

DIALLEL CROSS ANALYSIS FOR YIELD, ITS COMPONENTS AND RESISTANCE TO BORER IN CORN

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ABSTRACT

A half diallel set of crosses involved eight maize inbred lines were evaluated in normal and artificial infection by borer at the Agricultural Research and Experiment Center, Faculty of Agriculture, Benha University, Egypt. To estimate combining ability, improve productivity of maize and resistant to borer Mean squares of environments, genotypes and its fractions as well as general and specific combining abilities (GCA and SCA) reached the significance level of probability for all traits. Low GCA/SCA ratios than unity were obtained for grain yield and resistance to borer characters in artificial infection environment and across environments. Therefore, non-additive type of gene action seemed to be more prevalent. Regarding to grain yield/ plant the crosses P3xP5, P3xP6 and P3xP8 had significant superiority over the check hybrid SC pioneer 30k8 under both environments. P3 ranked the first best inbred line in grain yield/ plant in both environments. The best combinations were P3xP5, P3xP6, and P3xP8 for grain yield/plant at both environments.

Key words: Maize, Combining ability, Heterosis and borer

INTRODUCTION

Maize (*Zea mays* L.) is a major crop for both human and livestock feed. Moreover, it used for industrial purposes such as manufacturing diverse commodities including starch, cooking oils, glue, soap, paint, insecticides, toothpaste, shaving cream, rubber tires, rayon, molded plastics and fuels.

In Egypt, different species of lepidoptera pests, attack maize plants i.e, the pink stem borer *Sesamia cretica* Led. (Noctuidae), the European corn borer (ECB) *Ostrinia nubilalis* Hubn (pyroustidae) and the purple-lined corn borer *Chilo Agamemnon* Bles. (Crambidae). *Sesamia cretica*, the most prevalent corn borer in Egypt attacks young maize plants after emergence, causing death of these plants (dead hearts) and its capable of damaging older plants causing drastic yield losses. These losses are mainly attributed to the decrease in number of plants per unit area (Stand) at harvest because of the

large number of dead hearts, increase in plant lodging, ear drops and predisposing infested plants to disease organisms.

One of the most important methods for controlling insect pests in the context of integrated pest control is to grow insect-resistant cultivars. The first step in designing an efficient breeding program for resistance to a certain insect are to identify sources of resistance and to determine how plant behaves under insect attack is transmitted from the original parents to the improved cultivars. Considerable efforts have been devoted to identify and develop corn germplasm with resistance to damage by the pink stem borer *Sesamia cretica*.

Little information had been reported in the literature about the type of gene action controlling maize resistance to *Sesamia cretica*.

Diallel cross design is widely and extensively used for estimating the types of gene action. Several methods have been devised in this respect to estimate the genetic components in plant population, little information, however is available about comparing and relative efficiency of these methods.

The genetic parameter estimates (GCA and SCA) are essential in developing breeding strategies. Furthermore, the magnitude of genetic components for a certain trait would depend mainly upon the environmental fluctuations under which the breeding populations will be tested. Therefore, much effort has been devoted by corn breeders to estimate the interactions between genetic components and environments. **Therefore, the objectives of the work were 1)** To determine performance of hybrid for the eight selected inbred lines and identifying maize genotypes superior in both of high resistance to *S. cretica* and high yielding ability to be offered to maize breeding programs. **2)** To study the inheritance of studied characters and estimating combining ability and heterosis of the studied genotypes for maize resistance to *S. cretica*.

MATERIALS AND METHODS

The experimental work of this investigation during the two successive seasons of 2013 and 2014 was carried out at the Experimental Research Station of Moshtohor, Benha University, Qalyubiya Governorate, Egypt.

A total of eight inbred lines varying in the resistance to corn borer were used to establish the experiment materials for several characters. These lines were selected based on their variability toward corn borers *Sesamia cretica* and other desirable plant aspects. The designation, pedigree and origin of these inbred lines are presented in table (1).

Table (1): The Designation, pedigree and origin of the studied eight inbred lines.

Designation	Pedigree	Origin
P ₁	43	Produced by Prof. Dr Ali EL- Hosary Egypt
P ₂	83	
P ₃	24	
P ₄	122	
P ₅	CML135	Introduced CIMMYT Mexico
P ₆	CML67	
P ₇	191	
P ₈	193	

In the first early summer season 2013, seeds of the eight inbred lines were split planted in 5th, 12th and 19th May to avoid differences in flowering time and to secure enough hybrid seed. All possible cross combinations without reciprocals were made between the eight inbred lines by hand method giving a total of 28 crosses seeds.

