

## **COMBINING ABILITY AND GENETIC VARIANCE COMPONENTS OF A DIALLEL CROSSES AMONG SOME SQUASH VARIETIES**

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### **ABSTRACT**

Gene action for some economical traits in squash was examined by 6 x 6 diallel crossing excluding reciprocals using four foreign varieties, as well as, two local varieties. These varieties were belonging to the species of *Cucurbita pepo*, L. All 21 genotypes, included six parents and their 15 F<sub>1</sub> hybrids were evaluated in the following two locations; Sakha Research Station in Kafr El-sheakh and private farm at Mansoura- Dakahila governorate. Data of vegetative and flowering traits were recorded on plants within plots on the two types. The obtained results revealed that the mean squares of genotypes and its components, GCA and SCA were highly significant for all studied traits, indicating that additive and non-additive genetic variance contributed in the inheritance of the studied traits.

Both GCA and SCA genetic variances were found to be highly significant for all studied traits indicating the importance of both additive and non-additive gene action.

The parental, Zucchini Nova Verde di Milano were seemed to be the best combiner for number of leaves plant<sup>-1</sup> and No. of male flowers plant<sup>-1</sup>. While, Arab Marrow was the best combiner for stem length, leaf area (cm<sup>2</sup>) and No. of female flowers plant<sup>-1</sup>. The crosses involving the above parents were promising because they showed highly significant estimates of SCA effects.

### **INTRODUCTION**

Sumer squash is belonging to the family of vegetable *Cucurbitacea* having a wide range of variability. It is an interesting crop plant for genetical studies. In Egypt, there are only two local varieties of squash the first namely Ballady which is totally discarded for its prostrated growth habit and low yield, and the second namely Eskandarani which is characterized with high production based the satisfaction of both producers and consumers at the present time, but not may in future. So, knowledge about the mode of gene action of economical traits, which directly contributes towards yield, in any crop like summer squash (*Cucurbita pepo*, L.) helps to formulate the genetic basis for breeding. When the additive genetic variance is the main component of the total genetic variation, a maximum progress would be expected through selection programs. On the other hand, the presence of a relatively high non-additive genetic variance (including dominance) indicated that the production of hybrids should be the ultimate improvement as a result of the direct relationship between non-additive gene action and hetrotic effect, Abd El-Maksoud *et al* (2003).

Additive and non-additive genetic variances could be derived from the combining ability analysis. Therefore, the estimates of general and specific combining abilities are of great values in establishing the most proper

breeding approach. In this respect, Al-Araby (2004), reported that both GCA and SCA were highly significant for main stem length, and number of leaves per plant indicating that both additive and non-additive genetic variances were important for the inheritance of both traits on cucumber. In a diallel cross system among seven inbred lines derived from Eskandarani cultivar, El-Sharkawy (2000) regarded that a parental inbred line  $L_2$  could be considered as a good general combiner for harvesting early yield. This result also indicated that the two crosses  $L_2 \times L_5$  and  $L_2 \times L_6$  gave the earlier  $F_1$  hybrids and these crosses possessed the highest estimates of SCA effect. Mohanty (2000) on pumpkin, reported that the mean squares due to general (GCA) and specific (SCA) combining ability effects were significant for No. of leaves plant<sup>-1</sup> and No. of male flowers plant<sup>-1</sup>.

This investigation aimed to present further information dealing with nature of gene action and combining ability effects for some economical traits, as well as, estimation of genetic parameters for all studied traits in squash.

## **MATERIALS AND METHODS**

A partial diallel crosses was done using six varieties of squash. These varieties were: Eskandarani ( $P_1$ ), Zucchini mezza lung bianco ( $P_2$ ), Arab Marrow ( $P_3$ ), Marita ( $P_4$ ), Zucchini, Nano Verde di Milano ( $P_5$ ) and White Bush Scallop ( $P_6$ ). All the 15  $F_1$  hybrids along with their parents were evaluated in Randomized Complete Blocks Design (RCBD) with three replications. Spacing of 1.m between rows and 0.5m between plants were applied at the two following locations; Vegetables Research Farm, Kafr El-Sheikh, Egypt and private farm at Mansoura- Dakahlia governorate. The recommended cultural practices were followed.

Data were recorded on ten randomly plants from each plot and mean values were used for statistical analysis. Combining ability analysis was carried out according to method No. two and model No.1 of Griffing's (1956). The following genetic components of variation were calculated using Hayman's procedure (1954) and presented by Singh and Chaudhary (1977).

