over all the other parents for all studied traits with the exception of those of F.Sh.I and T.S.S.%. The two previous traits gave the highest mean values by the parent P<sub>3</sub>.

On the other hand, the parent P<sub>1</sub> has the lowest mean value for all studied traits except for F.Sh.I. The differences between the means of the lowest and the highest parent were always significant indicating the presence of genetic differences between the four parental varieties.

Concerning hybrids, the means of the F<sub>1</sub> hybrid (P<sub>3</sub>×P<sub>4</sub>) or (P<sub>4</sub>×P<sub>3</sub>) reflected the highest values for the same five traits F.L.cm, F.D.cm, W.F.kg, S.W.gm and T.Y./P.kg.

The reciprocal hybrid (P<sub>2</sub>×P<sub>1</sub>) gave the lowest mean values in most studied traits except in flesh thickness F.T.cm. The hybrids (P<sub>1</sub>×P<sub>2</sub>), (P<sub>1</sub>×P<sub>3</sub>), (P<sub>1</sub>×P<sub>4</sub>) and (P<sub>2</sub>×P<sub>4</sub>) showed the highest values for the traits; No.F./P., T.S.S.%, F.Sh.I. and F.T.cm, respectively.

Generally, the results indicated that the magnitudes of the mean performances of F<sub>1</sub> hybrids and their F<sub>1r</sub> (reciprocal) hybrids were close to each other for most studied traits.

**Table 4: The mean performances of four parental varieties, F<sub>1</sub> and F<sub>1r</sub> hybrids for yield and yield component traits for the combined data**

Genotypes	Yield and yield component traits								
	F.L.(cm)	F.D.(cm)	F.Sh.I.	T.S.S.(%)	F.T.(cm)	W.F.(kg)	S.W.(gm)	No.F./P.	T.Y./P.(kg)
P <sub>1</sub>	15.56 <sup>L</sup>	9.34 <sup>L</sup>	1.67	7.75 <sup>L</sup>	2.75 <sup>L</sup>	2.68 <sup>L</sup>	35.37 <sup>L</sup>	4.07 <sup>L</sup>	6.72 <sup>L</sup>
P <sub>2</sub>	22.95	14.25	1.61 <sup>L</sup>	8.15	3.81	3.73	43.75	5.63	18.54
P <sub>3</sub>	31.24	16.11	1.94 <sup>H</sup>	9.34 <sup>H</sup>	4.18	6.62	52.63	5.94	36.28
P <sub>4</sub>	35.52 <sup>H</sup>	19.53 <sup>H</sup>	1.82	9.08	4.45 <sup>H</sup>	8.13 <sup>H</sup>	59.27 <sup>H</sup>	6.29 <sup>H</sup>	47.17 <sup>H</sup>
P <sub>1</sub> × P <sub>2</sub>	25.36 <sup>L</sup>	16.34 <sup>L</sup>	1.55 <sup>L</sup>	10.23	4.17 <sup>L</sup>	5.59 <sup>L</sup>	67.36	9.54 <sup>H</sup>	50.26 <sup>L</sup>
P <sub>1</sub> × P <sub>3</sub>	32.54	18.64	1.75	11.65 <sup>H</sup>	4.89	7.54	72.65	8.69	61.22
P <sub>1</sub> × P <sub>4</sub>	37.65	17.87	2.11 <sup>H</sup>	10.47	5.06	9.72	78.39	7.52 <sup>L</sup>	68.34
P <sub>2</sub> × P <sub>3</sub>	34.52	18.34	1.88	9.89 <sup>L</sup>	5.22	8.44	64.84 <sup>L</sup>	9.18	73.42
P <sub>2</sub> × P <sub>4</sub>	38.64	18.66	2.07	10.15	5.35 <sup>H</sup>	9.68	80.67	8.27	76.36
P <sub>3</sub> × P <sub>4</sub>	40.75 <sup>H</sup>	19.87 <sup>H</sup>	2.05	10.56	4.95	10.08 <sup>H</sup>	83.42 <sup>H</sup>	9.39	90.62 <sup>H</sup>
P <sub>2</sub> × P <sub>1</sub>	26.24 <sup>L</sup>	17.06 <sup>L</sup>	1.54 <sup>L</sup>	9.94 <sup>L</sup>	4.74	6.98 <sup>L</sup>	70.69 <sup>L</sup>	8.42 <sup>L</sup>	54.39 <sup>L</sup>
P <sub>3</sub> × P <sub>1</sub>	33.89	18.73	1.81	10.75	4.57 <sup>L</sup>	8.94	85.24	9.14	78.14
P <sub>4</sub> × P <sub>1</sub>	38.04	18.24	2.09 <sup>H</sup>	11.03 <sup>H</sup>	5.12 <sup>H</sup>	9.28	81.37	8.87	80.76
P <sub>3</sub> × P <sub>2</sub>	35.64	19.15	1.86	10.86	4.87	8.17	78.68	9.33 <sup>H</sup>	72.21
P <sub>4</sub> × P <sub>2</sub>	37.65	19.46	1.93	10.39	5.08	9.87	88.67	8.97	85.37
P <sub>4</sub> × P <sub>3</sub>	38.84 <sup>H</sup>	20.32 <sup>H</sup>	1.91	10.69	4.79	10.29 <sup>H</sup>	90.62 <sup>H</sup>	9.02	89.54 <sup>H</sup>
LSD (5%)	0.361	0.265	0.222	0.175	0.450	3.634	6.312	1.436	6.72
LSD (1%)	0.480	0.353	0.295	0.232	0.608	4.833	8.395	1.910	18.54

