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COMBINING ABILITY FOR SOME IMPORTANT TRAITS IN RED MAIZE USING GRIFFING'S METHOD 2 AND 4

Sultan, M. S.*; A. A. El-Hosary; A. A. Lelah*; M. A. Abdel–Moneam* and * M.A. Hamouda**

*** Agron. Dept., Fac. of Agric. Mansoura Univ.**

**** Agron. Dept., Fac. of Agric. Moshtohor, Benha Univ.**

ABSTRACT

A half diallel cross among 9 inbred lines of maize (*Zea mays* L.) was evaluated under two locations (Fac. Agric. Moshtohor and Quesna menofiya Governorate) for some quantitative characters; i.e. Days to 50 % tasseling, plant height, No. of rows/ear, No of kernels/row,100-kernel weight and grain yield/plant. General and specific combining ability were estimated according to Griffings (1956) diallel cross analysis designated as method 2 and 4 model 1 for each location as well as the combined over them.

Locations mean squares were significant for all studied traits, except for no. of rows/ear, in both methods, with mean values in L1 being higher than those in L2 for all traits in both methods of analysis (M4 and M2), except no. of days to 50% tasseling. In both methods, genotypes mean squares were significant for all traits in both locations as well as the combined analysis. The mean squares due to general and specific combing ability were highly significant for all studied traits in both methods and both locations as well as the combined analysis.

In the method 4, high of GCA/SCA ratios which largely exceeded the unity were obtained for all studied traits in both locations as well as the combined analysis, except days to 50% tasseling at L2 only.

In method 2, no. of rows/ ear at L2 had GCA/SCA ratio equal unity. High ratios which largely exceeded the unity were obtained for days to 50% tasseling, 100-kernel weight and grain yield/ plant in both locations and the combined analysis. This finding coincided with that already reached from the combining ability analysis of Griffing method-4. For the other remain cases, GCA/SCA ratios, were less than unity. The mean squares of interaction between locations and both types of combining ability were significant for all traits in both methods of analysis.

The parental inbred lines no. 9, 1 and 8 seemed to be good combiners for yield and some of its components in both methods of analysis. The crosses P1xP4, P1xP8, P1xP9, P4xP7, P6xP9 and P8xP9 showed the highest values for SCA effects for grain yield and its components in both methods of analysis.

INTRODUCTION

Successful development of improved maize (*Zea mays* L.) hybrids is depended upon accurate evaluation of inbred lines under different environments.

The diallel analysis procedure suggested by (Griffing (1956) is the most common procedure to evaluate the combining ability of lines and to determine the usefulness of lines in hybrids development showing the superior performance of those hybrids under different environmental conditions. The environmental factors are usually daily changed; hence, the studying of genotype environment interaction for plant breeders is of prime importance for devoting these effects which help in selecting the elite materials. However,

location effect is one important factor which plays an important role in maize production.

The objectives of this investigation were to study: the magnitude of both general combining ability (GCA) and specific combining ability (SCA) effects and their interactions with two locations and to make comparison between the two Griffing's methods of diallel cross (method 2 and method 4) in the present investigation.

MATERIALS AND METHODS

Nine (*Zea mays* L.) red inbred lines developed by Quality Techno Seeds Company and were used to establish the experiment materials for several characters among inbred lines under study.

In the first summer season 2007, grains of the nine inbred lines were split sown in three planting dates to avoid differences in flowering time and to secure enough hybrid seed. All possible cross combinations without reciprocals were made between the nine inbred lines by hand method giving a total of 36 crosses.

In the second summer season 2008, nine inbred lines and their 36 hybrids were planted at two locations (Fac. of Agric. Moshtohor (L1) and district Quesna Menofiya Governorate (L2)). In each experiment, the 9 inbred lines and their 36 hybrids were grown in a randomized complete block design with three replications. Each plot consisted of three ridges of 3 m length and 75 cm width. Hill was spaced 25 cm apart with three kernels planted per hill and later thinned to one plant per hill. The plots were irrigated after sowing. The first irrigation was given after 21 days from sowing. The plants were then irrigated at intervals of 10-15 days. The plots were informally fertilized at the rate of 120 kg of nitrogen per feddan given before the first and second irrigations. The other cultural practices of maize growing were properly practiced.

Random sample of ten guarded plants in each plot were taken to evaluate tasseling date (days) in 50% of tasseled, plant height (cm.), no. of rows/ ear, no. of kernels/ row, 100-kernel weight and grain yield/ plant (g) which was adjusted for 15.5% moisture.

