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COMPARATIVE STUDY BETWEEN TWO MATING DESIGNS TO ESTIMATE DIFFERENT GENETIC PARAMETERS IN CORN *(Zea maize,* L.*)*

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ABSTRACT

In Egypt, as well as many other countries, corn is considered an important field crop. Due to the importance of corn, scientists in all countries gave corn breeding great concern. Many authors obtained high values for heterosis from the F_1 maize hybrids. It is found that the amounts of heterosis from the MP % for the diallel cross mating design were: 179.30, 17.78, 51.97 and 52.77% for Ear weight, No. of rows/ear, No. of kernels/row and 100 kernels weight at Mansoura location, respectively. The values of heterosis were: 107.13, 9.06, 31.07 and 65.30% for the same traits at the second location (Sohag), respectively. However, the estimated amounts of heterosis with respect to t BP % were: 152.48, 3.79, 26.36 and 38.7% for Ear weight, No. of rows/ear, No. of kernels/row and 100 kernels weight at Mansoura, respectively. They were: 68.70, -1.32, 23.05 and 51.12% for the same traits at Sohag, respectively. But for the line x tester mating design, it is appeared that the amounts of heterosis from the MP % were: 51.14, 3.20, 11.7 and 44.60% for ear weight, No. of rows/ear, No. of kernels/row and 100 kernels weight at Mansoura, respectively. The values of heterosis were: 121.1, 19.0, 42.6 and 50.17% for the same traits at Sohag, respectively. While the estimated amounts of heterosis with respect to the BP % were: 26.33, -16.13, 1.92 and 24.32% for ear weight, No. of rows/ear, No. of kernels/row and 100 kernels weight at Mansoura, respectively. They were: 89.7, -4.2, 5.5 and 21.82% for the same traits at Sohag, respectively.

GCA and SCA are usually used to estimate the types and the nature of gene action that present within hybrids. In this respect, there are different mating designs are known to obtain the estimates for these two components. Among these mating designs i.e. diallel crosses and line x testers mating designs. These two mating designs yield estimates for both GCA and SCA. The mean squares for GCA at Mansoura were highly significant for No. of kernels/row and 100 kernels weight. In general, the magnitudes of the mean squares at Sohag were larger than their corresponding estimates at Mansoura for Ear weight and No. of rows/ear while, it was the vice versa for No. of kernels/row and 100 kernels weight. The mean squares of the GCA of all yield component traits were larger in their magnitudes than their corresponding estimates of SCA at Mansoura. It is found that the results for the line x tester mating design indicated that the mean squares of GCA were highly significant. Therefore, both additive and additive by additive genetic variance appeared to be the most important and reliable component of genetic variances.

The presence of significant estimates of GCA and SCA suggest the importance of either additive (GCA) or non additive gene action (SCA). Indeed, superior hybrids depend on the presence of dominance genetic variance. In the same time, superior hybrids would depend on additive by additive genetic epistasis in case of the absence of the dominance variance. Therefore, it is very important to estimate the two types of gene action.

The utilization of two mating designs where used with the same inbred lines. These parental lines were planned to evaluate their validity to estimate both GCA and SCA using the homogeneity test of variance which declared that the estimates of GCA and consequently the additive genetic variance would be more valid if obtained from the mean squares of lines x tasters mating design while, the dominance genetic variances would be obtained with more validity from the diallel crosses mating design for most studied traits.

Keywords: Maize, general combining ability, specific combining ability, heterosis, hybrid and homogeneity test.

INTRODUCTION

Corn, *(Zea maize*, L.) , is one of the most important source of carbohydrates and oil for feeding for both human and animals. All countries which have a suitable atmosphere for corn plantation cultivate corn. In Egypt, as well as all other countries, corn is considered an important field crop where it is cultivated for an area about 1,60 million feddans to meet the demands of feeding human and animals. Due to the importance of corn, scientists in all countries gave corn breeding great concern and established programs to produce maize hybrids with high yielding ability. In this respect, many authors obtained high yielding hybrids showing large amounts of heterosis, among them: Alvi *et al*., (2003), Welcker *et al.*, (2005), Amiruzzaman *et al*., (2010) and El-Ghonemy and Ibrahim, (2010) who obtained heterosis values due to the high parent for yield trait were of about: 33.04, 32, 17.60 and 33.91%, respectively.

Melani and Carena (2005) indicated that the magnitudes of general combining ability were larger than those of specific combining ability indicating the predominance of additive gene effect. On the other hand, Brandon *et al*., (2007) found that the non-additive genetic variances including dominance were larger than the additive genetic variances for only grain yield. Rather *et al*., (2007) indicated that the pooled analysis of variance for combining ability revealed the presence of highly significant of mean squares due to GCA and SCA for all studied traits. The ratio of GCA to SCA variances indicated the preponderance of the latter component in controlling the expression of most studied traits.

However, Amiruzzaman *et al*., (2010) showed that the significant estimates of GCA and SCA genetic variances suggested the importance of both additive and non-additive gene actions for the expression of most studied traits. Preponderance of additive gene action was noticed for ear diameter and 1000-kernel weight where the other traits were controlled by non-additive types of gene action. From the heritability point of view, Rezaie and Roohi (2004) studied 90 F_1 hybrids of maize. They claimed that broad sense heritability estimates ranged from 68 to 91% for number of kernels/row and 100 kernels weight, respectively. Narrow sense heritability estimates ranged from 6.0 to 73% for grain yield per plant and days to tassel emergence, respectively.