## **RESULTS AND DISCUSSION**

Highly significant differences were found among genotypes, parents and crosses for all studied vegetative and flowering traits except for parents at the two locations and their combined data for No. of female flowers plant<sup>-1</sup> and No. of male flowers plant<sup>-1</sup> for parents vs. crosses as presented in Tables 1 and 2. These results indicated a wide range of genetic variations among parental varieties were used in this investigation. Parents vs. crosses mean squares indicated that the average of heterosis was significant in all crosses in the two locations and their combined data over locations for all vegetative and flowering traits. The interaction of genotypes, parents, crosses and parents vs. crosses with the locations were highly significant for all vegetative and flowering traits except for parents /locations for No. of female flowers plant<sup>-1</sup> and parents vs. crosses / locations for No. of male flowers plant<sup>-1</sup>, respectively.





It is important to evaluate the potentiality of parents for the expression of heterosis through the evaluation of their performances over a number of environmental conditions. Genetic diversity alone would not guarantee the expression of heterosis but suitability of the environmental conditions is required. Similar results were obtained by Al-Ballat (2008) and Al-Araby, (2010).

Both general and specific combining ability of genetic variances were found to be highly significant for all vegetative and flowering traits in the two locations and their combined data. Except for general combining ability of No. of female flowers plant<sup>-1</sup> in the first location as shown in Table 2. These results indicated the importance of both additive and non-additive genetic variances including dominance in determining the inheritance of these traits. The interactions of locations with GCA and SCA were found to be highly significant for all vegetative and flowering traits indicating that both additive and non-additive genetic variance tended to interact with the environments. Therefore, selection for these traits would not be effective in a single environment, but more environments would be required. This result was agreed with conclusions obtained by Al-Ballat (2008) and Al-Araby, (2010).

The ratio of  $\sigma^2$  GCA /  $\sigma^2$  SCA estimate were less than unity for all the traits indicating the preponderance of non-additive genetic variance. This finding suggests the importance of non-additive gene action in the production of squash hybrids. Similar results were obtained by Kumbhar *et al.* (2005), Obiadalla-Ali (2006) and Al-Araby, (2010).

As shown in Tables 3 and 4 high relative estimate of dominance genetic variance were achieved for all vegetative and flowering traits. The relative magnitude of the dominance genetic variance to additive genetic variance was very high. Consequently, such type of variance was very important contributor for vegetative and flowering traits. So, the dominance genetic variance played the most important role in the inheritance of these traits.

Tables 3 and 4 presents the genetic components of the six vegetative and flowering traits under investigation according to Hayman (1954). The additive component "D" was insignificant positive for No.of leaves plant<sup>-1</sup> in the first location; leaf area (cm<sup>2</sup>) in both second location and the combined data; both No. of male flowers plant<sup>-1</sup> and sex ratio in the second location and for No. of female flowers plant<sup>-1</sup> in the tow locations and their combined data. However, the values of dominance components "H<sub>1</sub>" and "H<sub>2</sub>" were highly significant for these traits, except for H<sub>2</sub> for No. of male flowers plant<sup>-1</sup> and sex ratio traits for the second location. These results indicated that dominance effects were relatively more important than additive component in the inheritance of these traits. The magnitude of "H<sub>1</sub>" was more than "H<sub>2</sub>" in all studied traits, indicating that the most loci, the positive and negative alleles, were in equal proportion. These results agree with those of Gendy (1991) and Al-Ballat (2008).

Dominance variance over all heterozygous loci "h<sup>2</sup>" was highly significant for all vegetative and flowering studied traits except for No. of male flowers plant<sup>-1</sup> in the first, second location and their combined data and for sex ratio in the first location indicating that dominance was unidirectional.





The values of "F" were insignificant for leaf area (cm<sup>2</sup>) and No. of female flowers plant<sup>-1</sup> at both locations and their combined data; No. of leaves plant<sup>-1</sup> in the first location; No. of male flowers plant<sup>-1</sup> and sex ratio in the second location. While it was significant for the other vegetative and flowering traits. Suggesting that dominant and recessive genes were in equal proportion. On the other hand, "F" values were significant for all vegetative and flowering traits, indicating that there was asymmetric gene distribution with an excess of dominant alleles as compared with recessive ones.