In the second summer, season 2014, two experiments were undertaken in two environments (under artificial infestation conditions and normal conditions). at the Agricultural Research and Experimental Station of the Fac. of Agric., Moshtohor. Each experiment included the eight inbred lines and 28 crosses as well as Single cross pioneer 30k8 which were sown on 22th of May. A randomized complete block design with three replications was used. Each plot consisted of two ridges of six m length and 70 cm width. Hills were spaced by 25 cm with three kernels per hill on one side of the ridge. The seedlings were thinned to one plant per hill. The dry method of planting was used. The first irrigation was given after 21 days from sowing. The plants were then irrigated at intervals of 10-15 days. The cultural practices were followed as usual for ordinary maize field in the area.

The traits studied were: number of kernels row-1, number of rows ear-1, 100-kernel weight and grain yield plant-1 adjusted to 15.5% grain moisture. Fifteen guarded plants from each plot were randomly taken as samples tested for the previous traits.

The ordinary analysis of variance for RCBD was firstly performed according to **Snedecor and Cochran (1989)**. General and specific combining ability estimates were obtained by employing **Griffing's (1956)** diallel cross analysis designated as method 2 mode 1 for yield, its components and losses and grain yield/ plant.

RESULTS AND DISCUSSIONS

The analysis of variances were recorded on all crosses in the two environments and the combined over them for agronomic traits are presented in **Table.2**.

Environment mean squares were significant for all the studied traits, with mean values in normal condition being higher than those in artificial infestation of borer for most studied traits. The increasing in the most of characters at normal condition may be due to favorable condition leading to great vegetative growth, yield and its components of corn plants.

The mean of squares for genotypes for all studied traits were found to be highly significant at the two environments as well as their combined analysis, indicating the presence of the true differences among these genotypes. The genotypes interactions with environment were also found to be highly significant for all studied traits. The significance of genotypes and genotypes interaction with the environments indicated that the behaviors of different studied genotypes were markedly different from an environment (Normal) to another (infestation environment).

Mean squares due to parents were found to be highly significant for all traits studied at the two irrigation treatments as well as their combined analysis except, no of rows/ ear in normal condition and grain yield / plant in infection environment . On the other hand, mean squares due to interactions between parents and the environments were insignificant for all studied traits except no of rows/ ear and 100-kernel weight. These findings indicated that parental cultivars differed in their mean performances in most studied traits. At the same time, the significance of parents and interaction parents with environments mean square indicating that the behavior of different studied parents were markedly different from one environment to another.

Crosses mean squares were significant for all the studied traits at both environments and the combined analysis, except, ear diameter in both and across environments.**Table.2**. This indicates the wide diversity between the parental materials used in this study.

Significant interaction mean squares between crosses and environments were detected for all studied traits except, No. of rows/ ear indicating that, these crosses behaved somewhat differently from environment to another. The crosses mean squares were found to be highly significant for all traits studied at the two environments as well as their combined analysis. Significant mean squares due to interaction between crosses and the environments found to be highly and/or significant for all studied traits except for, flowering characters, ear diameter and shelling percentage.

Table 2: Observed mean squares from analysis of variance, GCA and SCA mean squares for all studied traits.

SOV	d.f	Number of kernel / row	Number of rows / ear	100-Kernel weight	grain yield / plant
artificial infection environment					
Replication	2	4	0.09	3.87	49.6
Genotypes	35	163.18**	2.14**	129.55**	8353.79**
parent	7	46.28**	4.92**	25.95**	67.83
Cross	27	36.60**	1.38**	40.02**	1800.98**
Par.vs.cr.	1	4399.31**	3.38*	3271.87**	243281.56**
Error	70	10.37	0.52	5.64	64.17
GCA	7	12.87**	0.91**	7.47**	497.67**
SCA	28	64.77**	0.66**	52.11**	3356.33**
Error	70	3.46	0.17	1.88	21.39
GCA/SCA		0.2	1.37	0.14	0.15
chemical control environment					
Genotypes	35	7.3	0.78	56.48**	45.04
parent	7	125.65**	1.52**	236.82**	8745.23**
Cross	27	17.79**	0.63	9.21	335.15**
Par.vs.cr.	1	33.79**	1.03**	46.19**	1546.95**
Error	70	3360.73**	21.00**	6977.19**	261969.29**
GCA	7	5.92	0.49	4.96	52.54
SCA	28	9.06**	0.32**	9.82**	472.47**
Error	70	50.09**	0.55**	96.22**	3525.73**
GCA/SCA		1.97	0.16	1.65	17.51
GCA/SCA		0.18	0.59	0.1	0.13
combined analysis					
Environment(E)	1	279.48**	56.82**	1563.86**	5298.48**
Rep/E	4	5.65	0.43	30.17**	47.32
Genotypes(G)	35	254.42**	1.91**	326.41**	16916.48**
Parent(P)	7	49.51**	2.32**	4.48	301.77**
Cross(C)	27	30.86**	1.11**	55.21**	3143.95**
Par.vs.C.	1	7725.13**	20.62**	9902.44**	134738.71**
GXE	35	34.40**	1.75**	39.96**	182.54**
PXE	7	14.57	3.22**	30.68**	101.21
CXE	27	39.53**	1.30**	31.01**	203.98**
PXCXE	1	34.91*	3.76**	346.62**	172.86
Error	140	8.15	0.5	5.3	58.35
GCA	7	11.53**	0.55**	10.34**	919.81**
SCA	28	103.13**	0.66**	133.42**	6818.58**
GXE	35	34.40**	1.75**	39.96**	182.54**
GCA x E	7	10.40**	0.69**	6.96**	50.33*
SCA x E	28	11.74**	0.56**	14.91**	63.47*
Error	140	2.72	0.17	1.77	19.45
GCA/SCA		0.11	0.83	0.08	0.13
GCA x E/GCA		0.9	1.26	0.67	0.05
SCA x E/SCA		0.11	0.84	0.11	0.01