The objectives of this study were directed to determine heterosis under the two different environments (Mansoura and Sohag), and their combined data to obtain estimates of GCA and SCA using the two different mating designs. The utilized mating designs included diallel crosses and line x tester mating design. Both GCA and SCA were evaluated in a homogeneity test of variance to test the validity of each of them.

MATERIALS AND METHODS

Genetic materials:

In this investigation, seven inbred lines (Inb. L. 2, Inb. L. 21, Inb. L. 81, Inb. L. 122, Inb. L. 133, Inb. L. 144 and Inb. L. 147) and three testers (Giza 2, S.C.10 and T.W.C.310) of maize were used. The seeds of all inbred lines and testers were obtained from National Maize Program, Field Crops Research Institute, Agricultural Research Center (ARC), Egypt.

In the growing season of 2008, two mating designs were made utilizing these genetic materials. The first is a partial diallel crosses including the seven parental lines to produce 21 F_1 hybrids. The second is a line x tester mating design including the three testers crossed by the same seven parental lines to produce 21 F_1 hybrids. Thus, there will be two experiments; the first one included the 21 partial diallel cross hybrids and their seven parental lines. The second included the 21 F_1 hybrids obtained from the line x tester crossing in addition to their 10 parents (seven parental lines and three testers). The seeds of all genotypes were cultivated in two separate experiments at Mansoura and Sohag to be evaluated during the maize growing season of 2009.

Definition of traits:

Data were recorded on different yield component traits. These traits were:

1) Ear weight in grams (E.W. g.):
2) Number of rows/ear: (No. R. /E.):
3) Number of kernels/row: (No. K. /R.):
4) Weight of 100 kernels in grams. [W.100.k.(g)]

Statistical analysis:

A-Analysis of variance:-

In this study, several types of analysis of variance were made. The statistical procedures used in this study were done according to the analysis of variance for Randomized Complete Blocks Design (RCBD) outlined by Cochran and Cox (1957) for both experiments.

B-Genetic variance components:-

The analyses of variance utilizing the F_1 hybrids were executed according to the two methods of mating designs:

1- The first method was the partial diallel crosses mating design according to Griffing (1956), including the combined analysis over the two locations at Mansoura and Sohag and known as Experiment 1.

2- The second method was line x tester mating design which included the application of Comstock and Robinson (1952) mating design known as Experiment II where the mating design use three testers x seven lines to produce 21 crosses. The 21 F_1 hybrids and their 10 parents were evaluated at both locations.

Test of homogeneity of variance:-

In this study, the genetic materials were set up in two mating designs. The first was the partial diallel crosses and the second was the line x tester mating design. Both designs, makes it possible to obtain estimates for the genetic variance components utilizing the mean squares obtained from the analysis of variance tables. It is acceptable that both designs would present reliable estimates, therefore, it would be very useful to test the homogeneity of the variances (the mean squares) obtained from the two mating designs using F- test according to following formula :

$$\textbf{F value} = \frac{\text{The large mean squares (from one mating design)}}{\text{The small mean squares (from the second mating design)}}$$

The estimated F value would be compared to the tabulated F value with the degrees of freedom for the numerator and dominator. Thus, F value would be either significant or insignificant. When the F value is significant, it would indicate the importance of the numerator mean squares. Accordingly, the significance of homogeneity test would indicate the importance of the mating design used to estimate different genetic parameters.

RESULTS AND DISCUSSION

The mean performance of the seven parental lines and their F_1 hybrids resulted from the partial diallel crosses at both locations and their combined data for all studied traits are presented in Table 1. The means for ear weight for the seven parental lines at both locations showed lower values than the means of their F_1 hybrids. This quantitative trait is one of the most important yield component traits and therefore, it determines the yielding ability of a given genotype. In this study, it appeared that parent No. 3 (103.7g) and No. 5 (102.35g) yielded the highest F_1 hybrid 3x5 (273g). Looking into all the means, it appeared that this role is true for all parents and their F_1 hybrids i.e.; the high parents for ear weight produce a high F_1 hybrid for the same trait indicating that the choice of parent is of paramount importance to produce the superior F_1 hybrids. It should be indicated that for this trait all the F_1 hybrids exceeded their parents and all other parents with large values proving that heterosis is a true fact.

For No. of rows/ear, it was very clear that all F_1 hybrids exceeded their parents and all other parents. The parents ranged from 12.25 to 14.3 rows/ear while the hybrids ranged from 14.1 to 16.65 rows per ear which was an indication about the superiority of F_1 hybrids when compared with their parents. Concerning to No. of kernels/row almost showed similar behavior. Concerning to No. of kernels/row in the parents ranged from 22.7 to 30.25 while it is ranged in the F_1 hybrids from 35.2 to 39.4. These results showed that all hybrids had more kernels per row than the parents which intern increase the yielding ability of ears.

The superiority of F_1 hybrids could be also seen when the weight of 100 kernels trait was studied. The results in Table 1 appeared that the parents means for this trait ranged from 22.15g to 23.75g while it ranged in the F_1 hybrids from 31.35g to 40.7g. Thus, the weight of kernels in the F_1 hybrids once again declares the superiority of the F_1 hybrids. It should be also indicated here that the two parents No. 5 (22.15g) and No. 7 (23.75g) produced the highest F_1 hybrid 5x7 (40.7g) which once again declare that the high parent for a trait produce the highest F_1 hybrid for the same trait.