The influence of non-additive genetic variance as indicated by the relatively larger values of (H<sub>1</sub>) and (H<sub>2</sub>) than those of (D), suggesting that there is a possibility to break the yield plateau of squash by exploiting the dominance genetic components. This finding was further justified by the ratio of (H<sub>1</sub>/D)<sup>1/2</sup> which revealed over dominance. Al-Ballat (2008), also found over dominance for the same studied traits. The ratio of (H<sub>2</sub>/4H<sub>1</sub>) was less than 0.25, indicating that a symmetric distribution of positive and negative alleles is existed in the parents. The ratio of total number of dominant to recessive alleles in the parent (KD/KR) was greater than unity of all traits indicating that the proportion of dominant alleles was greater for these traits.

Data presented in Tables 3 and 4 showed that heritability estimates in broad sense (h<sup>2</sup><sub>b</sub>) were high for all vegetative and flowering traits, while heritability estimates in narrow sense (h<sup>2</sup><sub>n</sub>) were relatively low for all studied traits. This further suggests that a major part of the total phenotypic variance for these traits was due to dominance genetic variance and environmental effects. These findings lead to conclude that the production of squash hybrids is the most important suitable breeding program. On the other hand, selection for such characters must be done in the later generations. This result agrees with those obtained by El-Gendy (1999); Mohanty and Mishra (1999), and Saad (2003) and Obiadalla- Ali (2006).

#### **General combining ability effects:**

The estimates of general combining ability effects for the parental varieties for all studied traits were estimated and the results are presented in tables 5 and 6. The genotypes, Arab Marrow (P<sub>3</sub>) and White Bush Scallop (P<sub>6</sub>), were found to be good general combiners for vegetative and flowering traits as presented in Tables 5 and 6. Arab Marrow (P<sub>3</sub>) was a good combiner for stem length and leaf area with positive highly significant values for GCA effects. White Bush Scallop (P<sub>6</sub>) was a good combiner for No. of leaves plant<sup>-1</sup>, stem length(3.088) and No. of male flowers plant<sup>-1</sup> (2.88). Zucchini mezza lung bianco (P<sub>2</sub>) was best combiner for sex ratio (-0.220). So, could be used as the best parent to improve vegetative and flowering traits. The performance of parents was an indication of their GCA effects for all the above traits, which was reported earlier similar results by Sharma and Pathania (2000), Kamoooh (2002), Abd El-Maksoud *et al.* (2003), Obiadalla- Ali (2006) and Al-Araby (2010).

**Table 5: Estimates of general combining ability effects (gi) of the six parents for vegetative traits in the two locations and their combined data.**

Parents	G.C.A. effects								
	No. of leaves plant <sup>-1</sup>			Stem length(cm)			Leaf area(cm <sup>2</sup> )		
	L <sub>1</sub>	L <sub>2</sub>	Comb.	L <sub>1</sub>	L <sub>2</sub>	Comb.	L <sub>1</sub>	L <sub>2</sub>	Comb.
P <sub>1</sub>	2.088**	-1.278*	0.405	-0.187	1.215*	0.514	-25.87**	-21.34**	-23.60**
P <sub>2</sub>	-1.223*	-1.434*	-1.329**	-2.927**	0.278	-1.325**	15.79**	0.565	8.176*
P <sub>3</sub>	0.028	-1.783**	-0.877	4.063**	3.184**	3.623**	36.07**	30.73**	33.40**
P <sub>4</sub>	-2.115**	-1.804**	-1.960**	-5.021**	-1.814**	-3.417**	-1.701	17.82**	8.057*
P <sub>5</sub>	-1.221*	2.566**	0.673	0.240	-1.087	-0.424	-30.30**	-28.28**	-29.29**
P <sub>6</sub>	2.443**	3.732**	3.088**	3.833**	-1.776**	1.028*	6.012	0.503	3.257
LSD 0.05	1.038	1.243	0.887	1.439	1.152	0.854	11.21	10.58	6.862
0.01	1.389	1.663	1.187	1.925	1.541	1.142	14.99	14.16	9.182

\* And \*\* Significant at 0.05 and 0.01 levels, respectively.