H= The highest value

L= The lowest value

- **Analysis of combining ability variances:**

Analysis of variance for combining ability and the mean squares of complete diallel crosses are presented in **Table 5** for yield and yield component traits in the combined data.

The mean squares due to general combining ability (GCA) exhibited highly significant differences for all studied yield and yield components traits in the combined data. It means that the additive genetic variance was more important in the inheritance of these traits. The mean squares due to SCA combinations ability were highly significant for all studied yield and yield components traits for the combined data.

At the same time the mean squares due to reciprocal effect were highly significant for all studied traits.

The population of GCA was higher than SCA from their traits. The values of GCA mean squares were higher than those of SCA mean squares for all yield studied traits except T.Y./P.kg. It means that additive genetic variances were more important in the inheritance of these traits. Meanwhile, the combining ability interaction with locations (GCA × L), (SCA × L) and (Rec. × L) were not significant for most studied traits and could be negligible for these traits.

These results indicated that the two parents i.e. P<sub>3</sub> (Bugle Pumpkin) and P<sub>4</sub> (Long Island Cheese Pumpkin) had effective GCA and gave good combinations with the other parental lines to produce the highest F<sub>1</sub> hybrid.

The present results are in agreement in the reported by ([7], [14] and [15]).

**Table 5 Analysis of combining abilities and the mean squares of F<sub>1</sub> hybrids for yield and yield component traits for the combined data**

S.O.V.	d.f.	Yield and yield component traits								
		F.L.(cm)	F.D.(cm)	F.Sh.I.	T.S.S.(%)	F.T.(cm)	W.F.(kg)	S.W.(gm)	No.F./P.	T.Y./P.(kg)
G.C.A.	3	93.175**	38.845**	63.358**	75.128**	165.423**	218.90**	254.461**	619.526**	0.579**
S.C.A.	6	49.153**	9.223**	7.154**	14.956**	49.264**	244.62**	43.256**	242.171**	26.169**
R.E.	6	5.135**	2.354**	1.459**	2.259**	7.247**	161.58**	9.256**	14.634**	0.257**
G.C.A. × L	3	0.159**	0.004	0.008	0.057	0.157**	9.83	0.279**	3.292	0.016
S.C.A. × L	6	0.254**	0.042	0.007	0.043	0.123**	8.96	0.218**	1.646	0.098
R.E. × L	6	0.189**	0.036	0.057	0.064	0.146**	9.59	0.176**	2.567**	0.074
Polled Error L/comb.	60	0.087	0.064	0.043	0.034	0.076	1.656	0.054	1.547	0.039

G.C.A.: general combining ability, S.C.A.: specific combining ability, R.E.: reciprocal effects, L:location.

**- Genetic parameters and heritability:**

According to the expectations of mean squares, the variance components could be calculated and translated in terms of genetic variance components. Thus, the estimated values of additive ( $\delta^2A$ ), non-additive genetic variance including dominance ( $\delta^2D$ ), reciprocal effect ( $\delta^2r$ ), additive variance × location ( $\delta^2A \times L$ ), non-additive genetic variance × location ( $\delta^2D \times L$ ) and reciprocal effect × location ( $\delta^2r \times L$ ) were obtained.

The estimated magnitudes of total genetic variance as well as those of broad and narrow senses heritability percentage, for yield and yield component traits are presented in **Table 6**.