The previous results presented evidence about the superiority of F_1 hybrids for all yield component traits, however it should be indicated that the performances of the parents and their F_1 hybrids greatly varied at both locations. In general, the performances of their F_1 hybrids and the parents were better at Mansoura than at Sohag. Such an observation could be expected due to the atmospheric conditions and type of soil which greatly vary at both locations. Looking into the performances of the F_1 hybrids it appeared that the best F_1 hybrid that could be planted at Mansoura is the hybrid 4x6 and the best hybrid that could be planted at Sohag is the hybrid 3x5.

Table 1: The mean performance of the seven parental lines and their 21 F_1 hybrids resulted from the partial diallel crosses at both locations and from the combined data for yield component traits

Genotypes	Ear weight (g)			No. of rows/ear			No. of kernels/row			100 kernels weight (g)		
	M	S	C	M	S	C	M	S	C	M	S	C
L_1	126.7	69.6	98.15	12.9	11.6	12.25	26.3	19.1	22.7	21	18.2	22.15
L_2	127.2	69	98.1	13.8	12.2	13	25.3	24.9	25.1	23.5	15.3	22.15
L_3	126.1	81.3	103.7	14	12.2	13.1	25.8	23.8	24.8	26.9	19.7	22.15
L_4	112.2	87.7	99.95	12.4	12.2	12.3	27.6	25.8	26.7	26.2	19.4	22.15
L_5	113.9	90.8	102.35	15.3	13.3	14.3	28.8	26.5	27.65	27.4	16.9	22.15
L_6	99.4	99	99.2	14	13.8	13.9	31	27.6	29.3	28.6	17.2	22.9
L_7	99.4	105.8	102.6	14.4	13.5	13.95	32.7	27.8	30.25	28.1	19.4	23.75
1x2	295.5	206.3	250.9	16.2	12.2	14.2	43	34.5	38.75	42.5	26.2	34.35
1x3	303.9	147.2	225.6	16	12.5	14.25	41.9	36.9	39.4	37.6	26.1	31.85
1x4	323.9	144.7	234.3	16	12.9	14.45	43.4	34.1	38.75	34	29.9	31.95
1x5	347.8	140.2	244	15.1	14.7	14.9	40.6	37.4	39	35.7	27.2	31.45
1x6	307.2	149.8	228.5	15.3	12.9	14.1	37.7	33.8	35.75	38.9	26.8	32.85
1x7	332.8	167.8	250.3	15.8	13.5	14.65	41.2	34.8	38	37.2	27.6	32.4
2x3	318.9	179.1	249	16.7	16.2	16.45	41.4	37.2	39.3	38.6	24.1	31.35
2x4	306.7	152.3	229.5	16.4	15.6	16	43.8	33.1	38.45	34.3	31.3	32.8
2x5	315.6	177.1	246.35	15.8	12.5	14.15	42.9	33.1	38	37.5	27.4	32.45
2x6	307.8	171.2	16	17.3	16	16.65	39.7	36.2	37.95	39	26.1	32.55
2x7	326.7	164.7	245.7	16	14.7	15.35	38.3	32.1	35.2	47.4	29.5	38.45
3x4	323.9	203.3	263.6	15.8	13.3	14.55	39.3	34.3	36.8	37.9	29.9	32.4
3x5	317.8	228.2	273	16.4	13.1	14.75	39.9	35.7	37.8	44.5	25.4	34.95
3x6	313.3	208.7	261	17.5	14.9	16.2	32.1	41.6	36.85	32.8	42.4	37.6
3x7	315	204.9	259.95	16	14.2	15.1	43.3	32.5	37.9	44.6	33.4	39
4x5	322.2	165.6	243.9	15.6	14	14.8	44	31.1	37.55	42.2	33.3	37.75
4x6	335.6	184.3	259.95	15.3	14.6	14.95	39.8	31.9	35.85	34.5	33.8	34.15
4x7	332.8	159.2	246	16	14.2	15.1	39.6	36.7	38.15	36.5	35.9	36.2
5x6	332.2	183.9	258.1	15.6	14.5	15.1	38.9	36.3	37.6	37.9	29.1	33.5
5x7	346.7	193.8	270.25	14.9	14.9	14.9	43.4	30.2	36.8	47.8	33.6	40.7
6x7	317.8	215.8	266.8	16.9	13.8	15.35	43.9	34.3	39.1	42.5	35.2	38.85
LSD 5%	49.13	44.80	46.97	1.44	1.46	1.45	2.78	3.99	3.39	3.82	8.04	5.93
LSD 1%	65.43	59.66	62.55	1.92	1.94	1.93	3.70	5.31	4.51	5.10	10.7	7.91

The mean performance of all genotypes resulted from the line x tester mating design for the two different locations and their combined data for all studied traits are shown in Table 2. Ear weight which is the most important trait of yield components indicated without any doubt that all the F_1 hybrids at both locations and from the combined data exceeded not only the testers but also the inbred lines. The magnitudes of the means indicated that the inbred line No. 3 showed the largest mean (103.7g) and T_3 also showed the largest mean (151.05g). Their hybrid combination T_3xL_3 showed the largest mean among all F_1 hybrids (261.25g).

Table 2: The mean performance of lines, testers and their 21 F_1 hybrids resulted from line x tester mating design at both locations and from the combined data for yield component traits.