The obtained data were statistically analyzed for analysis of variance by using computer statistical program MSTAT-C. General and specific combining ability estimated according to Griffing's (1956) diallel cross analysis designated as method 2 and method 4 models 1 (fixed model) for each location. The combined analysis of the two locations was carried out whenever homogeneity of variance was detected (Gomez and Gomez, 1984). Simple correlation was used for comparison between the general and specific combining ability effects (Griffing method 2 and 4). F. test was used for comparison between GCA or SCA were determinded by Griffing method 2 and 4.

RESULTS AND DISCUSSION

The present investigation was conducted to asses the genetic basis and to compare genetical analysis of the two methods using half diallel cross.

The analysis of variance for all traits i.e. Days to 50 % tasseling, plant height, No. of rows/ear, No of kernels/row,100-kernel weight and grain yield/plant are presented in Tables (1 and 2).

Locations mean squares were significant for all studied traits, except for no. of rows/ear, in both methods, with mean values in L1 being higher than those in L2 for all traits in both methods of analysis (M4 and M2), except no. of days to 50% tasseling. It is clear that number of days from sowing to tasseling increased significantly with location 2. It could be concluded that location 1 showed positive effect on the previous traits on maize.

In both methods, genotypes mean squares were significant for all studied traits in both locations as well as the combined analysis. This indicates the wide diversity between the parental materials used in the present study. Significant genotypes x locations interaction mean squares were obtained for all studied traits, revealing that the performance of genotypes differed from location to another.

Significant parents', crosses and parent *vs.* crosses mean squares were obtained for all studied traits (Table 2). Significant interaction mean squares between parental inbred lines, cross and parent *vs.* crosses with location were detected for all studied traits, except no. of Kernel/ row and grain yield/ plant for parent x L and no. of rows/ear for parent *vs.* crosses mean squares (Table 2). This result revealing that the parental inbred lines, crosses and parent *vs.* crosses varied in their response to location to another. For the exceptional cases parental inbred lines and parent *vs.* crosses, interaction with locations were insignificant, revealing that repeatability of performance of these traits under different locations.

Griffing method 2 and method 4 model 1, 1956.

The analysis of variance for combining ability for each location as well as the combined analysis for all the traits studied in both methods is presented in Tables (1 and 2).

The mean squares due to general and specific combing ability were highly significant for all traits in both methods as well as the combined analysis.

If both general and specific combining ability mean squares are significant, one may ask which type and or types of gene action are important in determining the performance of single- cross progeny. To overcome such situation the size of mean squares can be used to assume the relative importance of both types of combining ability. Hence, GCA/SCA ratio was used as measure to reveal the nature of genetic variance involved.

In the method 4, high ratios which largely exceeded the unity were obtained for all traits in both locations as well as the combined analysis, except days to 50% tasseling at L2 only, whereas the ratio of GCA/SCA which was less than unity indicating that large part of the total genetic variability associated with those traits was additive and additive by additive gene action.

In method 2, no. of rows/ ear at L2 had GCA/SCA ratio equal unity, indicating that additive and non additive types of gene action have the same importance in the performance of this trait.

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High ratios which largely exceeded the unity were obtained for days to 50% tasseling, 100-kernel weight and grain yield/ plant in both locations and the combined analysis, indicating that large part of the total genetic variability associated with these traits was additive and additive by additive gene action. This finding coincided with that already reached from the combining ability analysis of Griffing method-4.

For the other remain cases, GCA/SCA ratios, were less than unity. Therefore, it could be concluded that the large portion of the total genetic variability associated with these traits is due to non-additive gene action. This finding disagreement with that already reached from method-4.

The mean squares of interaction between locations and both types of combining ability were significant for all studied traits in both methods of analysis. Such results showed that the magnitude of all types of gene action varied from location to another. It is fairly evident that ratio for SCAxL/SCA was higher than ratio of GCAxL/GCA for all traits in the method -4. This result indicated that non-additive genetic effects were more influenced by locations than additive genetic effects of these traits. This conclusion is in well agreement with those reported by Gilbert (1958). However, in the method-2 the ratio of SCAxL/SCA was higher than ratio of GCAxL/GCA was obtained for number of grains/ row and 100-kernel weight. As for grain yield/ plant in both ratios were equal, revealing that additive and non additive were similar changed by locations. For the other remain traits the ratio of GCAxL/GCA was higher than ratio of SCAxL/SCA, indicating that additive effects were more influenced by location than non-additive effects. This result indicate that additive effects were more influenced by the environmental conditions than non- additive effects. The genetic variance was previously reported to be mostly due to non-additive for plant height by Sadek *et al.* (2000) and Sedhom *et al.* (2007); no. of grains/row by Shafey *et al.* (2003), El-Shenawy (2003) and Sedhom *et al.* (2007) and for grain yield/plant by Sadek *et al.* (2000), Soliman (2000), Shafey *et al.* (2003), El-Hosary and El-Badawy (2005); El-Shenawy (2003) and El-Hosary *et al.* (2006), Sedhom *et al.* (2007) and El-Hosary (2011). On the other hand, the additive genetic variance was previously reported to be the most prevalent for earliness by Sadek *et al.* (2000); El-Hosary and El-Badawy (2005), El-Shenawy (2003), El-Hosary *et al.* (2006) and Sedhom *et al.* (2007); no. of rows/ear by Shafey *et al.* (2003) and El-Hosary and El-Badawy (2005) and Sedhom *et al.* (2007); for100-kernel weight by Shafey *et al.* (2003), El-Hosary and El-Badawy (2005) and Sedhom *et al.* (2007), El Badawy *et al.* (2010) and El-Hosary (2011).