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

The mean performances of eight parental inbred lines and their tested 28 Crosses and the check hybrids SC pioneer 30k8, Hytech 2031 and SC 10 at each environment and the combined over the environments are presented in **Table.3**.

For No. of rows/ ear , No. of kernels/ row and 100-kernel weight non crosses showed significant high mean values than the best check hybrids in artificial infestation, normal condition and the combined analysis. However, the combinations P1xP8 for No of kernels/ row was; P1xP4, P1xP5, P1xP6, P3xP6, P3xP7, P4xP5, P4xP7, P4xP8, P5xP6, P5xP7 and P5xP8 for No of rows/ ear; P4xP5 for 100-kernel weight had the highest values but did not differ significantly compared with the best check hybrids.

Concerning grain yield/ plant the crosses P3xP5, P3xP6 and P3xP8 had significant superiority over the high check hybrid SC Hytech 2031 under both and across environment. These crosses exhibited significant increase of one or more of traits contributing to grain yield **Table.3**. The fluctuation of Crosses from environment to another was detected for most traits. These results would be due to significant interaction between Crosses and environments.

Heterosis expressed as the percentage deviation of F₁ mean performance from SC. Pioneer 30k8, Hytech 2031 and SC 10 values for all traits studied at the artificial infestation condition, normal condition and across environments are presented in **Table.3**.

Concerning grain yield/plant, the useful heterotic effects relative to SC. Pioneer 30k8, SC Hytech 2031 and SC 10 ranged from 22.97 to 25.63%, 10.93 to 13.33 and 17.43 to 19.97 in the combined analysis, respectively. However, most desirable heterotic effects were detected for the crosses P₃xP₅, P₃xP₆ and P₃xP₈ at both and across environment.

Hence, it could be concluded that these crosses offer possibility for improving grain yield in maize. Several investigators reported high heterosis for yield of maize; i.e. **Sabljarevic (1997)**, **El-Zeir (1998)**, **Nawar et al. (1998)**, **Abdel-sattar et al. (1999)**, **Abd El-Azeem (2000)**, **El-Bagoury et al. (2004)**, **Nawar et al. (2002)**, and **El-Hosary et al. (2006)**.

Table 3. Mean performance of all genotypes for all studied traits at both and across environments as well as relative superior for grain yield relative to checks hybrids