Genotypes	Ear weight (g)			No. of rows/ear			No. of kernels/row			100 kernels weight (g)		
	M	S	C	M	S	C	M	S	C	M	S	C
L_1	126.7	69.3	98	12.9	11.6	12.25	26.3	19.1	22.7	21	18.2	19.6
L_2	127.2	69	98.1	13.8	12.2	13	25.3	24.9	25.1	23.5	15.3	19.4
L_3	126.1	81.3	103.7	14	12.2	13.1	25.8	23.8	24.8	26.9	19.7	23.3
L_4	112.2	87.7	99.95	12.4	12.2	12.3	25.8	25.6	25.7	26.2	19.4	22.8
L_5	113.9	90.8	102.35	15.3	13.3	14.3	28.8	26.5	27.65	27.4	16.9	22.15
L_6	99.4	99	99.2	14	13.8	13.9	31	27.6	29.3	28.6	17.2	22.9
L_7	99.4	62.8	81.1	14.4	13.5	13.95	32.7	27.8	30.25	28.1	19.4	23.75
T_1	206.1	87.2	146.65	14.9	13.3	14.1	35.3	29.3	32.3	31.6	13.4	22.5
T_2	213.9	58.1	136	17.3	4.7	11	35.1	13	24.05	31.6	9.9	20.75
T_3	228.3	73.8	151.05	14	6.7	10.35	36.4	10.9	23.65	33.3	27	30.15
T_1xL_1	235.6	150.8	193.2	12.7	12	12.35	36	25.2	30.6	32.2	25.1	28.65
T_1xL_2	232.2	130.4	181.3	15.8	12.5	14.15	36.1	26.8	31.45	32.1	31.7	31.9
T_1xL_3	232.2	134.8	183.5	15.6	12.9	14.25	36.8	28.4	32.6	32.1	31.7	31.9
T_1xL_4	256.5	128.9	192.8	14.2	12.4	13.3	36.1	29.8	32.95	32.4	33.3	32.85
T_1xL_5	288.9	190.1	239.5	17.5	14.2	15.85	38	30.1	34.05	39	35	37
T_1xL_6	337.2	161.2	249.2	14.7	14.4	14.55	37.4	35.9	36.65	37.2	34.7	35.95
T_1xL_7	276.7	177.1	226.9	14.9	14.7	14.8	37.6	36.6	37.1	43.1	36.1	39.6
T_2xL_1	285.6	195.7	240.65	14	13.5	13.75	38	36.8	37.4	41.1	34.9	38
T_2xL_2	300	158.3	229.15	14.7	14	14.35	37.7	33.2	35.45	37.2	35.4	36.3
T_2xL_3	311.1	185.2	248.15	15.3	12.2	13.75	37.5	37.3	37.4	51.8	34	42.9
T_2xL_4	317.8	171.9	244.85	15.1	14	14.55	37.4	36.7	37.05	41.5	34.3	37.9
T_2xL_5	282.2	166.5	224.35	15.8	14	14.9	37	37	37	44.5	36	40.25
T_2xL_6	309.5	212.5	261	15.5	13.5	14.5	36.2	33.8	35	37.9	33.5	35.7
T_2xL_7	302.5	154.1	228.3	14	12	13	37.7	36.6	37.15	39.2	34.9	37.05
T_3xL_1	311.1	189.6	250.35	15.1	13.5	14.3	37.3	37.1	37.2	48.4	35.4	41.9
T_3xL_2	287.8	170.8	229.3	13.8	13.3	13.55	37.7	33	35.35	42.7	36.8	39.75
T_3xL_3	290.6	231.9	261.25	13.3	13.1	13.2	37.8	36.3	37.05	49.6	35.3	42.45
T_3xL_4	297.8	203.7	250.75	14.2	14	14.1	37.7	37	37.35	51.7	33.3	42.5
T_3xL_5	280	176.8	228.4	15.6	14.7	15.15	37	37	37	48.6	33.6	41.1
T_3xL_6	327.8	176.2	252	17.1	13.3	15.2	37.7	37.1	37.4	47.7	39.2	43.45
T_3xL_7	292.8	194.1	243.45	14	13.3	13.65	39.2	37.1	38.15	50.4	36.4	43.5
LSD 5%	29.37	62.71	46.04	0.73	1.46	1.095	1.75	5.06	3.41	2.99	8.15	5.57
LSD 1%	39.06	83.40	61.23	0.97	1.95	1.46	2.32	6.73	4.53	3.98	10.8	7.39

The magnitudes of the means at Mansoura were always larger than their corresponding means at Sohag for all genotypes. However, it should be indicated that the best hybrid that would be cultivated at Sohag is the hybrid

T_3xL_3 (231.94g) while the best hybrid that would be cultivated at Mansoura is the hybrid T_1xL_6 (337.2g).

In general, the combined means showed that ear weight in the hybrids ranged from 181.1 to 261.25g while among parents including testers ranged from 98 to 151.05g. Therefore, these results clearly indicated that the superiority of the F_1 hybrids.

For No. of rows/ear, it was very clear that all F_1 hybrids exceeded their parents and all other parents. The parents ranged from 10.35 to 14.3 rows/ear while the hybrids ranged from 12.35 to 15.85 rows per ear which was an indication about the superiority of F_1 hybrids when compared with their parents.

No. of kernels/row almost showed similar behavior. In the parents it ranged from 22.7 to 32.3 kernels, while it is ranged in the F_1 hybrids from 30.6 to 38.15 kernels. These results showed that all the hybrids had more kernels per row than their parents which intern increase the yielding ability of ears.