**Table 6: Estimates of general combining ability effects (gi) of the six parents for flowering traits in the two locations and their combined data.**

Parents	G.C.A. effects								
	No. of male flowers plant <sup>-1</sup>			No. of female flowers plant <sup>-1</sup>			Sex ratio		
	L <sub>1</sub>	L <sub>2</sub>	Comb.	L <sub>1</sub>	L <sub>2</sub>	Comb.	L <sub>1</sub>	L <sub>2</sub>	Comb.
P <sub>1</sub>	3.447**	0.756*	2.101**	-0.037	1.065**	0.514**	-0.182**	0.202**	-0.052
P <sub>2</sub>	-2.203**	-1.486**	-1.844**	-0.004	-0.081	-0.042	0.396**	0.252**	0.355**
P <sub>3</sub>	-1.253**	-0.678*	-0.965**	-0.154	-1.631**	0.892**	-0.021	-0.258**	-0.105**
P <sub>4</sub>	-1.674**	-0.619*	-1.147**	-0.479	0.753**	0.137	0.019	0.025	0.035
P <sub>5</sub>	-1.403**	-0.503	-0.953**	0.313	-0.293	0.010	0.032	0.028	-0.013
P <sub>6</sub>	3.085**	2.531**	2.808**	0.363	0.186	0.274	-0.244**	-0.248**	-0.220**
LSD 0.05	0.500	0.585	0.369	0.582	0.385	0.364	0.074	0.107	0.056
0.01	0.669	0.783	0.494	0.778	0.515	0.487	0.100	0.143	0.074

\* And \*\* Significant at 0.05 and 0.01 levels, respectively.

**Specific combining ability effects:**

The estimated values of SCA effects for vegetative and flowering traits in the two locations and their combined data are presented in Tables 7 and 8. The results revealed that out of 15 cross combinations, The F<sub>1</sub> hybrids (P<sub>1</sub> x P<sub>3</sub>); (P<sub>2</sub> x P<sub>6</sub>); (P<sub>2</sub> x P<sub>4</sub>) and (P<sub>2</sub> x P<sub>3</sub>) showed significant and highly significant positive desirable of SCA effects for No. of leaves plant<sup>-1</sup> for both locations and their combined data. The F<sub>1</sub> hybrids (P<sub>1</sub> x P<sub>2</sub>); (P<sub>1</sub> x P<sub>3</sub>) and (P<sub>2</sub> x P<sub>6</sub>) showed highly significant values for stem length at the two locations and their combined data for leaf area (cm<sup>2</sup>), the two F<sub>1</sub> hybrids (P<sub>2</sub> x P<sub>4</sub>) and (P<sub>2</sub> x P<sub>5</sub>) gave the highest significant and highly significant positive values (desirable) for SCA effects. Four crosses also revealed positive and highly significant SCA effects for No. of male flowers plant<sup>-1</sup> for the combined data. In case of No. of female flower plant<sup>-1</sup>, significant positive SCA effects were recorded for nine F<sub>1</sub> hybrids from the combined data. The three F<sub>1</sub> hybrids (P<sub>1</sub> x P<sub>4</sub>); (P<sub>1</sub> x P<sub>3</sub>) and (P<sub>5</sub> x P<sub>6</sub>) were the best hybrid for this trait. The results cleared that seven cross combinations recorded significant and highly significant positive values of SCA effects for sex ratio trait. These crosses also showed good specific combinations for most of studied traits.



In this respect, many authors obtained variable estimates for both GCA and SCA effects in squash among them, Ahmed *et al.* (2003), Sadek (2003), Abd El-hadi *et al.* (2005), Obiadalla- Ali (2006), Al-Ballat (2008), Kumbhar *et al.* (2005) and Al-Araby(2010).

**Table 8: Estimates of specific combining ability effects (sij) for the 15 F<sub>1</sub> hybrids for flowering traits in the two locations and their combined data.**