Genotype	No. of kernel / row			NO of Rows/ ear			100-kernel weight		
	Inf.	Normal	Combined	Inf.	Normal	Combined	Inf.	Normal	Combined
P1	19	22.07	20.53	8.43	11.73	10.08	20.67	22.5	21.58
P2	24.33	21.93	23.13	10.4	12.4	11.4	22	22.07	22.03
P3	22.5	25.4	23.95	12.27	11.33	11.8	21.67	22.17	21.92
P4	13.67	19.8	16.73	12.34	12	12.17	21.33	22.5	21.92
P5	14	18.93	16.47	10.77	11.2	10.98	14.67	26.33	20.5
P6	17.67	24.13	20.9	11.17	12	11.58	22	24	23
P7	18	25.13	21.57	11.78	11.2	11.49	22	23.17	22.58
P8	22.33	24.33	23.33	11.72	11.27	11.49	23.13	23.33	23.23
P1xP2	25.33	38.07	31.7	11.22	12.8	12.01	37	44.33	40.67
P1xP3	37.1	31.8	34.45	11.94	12	11.97	38.67	40	39.33
P1xP4	34.23	31.93	33.08	12.03	12.4	12.21	32.33	45.33	38.83
P1xP5	36.33	37.47	36.9	12.14	13.47	12.8	38	40.33	39.17
P1xP6	32.67	35.6	34.13	13.08	11.87	12.48	37	43	40
P1xP7	36.6	37.87	37.23	11.25	12.53	11.89	40.1	42	41.05
P1xP8	38.77	42.73	40.75	11.21	12.8	12	31.33	46.33	38.83
P2xP3	37.33	34.73	36.03	10.75	13.07	11.91	35	47.67	41.33
P2xP4	36.5	36.53	36.52	11.53	12.4	11.97	33.33	42.33	37.83
P2xP5	34.5	38.87	36.68	11.37	13.73	12.55	34	42.67	38.33
P2xP6	35.37	33.47	34.42	10.92	12.93	11.93	39	41.67	40.33
P2xP7	34	38.47	36.23	11.94	12.67	12.31	30.67	44.33	37.5
P2xP8	40.17	34.33	37.25	11.33	12	11.67	28	40	34
P3xP4	37.07	31.93	34.5	11.22	12.67	11.94	31	31.33	31.17
P3xP5	33.43	38.07	35.75	11.22	12.27	11.74	32.33	34	33.17
P3xP6	37.6	32.6	35.1	11.07	13.2	12.14	33.33	43	38.17
P3xP7	29.33	38.47	33.9	12.14	13.6	12.87	30.67	35.33	33
P3xP8	32.23	33.4	32.82	10.81	12.4	11.6	34	43.33	38.67
P4xP5	30.5	42.67	36.58	12.44	13.07	12.76	43	42.67	42.83
P4xP6	32.43	30.33	31.38	12.92	12.53	12.73	39.33	42.67	41
P4xP7	34	33.73	33.87	11.86	12.8	12.33	35.77	46	40.88
P4xP8	37.07	40.8	38.93	12.64	12.27	12.46	35.53	37.33	36.43
P5xP6	34.67	33	33.83	11.19	13.07	12.13	36.33	46	41.17
P5xP7	35.17	37.07	36.12	11.28	13.33	12.31	40.33	45	42.67
P5xP8	25.5	36.47	30.98	10.79	13.6	12.19	35	45.67	40.33
P6xP7	33.43	40.27	36.85	10.66	12.53	11.59	30	38.33	34.17
P6xP8	32.6	33.23	32.92	10.64	11.13	10.89	37	38.67	37.83
P7xP8	36.17	37.87	37.02	11.39	12.53	11.96	32.33	39.67	36
30K08	36.93	40.2	38.57	10.64	12.93	11.79	39.33	33.33	36.33
HT2031	35	39.8	37.4	10.22	12.13	11.18	45	39	42
S.C10	37.23	41.27	39.25	11.33	12.13	11.73	36.33	36.67	36.5
mean of parents	18.94	22.72	20.83	11.11	11.64	11.38	21.78	22.42	22.1
mean of crosses	34.29	36.13	35.21	11.54	12.7	12.12	35.01	41.75	38.38
mean of Genotypes	30.88	33.15	32.02	11.44	12.47	11.95	31.89	37.64	34.76
L.S.D 5%	5.23	3.95	4.57	1.17	1.13	1.13	3.86	3.62	3.68
L.S.D 1%	6.94	5.24	5.99	1.55	1.5	1.48	5.11	4.8	4.83

Table 3. Cont.