The superiority of F_1 hybrids could be also seen when the weight of 100 kernels trait was studied. Form Table 2, it appeared that the 100 kernels weight for parents ranged from 19.4g to 30.15g while it ranged in the F_1 hybrids form 28.65g to 43.5g. Thus, the weight of kernels in the F_1 hybrids once again declared the superiority of the F_1 hybrids. It should be also indicated here that the two parents No. L_7 (23.75g) and T_3 (30.15g) produced the F_1 hybrid T_3xL_7 (43.5g) which once again declared that the high parents for this trait produce the highest F_1 hybrid.

1- The nature of variation:

a- The nature of variation from the partial diallel crosses:

During 2009 growing season, the seven inbred lines and their 21 F_1 hybrids resulted from the partial diallel crosses were evaluated at Mansoura and Sohag for several traits. The obtained data were set up in an analysis of variance for each location and for the combined analysis over both locations and the results were obtained for yield component traits are presented in Table 3.

Table 3: The combined analysis of variance of the diallel crosses for yield component traits.

S.V.	d.f	M.S.			
		Ear Weight	No. of rows/ear	No. of kernels/row	100 kernels weight
Loc.	**1**	547669**	79.13**	1256**	3726**
Reps x Loc.	**4**	2596**	0.383*	14.99**	33.12**
Crosses	**27**	26817**	7.030**	163.4**	231.2**
GCA	**6**	1395**	6.297**	6.477**	102.8**
SCA	**21**	34080**	7.239**	208.2**	267.9**
Crosses x Loc.	**27**	5043**	3.789	27.65**	33.56**
GCA x Loc.	**6**	1594**	1.278	27.12**	58.78**
SCA x Loc.	**21**	6028**	4.507	27.79**	26.35**
Error	**108**	824.9	0.783	4.414	14.80

*** and ** Significance at 5% and 1% levels of probability, respectively.**

Yield component traits showed significant interactions with all sources of variations indicating the important effects of locations on yield component traits. These results would be expected since all quantitative traits are highly affected by environments and show variable performances from one environment to another. The significant interactions with locations would reveal the importance of the choice of the suitable hybrid for each location. Plant breeders must consider the significant effects of both GCA and SCA when they planning their programs to produce superior maize hybrids.

b- The nature of variation from the line x tester crosses:

In the same growing season of 2009, the results of line x tester mating design were evaluated over both locations and the analyses of variance for yield component traits are presented in Table 4.

Table 4: The combined analysis of variance over both locations for yield component traits obtained from the line x tester mating design.

S.V.	d.f	M.S.			
		Ear Weight	No. of rows/ear	No. kernels/row	100 kernels weight
Loc.	**1**	70498**	2.240	102.8**	187.7**
Reps. x Loc.	**4**	69506**	105.6**	205.9**	304.8**
Crosses	**20**	78316**	292.5**	1901**	2185**
Lines	**6**	260157**	971.8**	6332**	7249**
Testers	**2**	631.8**	0.515	5.034**	23.05**
Lines x testers	**12**	343.9**	1.452**	2.513**	13.34**
Crosses x Loc.	**20**	5118**	2.254	18.74**	51.98**
Lines x Loc.	**6**	15825**	4.654	54.39**	121.2**
Testers x Loc.	**2**	393.6**	0.714	5.423*	36.02**
Lines x testers x Loc.	**12**	553.2**	1.311	3.134*	20.05**
Error	**120**	162.2	0.599	1.072	2.182

*** and ** Significance at 5% and 1% levels of probability, respectively.**

The analyses of variance for yield component traits showed that all the sources of variation were significant and highly significant with few exceptions such as testers and the interactions between crosses, lines, testers and lines x tasters by location for No. of rows per ear. Once more, the results indicated that quantitative traits such as yield component traits were highly affected by environment and would show variable performance from location to location. In this connection, the choice of the suitable hybrid for any given location is an important task of plant breeders.

2- The magnitudes of heterosis.

The estimated amounts of heterosis form each and both locations along from the mid and better parents were obtained and the results are presented in Table 5.

With respect to yield component traits in Table 3, the amounts of heterosis from the MP were: 179.30, 17.78, 51.97 and 52.77% for Ear weight, No. of rows/ear, No. of kernels/row and 100 kernels weight at Mansoura location, respectively. The values of heterosis were: 107.13, 9.06, 31.07 and 65.30% for the same traits at the second location at Sohag, respectively.

While the amounts of heterosis from the combined data for these traits were: 143.22, 13.42, 41.52 and 59.04%, respectively.

The estimated amounts of heterosis with respect to the BP were: 152.48, 3.79, 26.36 and 38.7% for Ear weight, No. of rows/ear, No. of kernels/row and 100 kernels weight at Mansoura, respectively. They were: 68.70, -1.32, 23.05 and 51.12% for the same traits at Sohag, respectively. While the values of heterosis from the combined data for the same traits were: 110.59, 1.24, 24.71 and 44.90%, respectively.

In general, it is an evident fact that heterosis exists with large amounts when related to the MP or the BP. It is very important to indicate that the lower ranges of the F_1 hybrids were larger than the upper ranges of the parental lines. This result in its self is an indication without any doubt that hybrids in corn are of great economical importance and should be used in corn plantation. In this respect, many authors among them Abd El-Aal (2002), Venugopal *et al*.,(2002), Mosa (2003), Alvi *et al*.,(2003), Pooja *et al*.,(2011) and El-Badawy (2013) obtained similar results.

Table 5: The estimates of heterosis at both locations and their combined data from the MP % and BP % and the ranges from diallel mating design.