The presented results appeared that both additive ( $\delta^2A$ ) and non-additive genetic variances including dominance ( $\delta^2D$ ) were positive for all studied yield and yield component traits except  $\delta^2A$  for F.T.cm, W.F.kg and S.W.gm, which were this indicated that these variances play a role in genetic expression of yield and yield component traits. In addition, although the magnitudes of additive genetic variance which was larger the dominance genetic variance for and F.D.cm and F.Sh.I., traits. It could be suggest that additive genetic variance predominated in the inheritance of these traits. while the dominance genetic variance was larger additive genetic variance for F.L.cm; T.S.S.%; F.T.cm; W.F.kg; S.W.gm, No.F./P. and T.Y./P.kg traits. The results also illustrated that the importance of reciprocal variances which were smaller than additive genetic variances for most traits. Thus the cytoplasmic genetic factors also contributed in the genetic expression of yield and yield component traits.

In general, the heritability in broad sense ( $h^2_b$ ) were larger than their corresponding values of heritability in narrow sense ( $h^2_n$ ) for all studied traits. In case of two traits fruit diameter (F.D.cm) and fruit shape index (F.Sh.I.); the estimated values of  $h^2_n$  (51.438% and 57.196%, respectively) were found to be around one-half or slightly higher, of those estimated for  $h^2_b$  (99.762% and 99.573%, respectively). Such a result means that both additive and non-additive gene effects seemed to have approximately equal importance on the inheritance of two traits. These results are according with the results obtained by ([2], [12] and [15]).

On the other hand, the  $h^2_b$  were estimated with the higher values than double, or more, of  $h^2_n$  values for the rest studied traits. This results, clearly indicated the greater important of the non-additive gene effect, compared with the additive gene effects, on the inheritance of these traits and consequently, on their general performances.

**Table 6 The relative magnitudes of different genetic parameters and heritability for yield and yield component traits for the combined data over the two locations**

Genetic parameters and heritability	Yield and yield component traits								
	F.L.(cm)	F.D.(cm)	F.Sh.I.	T.S.S.(%)	F.T.(cm)	W.F.(kg)	S.W.(gm)	No.F./P.	T.Y./P.(kg)
$\delta^2A$	6.045	1.538	1.352	1.364	-58.712	-145.686	-9.238	10.349	8.745
$\delta^2D$	7.182	1.239	0.889	3.165	125.622	352.121	64.458	36.142	52.231
$\delta^2r$	0.758	0.192	0.17	0.283	116.752	194.692	14.456	0.159	2.227
$\delta^2A \times L$	0.002	-0.008	-0.01	0.004	-60.226	0.158	-0.974	0.174	0.238
$\delta^2D \times L$	0.017	0.002	-0.025	-0.008	3.873	-2.242	1.169	0.079	0.148
$\delta^2r \times L$	0.015	-0.014	0.004	0.017	5.557	0.717	0.95	1.139	0.453
$\delta^2E$	0.018	0.009	0.005	0.004	1.148	1.753	0.359	0.354	0.471
$h^2_b$	99.224	99.762	99.573	99.235	99.624	99.466	99.567	99.443	99.338
$h^2_n$	34.455	51.438	57.196	28.459	9.192	3.343	11.849	14.437	12.625

$\delta^2A$ : Additive variance,  $\delta^2D$ : Dominance variance,  $\delta^2r$ : Reciprocal variance,  $\delta^2E$ : Environmental variance, L:location.,  $h^2_b$ : heritability in broad senses,  $h^2_n$ : heritability in narrow senses.

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

## Conclusions

The results showed that the importance of general (GCA) and specific (SCA) combining abilities. GCA was larger than their corresponding estimates of SCA for yield and yield component traits at both F<sub>1</sub> and F<sub>1r</sub> hybrids. These results indicated that the two parents i.e. P<sub>3</sub> (Bugle Pumpkin) and P<sub>4</sub> (Long Island Cheese Pumpkin) had effective GCA and gave good combinations with the other parental lines to produce the highest F<sub>1</sub> hybrid. Estimation of genetic parameters showed that additive genetic variance was very important for most studied traits. The importance of additive genetic variance in addition to cytoplasmic genetic factors were played the major role in the inheritance of these traits. The estimates of heritability in broad sense were larger in magnitudes than their corresponding values in narrow sense. The two traits total yield per plant and total soluble solid is the most important for pumpkin breeding program should be described. Therefore, vegetable breeders would design their programs to use F<sub>1</sub> hybrids with high yielding to select superior inbred lines in the advanced segregating generations.

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