Genotype	grain yield / plant			relative superior relative to		
	Inf.	Normal	Combined	SC 30 k 8	S.C.2031	SC 10
P1	36.43	50.53	43.48			
P2	39.63	42.43	41.03			
P3	48.6	68.17	58.38			
P4	44.17	44.9	44.53			
P5	33.37	33.83	33.6			
P6	41.53	44.07	42.8			
P7	43.97	41.6	42.78			
P8	41.83	56.47	49.15			
P1xP2	141.8	150.27	146.03	-16.29**	-24.49**	-20.06**
P1xP3	138.47	148.63	143.55	-17.71**	-25.77**	-21.42**
P1xP4	148.2	159.1	153.65	-11.92**	-20.55**	-15.89**
P1xP5	159.63	158.3	158.97	-8.88*	-17.80**	-12.98**
P1xP6	126.27	143.9	135.08	-22.57**	-30.15**	-26.06**
P1xP7	157.3	165.57	161.43	-7.46*	-16.52**	-11.63**
P1xP8	153.97	165.47	159.72	-8.45*	-17.41**	-12.57**
P2xP3	159.93	156.33	158.13	-9.35**	-18.23**	-13.44**
P2xP4	164.7	166.97	165.83	-4.94	-14.25**	-9.22**
P2xP5	170.63	157.4	164.02	-5.98	-15.19**	-10.22**
P2xP6	153.47	174.97	164.22	-5.87	-15.08**	-10.11**
P2xP7	166.07	173.7	169.88	-2.62	-12.15**	-7.01*
P2xP8	144.9	155.67	150.28	-13.85**	-22.29**	-17.74**
P3xP4	133.23	131.87	132.55	-24.02**	-31.46**	-27.44**
P3xP5	216.83	221.5	219.17	25.63**	13.33**	19.97**
P3xP6	215.87	219	217.43	24.64**	12.44**	19.02**
P3xP7	137.7	163.4	150.55	-13.70**	-22.15**	-17.59**
P3xP8	211.83	217.2	214.52	22.97**	10.93**	17.43**
P4xP5	153.77	169.47	161.62	-7.36*	-16.43**	-11.53**
P4xP6	135.73	144.43	140.08	-19.70**	-27.56**	-23.32**
P4xP7	138.53	163.9	151.22	-13.32**	-21.80**	-17.22**
P4xP8	145.83	170.37	158.1	-9.37**	-18.25**	-13.46**
P5xP6	154.97	172.13	163.55	-6.25	-15.43**	-10.47**
P5xP7	148.9	169.63	159.27	-8.70*	-17.64**	-12.82**
P5xP8	155.6	174.13	164.87	-5.49	-14.75**	-9.75**
P6xP7	166.43	168.77	167.6	-3.93	-13.33**	-8.26*
P6xP8	126.63	171.03	148.83	-14.68**	-23.04**	-18.53**
P7xP8	122.7	120.93	121.82	-30.17**	-37.01**	-33.32**
30K08	185.33	163.57	174.45			
HT2031	204.5	182.27	193.38			
S.C10	186.93	178.43	182.68			
mean of parents	41.19	47.75	44.47			
mean of crosses	155.35	166.22	160.78			
mean of Genotypes	129.98	139.89	134.94			
L.S.D 5%	13.01	11.77	12.22			
L.S.D 1%	17.25	15.61	16.03			

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

Analysis of variance for combining ability as outlined by Griffing (1956) Method 2 model-1 in each environment and their combined data for all the studied traits is shown in Table.2. The mean squares associated with general combining ability (GCA) and specific combining ability (SCA) were significant for all the studied traits. 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.

Low GCA/SCA ratio, which belloyed the unity, was obtained for all cases revealing the predominance of non-additive gene effects for all traits. The same trend of the results were reported by El-Hosary and El-Badawy (2005), El-Shenawy (2005), Mosa and Motawei (2005), Motawei (2005), Soliman et al. (2005), El-Hosary et al. (2006), Sedhom et al. (2007), Akbar et al. (2008), Motawei and Mosa (2009) and GuangJauh (2009).

The mean squares of interaction between environment and both types of combining ability were significant for all studied traits. Such results showed that the magnitude of all types of gene action varied from environment to another. It is fairly evident that the ratio for SCA×E/SCA was higher than ratio of GCA×E/GCA for these traits. This result indicated that non-additive genetic effects were more influenced by the environmental conditions than additive genetic effects of these traits. These conclusions are in well agreement with those reported by Gelbert (1958). The genetic variance was previously reported to be mostly due to non-additive for plant and ear heights by Sadek et al. (2000), Amer (2003), Shafey et al. (2003) and Sedhom et al. (2007); No. of grains/row by Amer (2003), Shafey et al. (2003), El-Shenawy (2005) and Sedhom et al. (2007) and grain yield/plant by Sadek et al. (2000), Soliman (2000), Dodiya and Joshi (2002), Amer (2003), Mosa (2003-a), Shafey et al. (2003), El-Hosary and El-Badawy (2005); El-Shenawy (2005) and El-Hosary et al. (2006), Sedhom et al.(2007) and El-Ghonemy and Ibrahim (2010). On the other hand, the additive genetic variance was previously reported to be the most prevalent for earliness by Sadek et al. (2000); Dubey et al. (2001); Amer (2003); Mosa (2003-a&b), El-Hosary and El-Badawy (2005), El-Shenawy (2005), El-Hosary et al. (2006) and Sedhom et al. (2007); No. of rows/ear by Amer (2003); , Shafey et al. (2003) and El-Hosary and El-Badawy (2005), El-Shenawy (2005) and Sedhom et al. (2007);100-kernel weight by Dubey et al. (2001), Shafey et al. (2003), El-Hosary and El-Badawy (2005), Sedhom et al. (2007) and Motawei and Mosa (2009).

Estimates of GCA effects (\hat{g}_i) for individual parental inbred lines for each trait at both environments as well as the combined analysis are

presented in Table.4. General combining ability effects estimated herein were found to differ significantly from zero. The obtained high positive values for all traits in question

The parental inbred line P1 exhibited significant positive effects for 100-kernel weight at infestation condition and the combined analysis.