General combining ability effects:

Estimates of GCA effects ($\hat{g}_i$) for individual parental inbred lines for each trait in combined analysis in both methods (Griffing M 4 and 2) are presented in Table (3). General combining ability effects estimated herein were found to differ significantly from zero. High positive values would be of interest under all traits in question, except tasseling days to 50% as well as plant height where high negative effects would be useful from the breeder's point of view.

The parental inbred line no. 1 showed significant positive ($\hat{g}_i$) effects for plant height, 100-kernel weight no. of Kernels/ row and grain yield/ plant in the combined data, in both methods (M4 and M2). Meanwhile, it gave undesirable ($\hat{g}_i$) effects for other traits. This inbred line could be considered as excellent combiner for developing high grain yield, its components at both locations.

The parental inbred line no.2 showed significant desirable ($\hat{g}_i$) effects for plant height, number of rows/ ear and 100-kernel weight, in both methods (M4 and M2), no. of Kernels/ row in M2 and grain yield/ plant in M4. This inbred line could be considered as a good combiner developing genotype for short plant, low height of ear and high grain yield/ plant. Meanwhile, it exhibited either significant undesirable or insignificant ($\hat{g}_i$) effects for other traits in both methods.

The parental inbred lines no. 3, 4 and 5 exhibited either significant undesirable or insignificant ($\hat{g}_i$) effects for all studied traits. In the combined analysis in both methods.

The parental inbred line no. 6 exhibited the highest significant negative ($\hat{g}_i$) effects for; days to 50% tasseling, plant height in both methods. These results indicate that this inbred line could be considered as a good combiner for developing early and short genotypes. Earliness of inflorescence is required for developing early maturing genotypes to escape from corn pests, and shorter plants and ear heights are required for lodging resistance. Also, it gave significant positive ($\hat{g}_i$) effects for 100-kernel weight in both locations in both methods.

The parental inbred line no. 7 gave significant negative effects for plant height at the combined analysis in both methods of analysis (M4 and M2). Also, it showed significant positive ($\hat{g}_i$) effects for grain yield/ plant in M2. Meanwhile, it exhibited either significant undesirable or insignificant ($\hat{g}_i$) effects for other traits in both methods.

The parental inbred line no. 8 showed significant desirable ($\hat{g}_i$) effects for plant height, no. of Kernels/ row and grain yield/ plant in the combined data in both methods of analysis (M4 and M2). However, it exhibited either significant undesirable or insignificant ($\hat{g}_i$) effects for the other traits, indicating that this inbred line could be considered as the xcellent combiner for developing high yield hybrid, dwarf plant and lower ear height.

The parental inbred line no. 9 seemed to be good combiner in both methods of analysis for plant height, no. of Kernels/ row, 100-kernel weight and grain yield / plant. Also, it showed significant positive ($\hat{g}_i$) effects for ear length in M2 at both locations, and at L2 in M4. However it gave undesirable ($\hat{g}_i$) effects for other cases.

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It is worth noting that the inbred line which possessed high ($\hat{g}_i$) effects for grain yield per plant showed also desirable effect for one or more of the traits contributing to grain yield. The same trend in both methods of analysis was obtained for ($\hat{g}_i$) effects for most studied traits.

In most traits, the values of ($\hat{g}_i$) effects mostly differed from location to another. This finding coincided with that reached above where significant GCA by location mean squares were detected Table (1 and 2).

From the previous result, it could be concluded that the parental inbred lines no. 1, 8 and 9 seemed to be the best general combiners for grain yield/plant and some of its components in the combined analysis of both locations in both methods of analysis. Also, the inbred line no. 6 seemed to be the best combiner for earliness and shortness of ear and plant heights.

Specific combining ability effects ($\hat{S}_{ij}$):

Specific combining ability effects of the parental combination were estimated for only when significant mean squares were obtained in the combined analysis by two methods: Griffing's method 4 and method 2 (Tables 4).