Hybrids	SCA effects								
	No. of male flowers plant <sup>-1</sup>			No. of female flowers plant <sup>-1</sup>			Sex ratio		
	L <sub>1</sub>	L <sub>2</sub>	Comb.	L <sub>1</sub>	L <sub>2</sub>	Comb.	Y <sub>1</sub>	Y <sub>2</sub>	Comb.
P <sub>1</sub> X P <sub>2</sub>	6.205**	11.53**	8.866**	3.089**	-0.782	1.154*	-0.515**	-1.070**	-0.718**
X P <sub>3</sub>	-4.612**	-0.881	-2.746**	2.306**	5.335**	3.821**	0.443**	0.351*	0.468**
X P <sub>4</sub>	-3.591**	-3.873**	-3.732**	3.364**	4.818**	4.091**	0.420**	0.871**	0.616**
X P <sub>5</sub>	-3.162**	-7.789**	-5.476**	-0.694	2.331**	0.818	0.066	2.036**	0.562**
X P <sub>6</sub>	-6.683**	-2.689**	-4.686**	-1.244	0.152	-0.546	0.238*	-0.082	0.153*
P <sub>2</sub> X P <sub>3</sub>	4.505**	2.361**	3.433**	1.406	1.548**	1.477**	-0.488**	-0.228	-0.376**
X P <sub>4</sub>	-1.941**	-1.198	-1.569**	1.064	4.198**	2.631**	0.219*	0.455**	0.328**
X P <sub>5</sub>	0.488	1.186	0.837	-1.027	-0.257	-0.642	-0.369**	-0.476**	-0.367**
X P <sub>6</sub>	2.634**	-3.081**	-0.224	3.223**	1.031	2.127**	-0.252*	0.104	-0.133
P <sub>3</sub> X P <sub>4</sub>	0.009	1.827*	0.918	-2.986**	-2.986**	-2.986**	-0.229*	-0.315*	-0.285**
X P <sub>5</sub>	-0.295	0.511	0.108	6.189**	-2.573**	1.808**	0.697**	-0.324*	0.227**
X P <sub>6</sub>	0.551	0.277	0.414	-0.427	-0.452	-0.440	-0.015	0.041	-0.003
P <sub>4</sub> X P <sub>5</sub>	0.026	3.252**	1.639**	-0.252	3.710**	1.729**	0.039	-0.073	0.052
X P <sub>6</sub>	3.371**	-1.948*	0.712	2.064*	2.264**	2.164**	-0.034	0.306*	0.095
P <sub>5</sub> X P <sub>6</sub>	1.167	1.569	1.368**	1.873*	5.143**	3.508**	0.088	0.135	0.170*
LSD 0.05	1.374	1.608	1.013	1.598	1.056	0.999	0.204	0.294	0.153
0.01	1.838	2.151	1.355	2.138	1.413	1.336	0.273	0.393	0.204

\* And \*\* significant at 0.05 and 0.01 levels, respectively.

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## القدرة علي الإنتلاف ومكونات التباين الوراثي للهجن الدورية بين بعض أصناف قرع الكوسة

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تم دراسة طبيعة الفعل الجيني لبعض الصفات الإقتصادية في قرع الكوسة من خلال 6 X 6 أباء للتهجين الدوري غير مشتملة علي الهجن العكسية وذلك بإستخدام أربعة أصناف أجنبية وإثنين من الأصناف المحلية. كل هذه الأصناف تابعة لجنس قرع الكوسة. تم تقسيم واحد وعشرون تركيب وراثي الي ستة أباء و خمسة عشر هجيناً لا تشمل الهجن العكسية، تم تقييم كل التركيب في موقعين مختلفين تحت الظروف المصرية وهما محطة البحوث الزراعية بسخا-محافظة كفر الشيخ، ومزرعة خاصة بالمنصورة بمحافظة الدقهلية. وتم تسجيل البيانات علي النباتات في كل منطقة تم تصميم التجربة في صورة القطاعات الكاملة العشوائية علي نوعين من الصفات وهما الصفات الخضرية ( عدد الأوراق لكل نبات ، طول النبات ، المساحة الورقية) و الصفات الزهرية ( عدد الأزهار المذكرة لكل نبات ، عدد الأزهار المؤنثة لكل نبات ، النسبة الجنسية).

أشارت النتائج المتحصل عليها إلي أن متوسط المربعات للتركيب الوراثية ومكوناتها من القدرة العامة علي التآلف والقدرة الخاصة علي التآلف كانت عالية المعنوية لكل الصفات المدروسة، مما يشير إلي أن كل من الفعل الجيني الإضافي و الفعل الجيني غير الإضافي شاملاً السيادة يلعب دوراً مهماً في توريث هذه الصفات.

أوضحت النتائج أن الصنف زوكينو نانوفير دي ميلانو كان أحسن الأصناف المدروسة من حيث القدرة العامة علي التآلف لصفات عدد الأوراق لكل نبات وعدد الأزهار المذكرة لكل نبات. بينما الصنف عرب مرو كان أكثر الأصناف قدرة عامة علي التآلف لصفات طول النبات والمساحة الورقية وعدد الأزهار المؤنثة علي النبات. أوضحت النتائج أن الهجن المحتوية علي الأباء سابقة الذكر كانت هجن مبشرة وذلك لأنها اظهرت قيماً عالية المعنوية لتأثيرات القدرة الخاصة علي التآلف.