The inbred line P2 showed significant significant positive (\hat{g}_i) effects for No. of kernels/ row at the infestation condition. However, it shows undesirable significant or insignificant (\hat{g}_i) effects for other traits.

The parental inbred line P3 showed significant positive (\hat{g}_i) effects for number of kernels/ row under infestation condition, and grain yield/ plant at both and across environments. P3 ranked the first best inbred line in grain yield/ plant in both and across environments. However, it exhibited either significant undesirable or insignificant (\hat{g}_i) effects for other traits.

The parental inbred line P4 expressed significant significant positive (\hat{g}_i) effects for number of rows/ ear under infestation condition as well as the combined analysis. However, it exhibited either significant undesirable or insignificant (\hat{g}_i) effects for other traits.

The parental inbred line P5 had significant positive (\hat{g}_i) effects for, no of rows/ ear at Normal environment, 100-kernel weight in Normal environment as well as the combined analysis and grain yield/ plant at both and across environments. On the contrary, it expressed significant undesirable or insignificant (\hat{g}_i) effects for the other traits.

The parental inbred line P6 exhibited significant desirable \hat{g}_i effects for 100-kernel weight at infestation environment and the combined analysis. However, significant undesirable or insignificant (\hat{g}_i) effects were detected for the other traits.

The parental inbred line P7 exhibited significant positive (\hat{g}_i) effects for; No of kernels/row at normal environment. Meanwhile, it was around the average of the other cases.

The parental inbred line No. 8 showed significant desirable (\hat{g}_i) effects for; grain yield/ plant at control environment and no of kernels/ row at control environment and the combined analysis. Meanwhile, it was around the average of the other cases.

It is worth noting that the inbred line which possessed high (\hat{g}_i) effects for grain yield per plant showed the same effect for one or more of the traits contributing to grain yield.

Table.4: General combining ability effects for all the studied traits at both environments and their combined.

Parent	num of kernel / row			no of rows / ear			100 Kernel weight			grain yield / plant		
	Inf.	Normal	Combined	Inf.	Normal	Combined	Inf.	Normal	Combined	Inf.	Normal	Combined
g1	0.11	0.12	0.12	-0.32*	-0.09	-0.20**	1.08**	0.56	0.82**	-7.14**	-6.67**	-6.90**
g2	1.40*	0	0.70**	-0.31*	0.22	-0.05	-0.75	0.99*	0.12	1.09	-3.88**	-1.40**
g3	1.12*	-0.66	0.23	0.07	-0.03	0.02	-0.93*	-1.91**	-1.42**	14.12**	13.53**	13.82**
g4	-0.88	-1.08*	-0.98**	0.64**	-0.01	0.32**	0.67	-0.68	-0.01	-6.15**	-6.31**	-6.23**
g5	-1.98**	0.31	-0.84**	-0.1	0.27*	0.09	-0.03	1.19**	0.58**	5.72**	3.12*	4.42**
g6	-0.38	-1.16**	-0.77**	-0.02	-0.09	-0.05	1.14**	0.03	0.58**	-0.74	2.34	0.8
g7	-0.32	1.56**	0.62**	0.11	0.02	0.07	-0.24	-0.24	-0.24	-4.43**	-4.99**	-4.71**
g8	0.93	0.91*	0.92**	-0.07	-0.29*	-0.18**	-0.92*	0.06	-0.43**	-2.47	2.87*	0.2
L.S.D(0.05) gi	1.09	0.83	0.38	0.24	0.24	0.09	0.81	0.76	0.31	2.72	2.46	1.02
L.S.D(0.01) gi	1.45	1.1	0.5	0.32	0.31	0.12	1.07	1	0.4	3.61	3.27	1.34
L.S.D(0.05) gi-gj	1.65	1.25	0.72	0.37	0.36	0.18	1.22	1.14	0.58	4.12	3.72	1.93
L.S.D(0.01) gi-gj	2.19	1.66	0.95	0.49	0.48	0.23	1.62	1.52	0.76	5.46	4.94	2.53

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

In most traits, the values of (\hat{g}_i) effects mostly differed from environment to another. These findings coincided with that reached above where significant GCA by environment mean squares were detected in Table.2.

From the previous result, it could be concluded that the parental inbred lines P3 and P5 seemed to be the best general combiners for grain yield/plant and some of its components.

Specific combining ability effects were only estimated whenever significant SCA variances were obtained, Table.5.

With respect to No. of kernel/ear eighteen crosses in the infestation, thirteen crosses in normal environment and twenty one crosses in the combined analysis expressed highest desirable significant positive (\hat{S}_{ij}) effects.