As for days to 50% tasseling, the crosses P1xP4, P1xP5, P4xP6, P7xP8 and P7xP9 in both methods of analysis had the best desirable $\hat{S}_{ij}$ effects.

For plant height, the crosses P3xP4, P4xP8, P4xP9 and P5xP7 gave the best $\hat{S}_{ij}$ effects for short plant in method-4.

Regarding number of rows/ear, the crosses P3xP6 and P4xP7 in the combined analysis in method-4, P1xP2, P1xP5 and P2xP5 in method-2 had the highest positive $\hat{S}_{ij}$ effects for this trait.

With regard to number of kernels/ row, the crosses P1xP8, P2xP4 and P3xP8 in method4, P1xP4, P1xP8, P3xP4, P3xP8, P5xP6, P7xP8 and P7xP9 in method 2 gave the highest positive $\hat{S}_{ij}$ effects.

As for 100-kernel weight, the crosses P1xP8 and P1xP9 in both methods of analysis expressed the highest desirable $\hat{S}_{ij}$ effects in both locations.

With regard to grain yield/ plant, the crosses P1xP9, P2xP5, P4xP7, P6xP9 and P8xP9 had the highest significant desirable $\hat{S}_{ij}$ effects at both locations in both methods of analysis. It could be concluded that the previous crosses seemed to be the best combinations.

In most traits, the values of SCA effects were mostly differed from location to another. This finding coincided with that reached before for SCA by locations mean squares Tables (1 and 2).

If cross showing high specific combining ability involve only one good combiner such combinations would throw out desirable transgressive segregates providing that the additive genetic system present in the good combiner and complementary and epistatic effects present in the crosses act in the same direction to reduce undesirable plant characteristics and maximize the character in view. Therefore, the most previous crosses might be prime importance in breeding program for traditional breeding procedures or produce inbred line.

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القدرة على التآلف لبعض الصفات الهامة فى الذرة الشامية الحمراء

محمود سليمان سلطان*، على عبد المقصود الحصرى، عبد الرحيم عبد الرحيم ليلة*، مأمون أحمد عبد المنعم* و ماجد عبد العظيم حمودة***
*** قسم المحاصيل - كلية الزراعة جامعة المنصورة**
**** قسم المحاصيل - كلية الزراعة جامعة بنها**

يهدف البحث الى تقييم تسعة سلالات جديدة و الهجن الناتجة منها بنظام التهجين النصف دائرى و ذلك فى موقعين هما كلية الزراعة – جامعة بنها و قويسنا - منوفية و تقدير القدرة العامة و الخاصة على التآلف تبعا لطريقتى جريفنج ١٩٥٦ الطريقة الثانية و الرابعة الموديل الأول لكل موقع على حده و التحليل التجميعى لصفات عدد الايام حتى طرد ٥٠% من النورة المذكرة ، ارتفاع النبات ، عدد السطور فى الكوز ، عدد الحبوب بالسطر، وزن ١٠٠ حبة و وزن محصول النبات.

كان تباين المواقع معنويا لكل الصفات المدروسة عدا عدد الصفوف / كوز لكلا الطريقتين و كان متوسط الموقع الاول اكبر من متوسط الموقع الثانى عدا عدد الايام لطرد ٥٠% من النورات المذكرة.

كان التباين الراجع الى التراكيب الوراثية معنويا فى كلا الطريقتين لكل الصفات المدروسة فى كلا الموقعين و كذلك التحليل التجميعى.

كان التباين الراجع الى القدرة العامة و الخاصة على التآلف معنويا لكل الصفات المدروسة فى كلا الطريقتين و ذلك لكلا الموقعين و التحليل التجميعى.

كانت النسبة للقدرة العامة / القدرة الخاصة على التآلف اكبر من الوحدة فى الطريقة الرابعة لكل الصفات المدروسة فى كلا الموقعين و كذلك التحليل التجميعى عدا عدد الايام حتى طرد ٥٠% من النورات المذكرة فى الموقع الثانى فقط.

أظهرت السلالات ٩ ، ١ و ٨ أفضل قدرة عامة على التآلف للمحصول و بعض مكوناته فى كلا الطريقتين للتحليل. و أظهرت الهجن P8xP9, P1xP9, P4xP7, P6xP9 ,P1xP8و P1xP4 أفضل قدرة خاصة على التآلف للمحصول و مكوناته فى كلا الطريقتين للتحليل.