Generations		L.	Ear weight	No. of rows/ear	No. of kernels/row	100 kernels weight
Parents (MP)		M	115.0	13.5	27.19	25.96
		S	86.17	13.03	26.1	18.01
		C	100.59	13.23	26.65	21.99
Range		M	99.4-127.2	11.6-15.3	19.1-32.7	21-28.6
		S	69-105.8	12.2-14.4	23.8-27.8	15.3-19.7
BP		M	127.2	15.3	32.7	28.6
		S	105.8	14.4	27.8	19.7
		C	116.5	14.85	30.25	24.15
F_1		M	321.2	15.9	41.32	39.66
		S	178.48	14.21	34.21	29.77
		C	249.84	15.06	37.77	34.72
Range		M	295.5-347.8	14.9-17.3	37.7-43.9	34-47.8
		S	140.2-228.2	12.2-17.5	30.2-37.4	24.1-36.5
Heterosis (MP)%		M	179.30	17.78	51.97	52.77
		S	107.13	9.06	31.07	65.30
		C	143.22	13.42	41.52	59.04
Heterosis (BP)%		M	152.48	3.79	26.36	38.67
		S	68.70	-1.32	23.05	51.12
		C	110.59	1.24	24.71	44.90
LSD MP	0.05	M	42.53	1.24	2.41	3.31
		S	38.78	1.26	3.45	6.96
	0.01	M	56.65	1.66	3.20	4.41
		S	51.65	1.68	4.60	9.27
LSD BP	0.05	M	49.11	1.44	2.78	3.83
		S	44.78	1.46	3.99	8.04
	0.01	M	65.41	1.91	3.70	5.10
		S	59.63	1.94	5.31	10.70

Where: M= Mansoura, S= Sohag and C= Combined

Table 6: The estimates of heterosis at both locations and their combined data from the MP % and BP % and the ranges from line x tester mating design.

Generations		L.	Ear weight	No. of rows/ear	No. of kernels/row	100 kernels weight
Parents (MP)		M	190.82	14.06	33.23	28.63
		S	77.9	11.6	24.2	23.2
		C	134.36	12.83	28.72	25.92
Range		M	99.4-228.3	11.6-17.3	23.8-36.4	15.3-33.3
		S	58.1-90.8	4.7-14.4	10.9-32.7	9.9-28.6
BP		M	228.3	17.3	36.4	33.3
		S	90.8	14.4	32.7	28.6
		C	159.55	15.85	34.6	30.95
F_1		M	288.4	14.51	37.1	41.4
		S	172.2	13.8	34.5	34.84
		C	230.3	14.16	35.8	38.12
Range		M	232.2-337.2	12-17.5	36.1-39.2	32.1-39.2
		S	105.8-231.9	12-15.6	25.2-37.7	25.1-51.8
Heterosis (MP)%		M	51.14	3.20	11.7	44.60
		S	121.1	19.0	42.6	50.17
		C	86.12	11.1	27.15	47.39
Heterosis (BP)%		M	26.33	-16.13	1.92	24.32
		S	89.7	-4.2	5.5	21.82
		C	58.02	-10.17	3.71	23.07
LSD MP	0.05	M	25.43	0.63	1.51	2.59
		S	54.30	1.27	4.38	7.05
	0.01	M	33.83	0.84	2.01	3.45
		S	72.22	1.68	5.83	9.38
LSD BP	0.05	M	29.37	0.73	1.75	2.99
		S	62.70	1.46	5.06	8.14
	0.01	M	39.06	0.96	2.32	3.98
		S	83.39	1.95	6.73	10.83

As appeared in Table 6, the amounts of heterosis from the MP were: 51.14, 3.20, 11.7 and 44.60% for ear weight, No. of rows/ear, No. of kernels/row and 100 kernels weight at Mansoura, respectively. The values of heterosis were: 121.1, 19.0, 42.6 and 50.17% for the same traits at Sohag, respectively. While the amounts of heterosis from the combined data for these traits were: 86.12, 11.1, 27.15 and 47.39%, respectively.

The estimated amounts of heterosis with respect to the BP % were: 26.33, -16.13, 1.92 and 24.32% for ear weight, No. of rows/ear, No. of kernels/row and 100 kernels weight at Mansoura, respectively. They were: 89.7, -4.2, 5.5 and 21.82% for the same traits at Sohag, respectively. While the values of heterosis from the combined data for the same traits were: 58.02, -10.17, 3.71 and 23.07%, respectively.

In general, yield component traits also presented evidence that heterosis exists with large amounts when related to the MP % or the BP %. Once more, it is very important to indicate that the lower ranges of the F_1 hybrids were larger than the upper ranges of the parental lines. This result suggests that hybrids in corn are of great economical importance and should be used in corn production. It should be indicated that many research workers such as Abd El-Aal (2002), Venugopal *et al.*,(2002), Mosa (2003), Alvi *et al*., (2003) and Kustanto *et al*.,(2012) obtained similar results which agreed with the results obtained from this investigation.

3- The magnitudes of the mean squares of GCA and SCA

A- GCA and SCA from the diallel mating design.