With regard to No. of rows/ear, four, five and four crosses expressed significant positive (\hat{S}_{ij}) effects at infestation, normal as well as the combined analysis, respectively. The results indicated that crosses P1xP5, P1xP6, P2xP4 and P3xP7 recorded the highest desirable (\hat{S}_{ij}) effects in the combined analysis. The other crosses had either significant positive or insignificant (\hat{S}_{ij}) effects.

Regarding to 100-kernel weight, seventeen, twenty and twenty three crosses expressed significant positive (\hat{S}_{ij}) effects at infestation, normal and the combined analysis, respectively. The other crosses had insignificant (\hat{S}_{ij}) effects.

With regard to grain yield/plant, twenty two, twenty four and twenty five crosses showed significantly positive (\hat{S}_{ij}) effects at infestation, normal and the combined analysis, respectively.

In conclusion, the best combinations were P3xP5, P3xP6, and P3xP8 for grain yield/plant at the combined analysis. These crosses also, had the highest mean values in the combined analysis. It could be concluded that the previous crosses seemed to be the best combinations, where they had significant SCA effects for grain yield/plant and most of the yield components over the two environments.

In these crosses showing high specific combining ability involving only one good combiner such combinations would show desirable transgressive segregates, providing that the additive genetic system present in the good combiner as well as the complementary and epistatic effects present in the cross, act in the same direction to reduce undesirable plant characteristics and maximize the character in view. Therefore, the previous crosses might be of prime importance in breeding program for traditional breeding procedures. In most traits, the values of SCA effects were mostly different from environment to another. This finding coincided with that reached above where significant SCA by environment mean squares were detected Table 2.

Table.5: Specific combining ability effects for all the studied traits at both environments and their combined.

Cross	Number of kernel / row			num of rows / ear			100 Kernel weight			grain yield / plant		
	Inf.	Normal	Combined	Inf.	Normal	Combined	Inf.	Normal	Combined	Inf.	Normal	Combined
P1xP2	-7.05**	4.80**	-1.13	0.41	0.2	0.31	4.60**	5.33**	4.97**	17.86**	20.93**	19.40**
P1xP3	4.99**	-0.82	2.09*	0.75*	-0.35	0.2	6.45**	3.90**	5.17**	1.5	1.89	1.69
P1xP4	4.12*	-0.26	1.93	0.27	0.03	0.15	-1.48	8.00**	3.26**	31.50**	32.19**	31.85**
P1xP5	7.32**	3.88**	5.60**	1.12**	0.81*	0.97**	4.88**	1.13	3.01**	31.06**	21.96**	26.51**
P1xP6	2.06	3.49**	2.77**	1.98**	-0.42	0.78**	2.71*	4.96**	3.84**	4.16	8.35**	6.25*
P1xP7	5.93**	3.03*	4.48**	0.02	0.13	0.08	7.19**	4.23**	5.71**	38.88**	37.34**	38.11**
P1xP8	6.85**	8.55**	7.70**	0.16	0.71	0.44	-0.9	8.26**	3.68**	33.59**	29.38**	31.48**
P2xP3	3.94*	2.24	3.09**	-0.45	0.41	-0.02	4.61**	11.13**	7.87**	14.74**	6.80**	10.77**
P2xP4	5.10**	4.47**	4.79**	-0.23	-0.28	-0.26	1.35	4.56**	2.96**	39.78**	37.27**	38.52**
P2xP5	4.21*	5.41**	4.81**	0.34	0.77*	0.55*	2.71*	3.03*	2.87**	33.84**	18.27**	26.05**
P2xP6	3.47*	1.48	2.48*	-0.2	0.34	0.07	6.54**	3.20**	4.87**	23.13**	36.63**	29.88**
P2xP7	2.05	3.76**	2.90**	0.7	-0.04	0.33	-0.41	6.13**	2.86**	39.42**	42.69**	41.05**
P2xP8	6.97**	0.27	3.62**	0.27	-0.39	-0.06	-2.4	1.5	-0.45	16.30**	16.79**	16.54**
P3xP4	5.95**	0.52	3.23**	-0.93*	0.24	-0.34	-0.81	-3.54**	-2.17*	-4.72	-15.24**	-9.98**
P3xP5	3.42*	5.26**	4.34**	-0.19	-0.44	-0.32	1.22	-2.74*	-0.76	67.01**	64.96**	65.98**
P3xP6	5.98**	1.27	3.62**	-0.43	0.86**	0.22	1.06	7.43**	4.24**	72.50**	63.25**	67.88**
P3xP7	-2.34	4.41**	1.03	0.52	1.15**	0.83**	-0.23	0.03	-0.1	-1.98	14.98**	6.50*
P3xP8	-0.69	-0.01	-0.35	-0.64	0.26	-0.19	3.78**	7.73**	5.75**	70.20**	60.91**	65.56**
P4xP5	2.48	10.29**	6.38**	0.47	0.33	0.4	10.29**	4.70**	7.50**	24.21**	32.77**	28.49**
P4xP6	2.81	-0.57	1.12	0.85*	0.17	0.51	5.46**	5.86**	5.66**	12.64**	8.52**	10.58**
P4xP7	4.32*	0.1	2.21*	-0.33	0.32	0	3.27*	9.46**	6.37**	19.13**	35.31**	27.22**
P4xP8	6.14**	7.82**	6.98**	0.64	0.1	0.37	3.71**	0.5	2.11*	24.47**	33.92**	29.19**
P5xP6	6.15**	0.7	3.42**	-0.13	0.42	0.14	3.16*	7.33**	5.24**	20.00**	26.79**	23.39**
P5xP7	6.59**	2.04	4.32**	-0.17	0.57	0.2	8.54**	6.60**	7.57**	17.62**	31.61**	24.62**
P5xP8	-4.32*	2.09	-1.12	-0.48	1.15**	0.34	3.88**	6.96**	5.42**	22.37**	28.25**	25.31**
P6xP7	3.26	6.71**	4.98**	-0.88*	0.14	-0.37	-2.96*	1.1	-0.93	41.62**	31.53**	36.58**
P6xP8	1.18	0.33	0.75	-0.71	-0.95*	-0.83**	4.71**	1.13	2.92**	-0.14	25.94**	12.90**
P7xP8	4.68**	2.24	3.46**	-0.09	0.34	0.12	1.42	2.40*	1.91*	-0.38	-16.84**	-8.61**
LSD5%(sij)	3.35	2.54	2.07	0.75	0.73	0.51	2.47	2.32	1.67	8.35	7.55	5.54
LSD1%(sij)	4.45	3.36	2.72	0.99	0.96	0.67	3.28	3.08	2.19	11.07	10.02	7.27
LSD5%(sij-sik)	4.96	3.75	3.06	1.11	1.07	0.76	3.66	3.43	2.47	12.35	11.17	8.2
LSD1%(sij-sik)	6.58	4.98	4.02	1.47	1.43	1	4.85	4.55	3.24	16.38	14.82	10.75
LSD5%(sij-skl)	4.68	3.54	1.02	1.04	1.01	0.25	3.45	3.24	0.82	11.64	10.53	2.73
LSD1%(sij-skl)	6.21	4.69	1.34	1.38	1.34	0.33	4.58	4.29	1.08	15.44	13.97	3.58