فى الطريقة الثانية لجريفنج، بالنسبة لصفة عدد سطور الكوز فى الموقع الثانى كانت النسبة للقدرة العامة/ القدرة الخاصة على التآلف تؤل الى الوحدة. أما النسبة كانت تزيد عن الوحدة لصفة عدد الأيام لطرد ٥٠% من النورات المذكرة ، وزن ١٠٠ حبة و محصول النبات الفردى فى كلا الموقعين و التحليل التجميعى. بالنسبة لباقى الصفات كانت النسبة تقل عن الوحدة .

كان تباين التفاعل بين المواقع وكلا من القدرة العامة و الخاصة على التآلف معنوياً لكل الصفات المدروسة فى كلا الطريقتين من طرق التحليل.

قام بتحكيم البحث

أ.د / عادل محمد عبد الجواد سلامة — كلية الزراعة – جامعة المنصورة
أ.د / حسان عبد الجيد دوام — كلية زراعة شبين الكوم – جامعة المنوفية

Table (1): Observed mean squares from ordinary analysis and combining ability for the traits studied in each location and the combined over them Griffing m-4.

	d.f.		Days to 50% tasseling			Plant height			No of rows/ ear		
S.O.V	S.	c.	L1	L2	Comb.	L1	L2	Comb.	L1	L2	Comb.
Location		1			682.66**			15100.16**			0.17
blocks/L.	2	4	0.48	0.04	0.26	19.44	97.027*	58.24	8.92**	0.26	4.592**
Genotype	35	35	13.93**	14.71**	24.44**	467.32**	1012.76**	1200.34**	2.70**	5.37**	5.80**
GenotpexL.		35			4.209**			279.74**			2.261**
Error	70	140	0.66	0.41	0.54	72.30	25.48	48.89	1.31	0.68	0.99
GCA	8	8	6.12**	4.06**	9.018**	376.58**	566.48**	901.01**	1.38**	4.40**	4.895**
SCA	27	27	4.20***	5.15**	7.88**	90.34**	269.77**	251.70**	0.75*	1.01**	1.05**
GCAxL.		8			1.17**			42.063*			0.89**
SCAxL.		27			1.46**			108.45**			0.71**
Error	70	140	0.22	0.14	0.18	24.10	8.49	16.30	0.44	0.23	0.33
GCA/SCA			1.46	0.79	1.14	4.17	2.10	3.58	1.83	4.35	4.62
GCAxL./GCA					0.13			0.05			0.18
SCAxL./SCA					0.19			0.43			0.67

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

Table (1): Cont.

	d.f.		No of kernels/ row			100-Kernel Weight			Grain weight/ plant		
S.O.V	S.	c.	L1	L2	Comb.	L1	L2	Comb.	L1	L2	Comb.
Location		1			118.51**			224.07**			2276.30**
blocks/L.	2	4	4.93	0.78	2.85	2.53	2.40	2.46*	5.32	2.88	4.10
Genotype	35	35	17.62**	29.15**	36.67**	30.64**	20.58**	47.56**	818.88**	751.76**	1465.12**
GenotpexL.		35			10.09**			3.66**			105.52**
Error	70	140	1.72	1.04	1.38	0.83	1.06	0.95	6.88	12.89	9.89
GCA	8	8	13.95**	15.62**	26.30**	28.79**	18.69**	45.87**	838.53**	585.19**	1362.36**
SCA	27	27	3.47**	7.96**	8.05**	4.71**	3.356**	6.96**	105.38**	151.44**	229.41**
GCAxL.		8			3.27**			1.612**			61.36**
SCAxL.		27			3.39**			1.11**			27.41**
Error	70	140	0.57	0.35	0.46	0.28	0.35	0.32	2.29	4.30	3.30
GCA/SCA			4.01	1.96	3.27	6.11	5.57	6.59	7.96	3.86	5.94
GCAxL./GCA					0.13			0.04			0.06
SCAxL./SCA					0.42			0.16			0.12
*** and ** significant at 0.05 and 0.01 levels of probability, respectively.**											

Table (2): Observed mean squares from analysis for the traits studied in both locations as well as the combined over them Griffing m-2.