The statistical analyses of variance of the F_1 hybrids resulted from the partial diallel crosses for yield component traits were obtained and the results are presented in Table 7. In these analyses of variance, the sum squares were partitioned into GCA and SCA. The mean squares of these components are an estimate of additive and dominance genetic variances, respectively. The GCA mean squares also contain additive by additive genetic variance which in many cases explains the superiority of F_1 hybrids. The mean squares of GCA for yield and yield component traits were larger in magnitudes and significant for all studied traits at Sohag except No. of kernels/row. The mean squares for GCA at Mansoura were highly significant for No. of kernels/row and 100 kernels weight. In general, the magnitudes of the mean squares at Sohag were larger than their corresponding estimates at Mansoura for ear weight and No. of rows/ear while it was the vice versa for No. of kernels/row and 100 kernels weight. The mean squares of the GCA of all yield component traits were larger in their magnitudes than their corresponding estimates of SCA at Mansoura. At Sohag, the three traits ear weight, No. of rows/ear and 100 kernels weight showed the same behavior, while it was the opposite for No. of kernels/row where SCA mean squares were larger than those of GCA. Generally, all traits for yield component traits with the exception of No. of kernels/row indicated the importance of GCA and appeared to be of larger magnitudes than SCA. Thus, it would be expected that additive and additive by additive genetic variances were more important than dominance genetic variance which is contained within SCA. In this respect, many authors obtained similar results among them Desai and Singh (2001), El-Shenawy *et al*.,(2003), Melani and Carena (2005), Katta *et al*.,(2007) Rather *et al*. (2007), Moterle *et al*.,(2011), Borghi *et al*.,(2012), Ezatollah *et al*.,(2012), Gakunga *et al*.,(2012) and Haddadi *et al*.,(2012).

Table 7: The analysis of variance and mean squares for yield component traits at both locations obtained from diallel mating design.

S.V.	d.f		M.S.			
			Ear weight	No. of rows/ear	No. of kernels/row	100 kernels weight
Hybrids	**20**	**M**	555.7	1.106	14.70*	38.76**
		S	1973	5.912**	12.18*	51.81*
GCA	**6**	**M**	1009	1.199	14.90**	104.5**
		S	3090**	7.288**	5.424	94.36**
SCA	**14**	**M**	361.3	1.066	14.61**	10.58*
		S	1495	5.322**	15.07*	33.57
Error	**40**	**M**	900.9	0.771	2.887	5.472
		S	972.5	0.807	6.294	29.85

*** and ** Significance at 5% and 1% levels of probability, respectively.**

B- GCA and SCA from the line x tester mating design.

The estimates of GCA and SCA from line x tester mating design were obtained and the results are presented in Table 8. The obtained results indicated that the mean squares of GCA were highly significant. Therefore, both additive and additive by additive genetic variance appeared to be the most important and reliable component of genetic variances. These results were supported by the absence of SCA where, the mean squares of lines x testers were insignificant. This also would indicate the absence of dominance genetic variance. Therefore, the high performances of the hybrids in this mating design would be due to additive by additive genetic variance rather than dominance variance. These results would be considered favorable to plant breeders because they can initiate selecting programs based on the large magnitudes of additive by additive genetic variance to make use of transgressive segregation.

Table 8: The analyses of variance and mean squares for yield component traits from both locations obtained from line x tester mating design.

S.V.	d.f	M.S.				
		Ear weight		No. of rows/ear	No. of kernels/row	100 kernels weight
Hybrids	20	M	**60207	154.22**	1059.8**	906.81**
		S	23228**	140.48**	860.79**	1330.46**
GCA (lines)	6	M	20036**	509.21**	3532.1**	3021.4**
		S	75621**	467.21**	2855.07**	4349.69**
GCA (testers)	2	M	24.69	0.6535**	0.5632	0.9568
		S	1000.7	0.576	9.893	58.107*
SCA	12	M	160.85	2.325**	0.1782	0.4819
		S	736.35	0.439	5.468	32.906
Error	40	M	397.4	0.1998	0.9710	3.5102
		S	1695.17	0.658	9.173	32.023

*** and ** Significance at 5% and 1% levels of probability, respectively.**

6- Test of homogeneity of variances for the genetic parameters from both designs.

An important objective of this investigation was the identification of the relative importance of the variances obtained for the same genetic parameter from both mating designs. In this respect, the homogeneity tests of the variances for yield component traits were obtained for genetic parameters in terms of GCA and SCA at both locations and from the combined analysis for diallel and line x testers mating designs and the results are presented in Table 9.

The results of homogeneity test using the F test utilizing the larger mean squares for either mating design with its degrees of freedom in the numerator, while the smaller mean square with its degrees of freedom in the dominator. The significance would be determined by comparing the calculated F test with its corresponding tabulated F value at 1% and 5% levels of significance. Therefore, the estimates of GCA and consequently the additive genetic variance would be more valid if obtained from the mean squares of lines x tasters mating design while, the dominance genetic variances would be obtained with more validity from the diallel crosses mating design for most studied traits. In this respect, it should be indicated that the lines used in the diallel crosses were the same lines used in lines x testers mating design which would remove any doubt about these results.

Table 9: Test of homogeneity of variances between the diallel crosses and lines x testers for yield component traits at both locations and their combined analysis over both locations.