* and ** indicate $p < 0.05$ and $p < 0.01$, respectively.

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تحليل الهجن النصف تبادلية فى الذرة الشامية للمحصول و مكوناته و المقاومة للثاقبات فى الذرة الشامية

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أجرى تقييم للهجن الناتجة من التهجين النصف دائرى لثمانية سلالات من الذرة وذلك فى تحت بيئتين مختلفتين (تحت ظروف العدوى الصناعية بالثاقبات و تحت الظروف العادية) فى تصميم قطاعات كاملة العشوائية بثلاث مكررات بمركز البحوث و التجارب الزراعية التابع لكلية الزراعة بمشتهر - جامعة بنها. بهدف تقدير القدرة على التألف و متوسط اداء التراكيب الوراثية و مقاومة الهجن للثاقبات. كان متوسط التباين لكل من التراكيب الوراثية و الابعاء و الهجن معنوية فى كل الصفات الخاصة بالثاقبات. و كانت التباينات للقدرة العامة والخاصة على التألف معنوية لكل الصفات تحت الدراسة. وكانت النسبة بين القدرة العامة والقدرة الخاصة أقل من الوحدة لكل الصفات تحت الدراسة. و لذلك كان الفعل الجينى الغير مضيف هو المسؤول عن اظهار تلك الصفات. تفوقت الهجن P3xP5, P3xP6 , P3xP8 فى محصول الحبوب / النبات عن صنف المقارنة 30 ك 8 تحت ظروف العدوى الصناعية و المقاومة. اعطى الاب رقم 3 اعلى قدرة عامة على التألف مرغوبة لمحصول الحبوب/ نبات. و السلالة 3 اعطت قدرة اعلى قدرة عامة مرغوبة لصفة محصول الحبوب / نبات فى كلا البيئتين. أعطت الهجن التالية قدرة خاصه على التألف P6xP3 و P5xP3 و P8xP3 لصفة المحصول تحت ظروف العادية المقاومة الكيماوية للثاقبات.