S.O.V.			Days to 50% tasseling			Plant height			No. of rows/ ear		
	S.	C.	L1	L2	Comb	L1	L2	Comb	L1	L2	Comb
Location		1			763.39 **			15052.80 **			0.53
Rep/L	2	4	0.05	0.99	0.52	106.85	152.03	129.44	12.21 **	0.03	6.12 **
Genotypes	44	44	33.41 **	35.76 **	62.97 **	4552.63 **	4375.04 **	8622.82 **	4.51 **	7.39 **	9.71 **
parent	8	8	33.83 **	70.68 **	90.02 **	1505.79 **	2235.65 **	3396.64 **	3.00 *	5.33 **	6.17 **
Cross	35	35	13.93 **	14.72 **	24.44 **	467.32 **	1012.77 **	1200.34 **	2.70 **	5.37 **	5.81 **
Par.vs.cr.	1	1	711.85 **	493.07 **	1194.90 *	171913.38 **	139169.56 **	310218.90 *	80.12 **	94.59 **	174.40 *
G/L		44			6.21 **			304.85 **			2.20 **
par./L		8			14.49 **			344.79 **			2.17 *
Cr./L		35			4.21 **			279.75 **			2.26 **
Par.vs.cr./.L		1			10.01 *			864.03 *			0.30
Error	88	176	0.74	1.22	0.98	73.33	42.89	58.11	1.36	0.82	1.09
GCA	8	8	13.70 **	18.11 **	28.42 **	699.82 **	1114.80 **	1733.16 **	0.46	2.46 **	2.12 **
SCA	36	36	10.57 **	10.55 **	19.34 **	1699.26 **	1534.69 **	3127.85 **	1.74 **	2.47 **	3.48 **
GCA x L		8			3.39 **			81.46 **			0.80 *
SCA x L		36			1.78 **			106.10 **			0.72 **
Error	88	176	0.25	0.41	0.33	24.44	14.30	19.37	0.45	0.27	0.36
GCA/SCA			1.30	1.72	1.47	0.41	0.73	0.55	0.27	1.00	0.61
GCA x L/GCA					0.12			0.05			0.38
SCA x L/SCA					0.09			0.03			0.21

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

Table (2):Cont.

S.O.V.			No. of kernels /row			100-Kernel Weight			Grain yield / plant (gm)		
	S	C	L1	L2	Comb	L1	L2	Comb	L1	L2	Comb
Location		1			60.68 **			238.95 **			1684.50 **
Rep/L	2	4	4.83	1.54	3.19	2.05	0.42	1.24	12.56	10.85	11.71
Genotypes	44	44	69.75 **	59.26 **	118.75 **	39.77 **	28.64 **	63.90 **	1581.53 **	1239.36 **	2723.14 **
parent	8	8	33.00 **	50.65 **	80.98 **	13.09 **	15.90 **	21.00 **	189.10 **	176.08 **	364.86 **
Cross	35	35	17.62 **	29.15 **	36.67 **	30.65 **	20.59 **	47.57 **	818.88 **	751.77 **	1465.12 **
Par.vs.cr.	1	1	2188.09 **	1182.22 **	3293.51 *	572.47 **	412.56 **	978.50 *	39413.81 **	26811.16 **	65619.87 *
G/L		44			10.26 **			4.52 **			97.75 **
par./L		8			2.67			7.99 **			0.31
Cr./L		35			10.10 **			3.66 **			105.53 **
Par.vs.cr./.L		1			76.80 *			6.53 *			605.10 *
Error	88	176	1.85	1.68	1.77	0.84	1.18	1.01	5.81	10.91	8.36
GCA	8	8	12.30 **	13.49 **	23.93 **	21.65 **	19.34 **	39.97 **	616.89 **	470.30 **	1048.97 **
SCA	36	36	25.68 **	21.15 **	43.06 **	11.39 **	7.37 **	17.15 **	507.24 **	400.41 **	876.32 **
GCA x L		8			1.87 **			1.02 **			38.22 **
SCA x L		36			3.77 **			1.61 **			31.33 **
Error	88	176	0.62	0.56	0.59	0.28	0.39	0.34	1.94	3.64	2.79
GCA/SCA			0.48	0.64	0.56	1.90	2.62	2.33	1.22	1.17	1.20
GCA x L/GCA					0.08			0.03			0.04
SCA x L/SCA					0.09			0.09			0.04

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

Table (3): General combining ability effects for all parents at both locations (combined analysis) in method 4 and method 2 for all the traits studied .