Location		Design	d.f	Ear weight	Homogeneity	No. of rows/ear	Homogeneity	No. of kernels/row	Homogeneity	100 kernels weight	Homogeneity
Mansoura	GCA	Diallel	6	1009		1.199		14.90		104.5	
		lines	6	20036	19.86**	509.21	424.70**	3532.1	237.05**	3021.4	28.91**
	SCA	Diallel	14	361.3		1.066		14.61		10.58	
		L x T	12	160.85	2.25	2.325	2.18	0.178	82.08**	0.482	21.95**
Sohag	GCA	Diallel	6	3090		7.288		5.424		94.36	
		lines	6	75621	24.47**	467.21	64.11**	2855.1	526.38**	4349.7	46.10**
	SCA	Diallel	14	1495		5.322		15.07		33.57	
		L x T	12	736.35	2.03	0.439	12.12**	5.468	2.76*	32.91	1.02
Combined data	GCA	Diallel	6	1395		6.297		6.477		102.8	
		lines	6	260157	186.5**	971.8	154.3**	6332	977.6**	7249	70.52**
	SCA	Diallel	21	34080		7.239		208.2		267.9	
		L x T	12	343.9	99.10**	1.452	4.99	2.513	82.85**	13.34	20.08**

*** and ** Significance at 5% and 1% levels of probability, respectively.**

The homogeneity test of variances was one of the important objectives of this investigation and it was intended to throw a light about the prober and suitable mating design to estimate the genetic variance components.

Tests of homogeneity were also obtained from the combined analyses to determine the validity of the genetic parameters and to indicate which mating design was the most appropriable. The magnitudes of F values followed the same pattern obtained earlier at each location. Homogeneity test for GCA was more accurate when line x tester analysis was used, while SCA appeared to be more accurate when estimated from the diallel crosses. In general, the results of the combined analyses over both locations insured the previous results obtained from each location.

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دراسة مقارنة لنظامين من نظم التزاوج لقياس مكونات التباين الوراثي المختلفة في الذرة الشامية

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في مصر كما في معظم دول العالم, يعتبر محصول الذرة الشامية من أهم المحاصيل الحقلية لأهميته كغذاء لكل من الإنسان و الحيوان. و نظرا لذلك, فمنذ إكتشاف ظاهرة قوة الهجين, فإن مربي النبات في محاولات مستمرة لإنتاج هجن عالية المحصول. و عادة ما ينجح معظم مربو النبات في الحصول علي هجن فائقة و خاصة عند التهجين بين سلالات متباعدة المنشأ.

و حيث أن قوة الهجين تعتمد علي التباين الوراثي الراجع للسيادة و في حالة غيابه فإنها تعتمد علي التباين التفاعلي التجميعي x التجميعي و هذا يتطلب قياس كل من القدرة العامة و القدرة الخاصة علي التآلف. و في هذا الصدد, فهناك العديد من نظم التزاوج التي يتم بها الحصول علي قياسات لكل منهما. و من أهم هذه النظم تلك المستخدمة في هذه الدراسة و هي نظام التزاوج نصف الدوري و نظام السلالة x الكشاف و كان إستخدام كلا النظامين بغرض تقييمهما لتحديد أيهما أكثر دقة في قياس هذه المكونات الوراثية. و قد تمت التجربة علي سبع سلالات من الذرة هي Inb. L. 2 , Inb. L. 21 , Inb. L. 81 , Inb. L. 122 , Inb. L. 133 , Inb. L. 144 و Inb. L. 147 بالإضافة إلي ثلاثة كشافات هي Giza 2 , S.C.10 , T.W.C.310 و ذلك في الموسمين

2008 و 2009 في كل من المنصورة (الموقع الأول) و سوهاج (الموقع الثاني). و في هذه الصدد تم إستخدام إختبار تجانس التباينات لتحديد أي النظامين من التزاوج أكثر دقة.

أظهرت النتائج وجود تباين لصفات المحصول في كلا الموقعين المنصورة و سوهاج كما تباينت قيمة قوة الهجين في كلا الموقعين و إن كانت القياسات توضح أنها كانت أعلي في المنصورة عنها في سوهاج حيث كانت قيم قوة الهجين بالنسبة لمتوسط الآباء في نظام التزاوج الدوري هي: 179.13, 17.78, 51.79 و 52.77 % فـــي المنصـــورة و 107.13, 9.06, 31.07 و 65.30 % في سوهاج لصفات وزن الكوز, عدد الصفوف في الكوز, عدد الحبوب في الصف و وزن 100 حبة علي الترتيب . أما بالنسبة لقيم قوة الهجين بالنسبة للأب الأعلى لنفس نظام التزاوج فكانـت: 152.48, 3.79, 26.36 و 38.7 % فـي المنصـورة و 68.70, -1.32, 23.05 و 51.12% في سوهاج لنفس الصفات علي الترتيب . أما بالنسبة لنظام السلالة x الكشاف فقد كانت قيم قوة الهجين بالنسبة لمتوسط الآباء هي: 51.14, 3.20, 11.7 و 44.60 % في المنصورة و 121.1, 19.0, 42.6 و 50.17 % في سوهاج لنفس الصفات علي الترتيب . أما بالنسبة لقيم قوة الهجين بالنسبة للأب الأعلى فكانت هي: 26.33, -16.13, 1.92 و 24.32 % في المنصورة و 89.7, -4.2, 5.5 و 21.82 % في سوهاج لنفس الصفات علي الترتيب.

أوضحت قياسات القدرة علي التآلف في كلا نظامي التزاوج إلي أهمية كلا من القدرتين العامة و الخاصة علي التآلف. و أثبت إختبار التجانس أن القدرة العامة علي التآلف كانت أكثر دقة عندما قيست من نظام السلالة x الكشاف , أما القدرة الخاصة علي التآلف فكانت أكثر دقة عندما قيست من نظام التزاوج نصف الدوري. و بالرغم من ذلك فإن كلا النظامين صالحين لقياس القدرة العامة و الخاصة علي التآلف و ما يتبعهما من قياس للثوابت الوراثية.

قام بتحكيم البحث

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