### قام بتحكيم البحث

كلية الزراعة – جامعة المنصورة  
مركز البحوث الزراعيه

أ.د / خليفه عبد المقصود زايد  
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**Table 1: Mean square estimates of ordinary and combining ability analysis for vegetative traits in the two locations and their combined data.**

S . O . V	d . f		No.of leaves plant <sup>-1</sup>			Stem length (cm)			Leaf area (cm <sup>2</sup> )		
	Single	Comb.	L <sub>1</sub>	L <sub>2</sub>	Comb.	L <sub>1</sub>	L <sub>2</sub>	Comb.	L <sub>1</sub>	L <sub>2</sub>	Comb.
Locations	1	1	-	-	8.711	-	-	221.3**			8980**
Reps with Locations	2	4	-	-	4.731	-	-	14.88			1052
Genotypes	20	20	171.4**	307.1**	177.3**	238.9**	225.6**	173.6**	19747**	16051**	12010**
Parents	5	5	193.6**	345.9**	261.8**	371.8**	290.5**	298.6**	22108**	9126**	12383**
Crosses	14	14	133.7**	236.7**	101.1**	197.5**	215.8**	135.1**	18702**	19065**	11685**
P. vs crosses	1	1	587.3**	1099**	823.2**	153.8**	38.50*	86.54**	22570**	8487**	14685**
Genotypes/ locations		20			301.2**			290.9**			23788**
Parents/ locations		5			277.7**			363.7**			18851**
Crosses/ location		14			269.3**			278.2**			26082**
P. vs crosses/ locations		1			863.1**			105.8**			16372**
G.C.A	5	5	28.47**	49.02**	26.44**	104.2**	30.91**	44.90**	5081**	4027**	4276**
S.C.A	14	14	66.68**	120.2**	70.01**	71.46**	89.97**	62.20**	7082**	5791**	3912**
G.C.A / locations		5			51.05**			126.2**			4932**
S.C.A / locations		14			116.9**			99.23**			8961**
Error	40	80	7.601	10.89	5.549	14.60	9.358	5.141	885.4	790.0	332.1
GCA/SCA. ratio			0.051	0.049	0.045	0.186	0.041	0.089	0.088	0.085	0.137

\*And \*\* significant at 0.05 and 0.01 levels, respectively.

Table 2: Mean square estimates of ordinary and combining ability analysis for flowering traits in the two locations and their combined data.

S . O . V	d . f		No.of male flowers plant <sup>-1</sup>			No.of female flowers plant <sup>-1</sup>			Sex ratio		
	single	Comb.	L <sub>1</sub>	L <sub>2</sub>	Comb.	L <sub>1</sub>	L <sub>2</sub>	Comb.	L <sub>1</sub>	L <sub>2</sub>	Comb.
Locations	1	1	-	-	111.5**	-	-	89.85**	-	-	0.152
Reps with Locations	2	4	-	-	4.107	-	-	2.532	-	-	0.140
Genotypes	20	20	75.75**	57.59**	56.31**	23.78**	43.42**	24.76**	0.675**	1.691**	0.678**
Parents	5	5	191.1**	94.15**	126.9**	1.678	1.170	0.268	1.843**	1.486**	1.638**
Crosses	14	14	39.86**	48.59**	35.12**	17.26**	34.04**	13.82**	0.301**	1.736**	0.353**
P. vs crosses	1	1	1.236	0.775	0.013	225.5**	385.9**	300.4**	0.067	2.104**	0.434**
Genotypes/ locations		20			77.03**			42.44**			1.688**
Parents/ locations		5			158.4**			2.580			1.691**
Crosses/ location		14			53.33**			37.48**			1.684**
P. vs crosses/ locations		1			1.998			311.0**			1.737**
G.C.A	5	5	52.14**	16.45**	30.17**	0.774	7.180**	1.850**	0.402**	0.374**	0.303**
S.C.A	14	14	16.29**	20.11**	14.97**	10.31**	16.90**	10.39**	0.166**	0.627**	0.200**
G.C.A / locations		5			38.42**			6.104**			0.473**
S.C.A / locations		14			21.43**			16.82**			0.593**
Error	40	80	1.764	2.417	0.959	2.387	1.043	0.933	0.039	0.081	0.022
GCA/SCA. ratio			0.411	0.101	0.255	0.001	0.052	0.019	0.318	0.072	0.191

\*And \*\* significant at 0.05 and 0.01 levels, respectively.