parental	days to 50% tasseling		Plant height		No of rows/ ear		No of grains/ row		100-Kernel Weight		grain yield/ plant	
inbred line	M4	M2	M4	M2	M4	M2	M4	M2	M4	M2	M4	M2
p1	-0.01	0.11	6.37 **	9.24 **	0.47 *	0.42 *	1.38 **	0.67 **	1.59 **	1.58 **	13.79 **	8.43 **
p2	-0.32 *	0.04	-8.97 **	-9.61 **	1.13 **	0.48 **	-0.29	0.85 **	0.78 **	1.03 **	2.38 **	-1.21 *
p3	0.30	0.07	0.06	3.40 **	-0.06	0.02	-1.20 **	-1.27 **	-1.74 **	-1.12 **	-14.65 **	-10.54 **
p4	-0.08	-0.18	7.27 **	5.72 **	-0.53 *	-0.40 *	-0.72 **	-1.15 **	-1.93 **	-1.54 **	-14.37 **	-9.70 **
p5	1.28 **	1.69 **	15.15 **	15.74 **	0.32	0.02	-0.03	-0.02	-2.19 **	-1.77 **	-2.92 **	-2.01 **
p6	-1.75 **	-2.39 **	-4.90 **	-3.69 **	-0.20	-0.31	-1.15 **	-1.03 **	1.00 **	0.69 **	-0.03	0.66
p7	0.51 **	0.38 **	-5.80 **	-6.08 **	-0.15	-0.10	-0.22	-0.44 **	-0.79 **	-0.69 **	-0.06	1.21 *
p8	0.08	1.02 **	-2.16	-8.31 **	-0.92 **	-0.28	3.02 **	1.68 **	0.14	0.02	4.23 **	4.24 **
p9	-0.01	-0.74 **	-7.02 **	-6.40 **	-0.06	0.14	-0.79 **	0.71 **	3.14 **	1.81 **	11.63 **	8.92 **
LSD5%(gi)	0.30	0.32	2.86	2.45	0.41	0.34	0.48	0.43	0.40	0.32	1.28	0.93
LSD1%(gi)	0.40	0.42	3.78	3.22	0.54	0.44	0.64	0.56	0.53	0.42	1.70	1.22
LSD5%(gi-gj)	0.45	0.48	4.29	3.68	0.61	0.50	0.72	0.64	0.60	0.48	1.93	1.40
LSD1%(gi-gj)	0.59	0.63	5.68	4.82	0.81	0.66	0.95	0.84	0.79	0.64	2.55	1.83

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

Table (4): Specific combining ability effects for all crosses at both locations (combined analysis) in method 4 and method 2 for all the studied traits.

	Days to 50% tasseling		Plant Height		No of rows/ ear		No of Kernels/ row		100-Kernel Weight		grain weight/ plant	
Crosses	**M4**	**M2**	**M4**	**M2**	**M4**	**M2**	**M4**	**M2**	**M4**	**M2**	**M4**	**M2**
P1xP2	0.40	-1.12 *	-0.79	13.94 **	0.73	1.83 **	0.04	1.35	-1.86 **	-1.14 *	-6.32 **	10.42 **
P1xP3	0.45	-0.49	5.36	16.09 **	0.25	0.62	-2.23 **	0.31	-0.17	0.18	-1.49	7.56 **
P1xP4	-2.33 **	-3.41 **	-4.19	11.44 **	-0.61	-0.29	0.96	3.85 **	0.19	0.77	4.97 **	13.45 **
P1xP5	-2.86 **	-4.44 **	-4.40	9.09 *	0.87	1.62 **	0.27	2.72 **	-4.05 **	-3.51 **	-13.25 **	-1.01
P1xP6	2.83 **	2.30 *	-2.19	10.68 **	-0.27	0.28	-0.94	1.40 *	-3.07 **	-1.79 **	-10.90 **	1.56
P1xP7	-0.10	-1.14 *	-0.95	13.41 **	-0.32	0.07	-0.54	2.14 **	1.21 *	2.08 **	4.09 *	15.97 **
P1xP8	1.00 **	-1.11 *	-0.43	19.80 **	-0.23	-0.41	2.73 **	6.52 **	3.45 **	4.54 **	6.93 **	20.07 **
P1xP9	0.60	0.15	7.60 *	21.06 **	-0.42	-0.17	-0.30	0.65	4.29 **	6.58 **	15.97 **	31.82 **
P2xP3	0.60	-0.58	0.19	14.44 **	-1.08 *	-0.11	-0.39	0.29	1.48 **	1.55 **	2.25	9.53 **
P2xP4	-1.86 **	-3.17 **	1.31	20.45 **	0.06	0.98	3.13 **	4.17 **	-0.33	-0.02	8.44 **	15.16 **
P2xP5	0.12	-1.70 **	8.43 *	25.44 **	1.20 *	2.56 *	1.77 **	2.37 **	1.43 **	1.71 **	21.09 **	31.56 **
P2xP6	-1.02 **	-1.79 **	-9.02 *	7.36	0.39	1.56 *	0.06	0.55	0.74	1.75 **	7.13 **	17.83 **
P2xP7	-1.12 **	-2.40 **	-5.62	12.25 **	-0.32	0.68	-0.87	-0.04	-1.48 **	-0.87	-5.48 **	4.65 **
P2xP8	0.31	-2.03 **	5.74	29.48 **	-0.23	0.19	0.56	2.50 **	0.10	0.92	-1.66	9.71 **
P2xP9	2.57 **	1.89 **	-0.24	16.74 *	-0.75	0.10	-4.30 **	-5.19 **	-0.07	1.96 **	-25.46 **	-11.37 **
P3xP4	0.36	-0.37	-20.21 **	-5.06	-0.75	-0.56	1.20 *	3.46 **	-0.81	-0.87	-1.93	-2.91
P3xP5	0.17	-1.06 **	2.74	15.75 **	-0.61	0.01	-0.99	0.82	1.12 *	1.02	0.36	3.13 *
P3xP6	-2.14 **	-2.32 **	8.62 *	21.01 **	1.25 *	1.68 *	0.80	2.50 **	0.93	1.57 **	0.13	3.13 *
P3xP7	-1.40 **	-2.09 **	5.36	19.24 **	-0.46	-0.20	-0.80	1.25	-0.62	-0.38	-1.48	0.95
P3xP8	1.02 **	-0.73	3.88	23.63 **	0.63	0.32	3.63 **	6.79 **	-0.71	-0.26	7.40 **	11.08 **
P3xP9	0.95 *	0.86	-5.93	7.06	0.77	0.89	-1.23 *	-0.91	-1.21 *	0.45	-5.26 **	1.13
P4xP5	2.05 **	0.68	6.36	24.27 **	-0.13	0.44	-1.80 **	0.37	0.14	0.28	-1.36	0.86
P4xP6	-1.76 **	-2.08 **	17.24 **	34.53 **	0.39	0.77	-0.68	1.38 *	1.95 **	2.83 **	1.65	4.09 **
P4xP7	2.31 **	1.48 **	20.64 **	39.42 **	1.01 *	1.22 *	-0.27	2.12 **	-0.43	0.04	9.51 **	11.38 **
P4xP8	0.90 *	-0.99	-16.33 **	8.32 *	0.11	-0.26	-3.18 **	0.34	1.14 *	1.83 **	-6.51 **	-3.39 *
P4xP9	0.33	0.10	-4.81	13.07 **	-0.08	-0.02	0.63	1.31	-1.86 **	0.04	-14.77 **	-8.94 **
P5xP6	-0.45	-1.28 *	-16.48 **	-1.32	-1.46 **	-0.65	1.96 **	3.58 **	0.71	1.55 **	-2.03	4.17 **
P5xP7	1.45 **	0.12	-15.57 **	1.07	0.49	1.13 *	-0.13	1.82 **	1.00 *	1.43 **	-3.00	2.62
P5xP8	0.21	-2.18 **	19.95 **	42.47 **	-0.75	-0.68	-2.54 **	0.53	-1.26 *	-0.61	-9.72 **	-2.85
P5xP9	-0.69	-1.43 **	-1.02	14.72 **	0.39	0.89	1.44 *	1.67 *	0.90	2.77 **	7.91 **	17.50 **
P6xP7	4.81 **	4.53 **	-0.52	15.50 **	-0.32	0.13	-1.35 *	0.50	0.64	1.81 **	0.50	6.35 **
P6xP8	-0.43	-1.78 **	-13.33 **	8.56 *	-0.23	-0.35	-1.08	1.88 **	-2.12 **	-0.73	-11.21 **	-4.12 **
P6xP9	-1.83 **	-1.52 **	15.69 **	30.82 **	0.25	0.56	1.23 *	1.35	0.21	2.81 **	14.72 **	24.53 **
P7xP8	-3.52 **	-5.38 **	4.24	27.62 **	0.39	0.10	0.65	3.96 **	0.67	1.65 **	1.88	8.40 **
P7xP9	-2.43 **	-2.62 **	-7.57 *	9.04 *	-0.46	-0.32	3.30 **	3.76 **	-1.00 *	1.19 *	-6.02 **	3.22 *
P8xP9	0.50	-0.76	-3.71	18.77 *	0.30	-0.14	-0.77	0.81	-1.26 *	1.15 *	12.90 **	23.38 **
LSD5%(sij)	0.73	1.02	6.94	7.85	0.99	1.07	1.17	1.37	0.97	1.03	3.12	2.98
LSD1%(sij)	0.96	1.34	9.20	10.34	1.31	1.42	1.55	1.80	1.28	1.36	4.14	3.92
LSD5%(sij-sik)	1.10	1.50	10.50	11.57	1.50	1.58	1.76	2.02	1.46	1.53	4.72	4.39
LSD1%(sij-sik)	1.46	1.98	13.91	15.25	1.98	2.09	2.34	2.66	1.94	2.01	6.25	5.79
LSD5%(sij-ski)	1.00	1.43	9.58	10.98	1.37	1.50	1.61	1.92	1.33	1.45	4.31	4.16
LSD1%(sij-ski)	1.33	1.88	12.70	14.47	1.81	1.98	2.13	2.52	1.77	1.91	5.71	5.49

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