**Table 3: Estimates of different genetic parameters for vegetative traits from the two locations and their combined data.**

Genetic parameters	Estimates ± S.E.								
	No. of leaves plant <sup>-1</sup>			Stem length			Leaf area (cm <sup>2</sup> )		
	L <sub>1</sub>	L <sub>2</sub>	Comb.	L <sub>1</sub>	L <sub>2</sub>	Comb.	L <sub>1</sub>	L <sub>2</sub>	Comb.
(D)	142.7 ± 91.70	255.9** ± 74.25	194.4** ± 33.06	273.9**± 49.88	214.7**± 65.62	222.3**± 42.69	16273**± 5011.5	6586 ± 5565	9178.1± 6072
(H)									
H <sub>1</sub>	645.9** ± 232.2	1125.3** ± 188.1	658.7** ± 83.71	715.8**± 126.3	949.4**± 166.2	646.7**± 108.1	66443**± 12690	56432**± 14092	36146**± 15377
H <sub>2</sub>	444.8** ± 208.0	837.9** ± 168.4	455.6** ± 74.96	522.1**± 113.1	648.7**± 148.8	450.2**± 96.82	55851**± 11365	45195**± 12620	31320** ± 13771
h <sup>2</sup>	1140.5** ± 139.9	2134.6**± 113.2	1599** ± 50.42	296.3**± 76.08	73.09**± 0.731	167.3**± 65.12	43715**± 7643.7	16359**± 8487.8	28492**± 9261.9
(F)	299.7 ± 221.6	484.99**± 179.4	372.9** ± 79.89	356.9** ± 120.6	467.1** ± 158.6	377.3** ± 103.2	22173 ± 12112	11297± 13449	9496± 14676.6
(E)	2.491 ± 34.66	3.5304 ± 28.06	1.386 ± 12.494	4.881 ± 18.85	3.198 ± 24.81	1.769 ± 16.14	307.49 ± 1894.2	257.79 ± 2103	109.65 ± 2295
(H <sub>1</sub> /D) <sup>1/2</sup>	2.1272	2.0968	1.8401	1.6165	2.1031	1.7057	2.0206	2.9271	1.9845
(H <sub>2</sub> /4H <sub>1</sub> )	0.1722	0.1862	0.1729	0.1823	0.1708	0.1741	0.21015	0.2002	0.2166
(K <sub>D</sub> /K <sub>R</sub> )	2.9482	2.6487	3.175	2.3496	3.1427	2.9809	2.01734	1.8288	1.7053
(h <sub>bs</sub> )	0.9817	0.9854	0.9857	0.9744	0.9831	0.9869	0.98149	0.9826	0.9892
(h <sub>ns</sub> )	0.1625	0.1203	0.0964	0.2904	0.1276	0.1537	0.14119	0.2202	0.2211

\*And \*\* Significant at 0.05 and 0.01 levels, respectively.

$$(K_D/K_R) = \{(4DH_1)^{1/2} + F\} / \{(4DH_1)^{1/2} - F\}$$

Table 4: Estimates of different genetic parameters for flowering traits from the two locations and their combined data.

Genetic parameters	Estimates ± S.E.								
	No. of male flowers plant <sup>-1</sup>			No. of female flower plant <sup>-1</sup>			Sex ratio		
	L <sub>1</sub>	L <sub>2</sub>	Comb.	L <sub>1</sub>	L <sub>2</sub>	Comb.	L <sub>1</sub>	L <sub>2</sub>	Comb.
(D)	142.72** ± 18.22	69.802 ± 36.48	94.837** ± 23.47	0.4572± 5.589	0.5097± 8.895	-0.0969± 4.391	1.3688** ± 0.190	1.0848 ± 1.202	1.2226** ± 0.236
(H)									
H <sub>1</sub>	173.68** ± 46.15	197.39**± 92.39	154.42** ± 59.44	73.03**1± 14.15	127.68**± 22.53	69.348**± 11.12	1.7452**± 0.482	6.1521**± 3.043	2.0975** ± 0.597
H <sub>2</sub>	116.26**± 41.32	160.71± 82.74	113.47** ± 53.33	71.206**± 12.67	110.56**± 20.17	66.150**± 9.958	1.1648** ± 0.431	4.6463± 2.725	1.4027** ± 0.535
h <sup>2</sup>	2.0467± 27.79	1.0535± 55.64	-0.1644± 35.80	437.99**± 8.524	750.25**± 13.57	583.86**± 6.698	0.1222± 0.290	4.0742**± 1.833	0.8406**± 0.360
(F)	155.46** ± 44.05	96.316 ± 88.17	112.08** ± 56.73	1.2178 ± 13.51	2.9295± 21.50	-03570± 10.61	1.6642** ± 0.460	2.0292 ± 2.904	1.7003** ± 0.560
(E)	0.6404 ± 6.888	0.8171 ± 13.78	0.3426 ± 8.871	0.8012 ± 2.112	0.3681 ± 3.362	0.2975 ± 1.660	0.0135 ± 0.072	0.0210 ± 0.454	0.0075 ± 0.089
(H <sub>1</sub> /D) <sup>1/2</sup>	1.1032	1.6817	1.2760	12.639	15.828	13.106	1.1292	2.3814	1.3098
(H <sub>2</sub> /4H <sub>1</sub> )	0.1673	0.2035	0.1837	0.2438	0.2165	0.2132	0.1669	0.1888	0.1672
(K <sub>D</sub> /K <sub>R</sub> )	2.9504	2.3915	2.7250	1.2356	1.4437	1.837	3.3325	2.2934	3.2636
(h <sub>bs</sub> )	0.9877	0.9823	0.9916	0.9581	0.9896	0.9840	0.9698	0.9803	0.9838
(h <sub>ns</sub> )	0.4292	0.1103	0.2922	0.0278	0.2078	0.0931	0.3186	0.1908	0.2325

\*And \*\* Significant at 0.05 and 0.01 levels, respectively.  
 $(K_D/K_R) = \{(4DH_1)^{1/2} + F\} / \{(4DH_1)^{1/2} - F\}$

**Table 7: Estimates of specific combining ability effects (sij) for the 15 F<sub>1</sub> hybrids for vegetative traits in the two locations and their combined data.**

Hybrids	S.C.A. effects								
	No. of leaves plant <sup>-1</sup>			Stem length (cm)			Leaf area (cm <sup>2</sup> )		
	L <sub>1</sub>	L <sub>2</sub>	Comb.	L <sub>1</sub>	L <sub>2</sub>	Comb.	L <sub>1</sub>	L <sub>2</sub>	Comb.
P <sub>1</sub> X P <sub>2</sub>	14.64**	-2.058	6.291**	9.103**	4.896**	6.999**	10.23	-8.058	1.085
X P <sub>3</sub>	10.97**	14.04**	12.51**	12.28**	9.573**	10.93**	-22.72	-49.69**	-36.20**
X P <sub>4</sub>	-2.717	-5.938**	-4.328**	-7.804**	-6.096**	-6.950**	-23.49	46.94**	11.73
X P <sub>5</sub>	-5.445**	-6.975**	-6.210**	-1.314	-1.573	-1.443	23.78	17.07	20.42*
X P <sub>6</sub>	-7.442**	-5.141**	-6.292**	-5.824**	-13.55**	-9.687**	97.44**	-27.72	34.86**
P <sub>2</sub> X P <sub>3</sub>	9.161**	4.197*	6.679**	1.686	10.01**	5.848**	94.53**	-85.53**	4.498
X P <sub>4</sub>	5.261**	8.218**	6.739**	3.936	8.342**	6.139**	48.79**	36.60*	42.70**
X P <sub>5</sub>	0.497	16.35**	8.422**	11.09**	2.865	6.978**	66.96**	94.54**	80.75**
X P <sub>6</sub>	3.536*	17.77**	10.65**	4.832**	7.054**	5.943**	-167.7**	-146.4**	-157.1**
P <sub>3</sub> X P <sub>4</sub>	-2.431	5.733**	1.651	-1.137	-7.731**	-4.434**	-128.3**	94.54**	-16.89
X P <sub>5</sub>	-4.385**	2.407	-0.989	-11.65**	-8.208**	-9.928**	-65.12**	-23.47	-44.30**
X P <sub>6</sub>	4.118**	-12.30**	-4.092**	-1.908	-11.52**	-6.713**	-46.40**	62.09**	7.848
P <sub>4</sub> X P <sub>5</sub>	-1.181	-0.656	-0.918	-7.731**	11.56**	1.913	-48.42**	-64.40**	-56.41**
X P <sub>6</sub>	1.095	1.468	1.282	9.676**	1.229	5.452**	48.87**	29.43	39.15**
P <sub>5</sub> X P <sub>6</sub>	3.284*	2.515	2.899*	-0.418	0.569	0.075	-67.97**	-86.06**	-77.01**
LSD 0.05	2.852	3.413	2.436	3.952	3.164	2.345	30.78	29.07	18.85
0.01	3.815	4.567	3.260	5.288	4.233	3.138	41.18	38.90	25.22

\* And \*\* Significant at 0.05 and 0.01 levels, respectively.