COMBINING ABILITY, HETEROSIS AND ASSESSING GENETIC DIVERSITY USING RAPD MARKER IN MAIZE

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ABSTRACT: *A half diallel cross between seven inbred lines of maize were evaluated under two different sowing datess for grain yield and its components i.e. No. of rows ear, No. of kernels row, 100-kernel weight and grain yield/plant.*
The results showed that the mean squares for sowing dates, genotypes, parental inbred lines, crosses and parent vs crosses were found to be highly significant for all traits studied. The crosses P_3xP_5, P_4xP_5, P_4xP_7, P_5xP_7 and P_6xP_7 in early sowing dates, P_5xP_7 in late sowing dates and P_4xP_5, P_4xP_7 and P_5xP_7 in the combined analysis, had significant out yielded (heterosis) than the best check hybrid (SC Pioneer 30k8). The mean squares associated with general and specific combining abilities were significant for all traits. GCA/SCA ratio was less the unity for all traits except no. of rows ear^{-1}, indicating that greatest role of the non-additive type of gene action in the expression of these traits. The parental inbred lines P4 and P7 seemed to be the best general combiners for grain yield plant^{-1} and some of its components in the combined analysis of both sowing datess. The parental combinations P_3xP_5, P_4xP_5, P_4xP_6, P_5xP_6, P_5xP_7, P_1xP_4 and P_2xP_4 had the best SCA effects for grain yield plant^{-1} in the combined analysis. The genetic diversity (GD) among seven parental inbred lines was investigated using Random Amplified Polymorphic DNA (RAPD). The genetic diversity among the seven parental inbred lines ranged from 0.19 to 0.49. The correlation between GD and mean performance for grain yield which computed for 21 hybrids combination were found to be positive values (r = 0.07). Therefore, this specified tendency could be predicted about the relationship of GD for grain yield plant^{-1} in this study. We recommended that the hybrid P_5xP_7 could be used in the programs maize hybrid production. RAPD marker can be used as a tool for determining fingerprint for each line and the extent of genetic diversity among maize inbred lines and for genotypes into different groups but when used a large number of primers to detect the variation over all DNA or used a new marker like SSR or AFLP.

Key words: *Maize, Heterosis, Combining ability, additive, sowing dates, RAPD, Genetic diversity.*

INTRODUCTION

To establish a sound basis for any breeding program, aimed at achieving high yield, breeders must have information on the nature of combining ability of parents, their behavior and hybrid combination performance (Chawla and Gupta, 1984).

Diallel analysis technique is the choice of providing such detailed genetic information for selecting breeding materials that show great promise for success (Lonnquit and Gardner, 1961).

The genetic parameter general combining ability (GCA) and specific combining ability (SCA) were defined by Sprague and Tatum, (1942). Both GCA and SCA effects should be taken into consideration when planning maize breeding programs to produce and release new inbred lines and crosses. Furthermore, the magnitude of genetic components for a certain trait would depend mainly upon the environmental changed under which the breeding genotypes will be tested. In this respect, many researchers (EL-Hosary et al. 2006; Sedhom et al. 2007; Ngaboyisonga et al. 2009; Hefny 2010 and Irshad-El-Haq et al. 2010) concluded that the additive genetic (GCA) variance was more affected by environmental changed than the non-additive (SCA) variance for grain yield plant^{-1}.

On the contrary, Sofi and Rather (2006) and El-Badawy (2013) reported that the non-additive effects were more changed by interaction with environments than the additive effects for grain yield plant^{-1}.

Molecular markers that reveal polymorphism at the DNA level have been shown to be a very powerful tool for genetic diversity, since they were independent of the confounding effects of environmental factors. Molecular techniques are now a valuable tool for achieving advances in genome research and generating considerable polymorphic DNA (RAPD) analysis which is relatively simple rapid and cost effective (Parentoni *et al.* 2001, Vladislava *et al.* 2004 El-Amin and Hamza 2013). Therefore, the objectives of our study were: 1) to establish the magnitude of both general combining ability GCA and specific combining ability SCA effects and their interaction with the two sowing datess, 2) to estimate the relative superior of the investigated crosses than both check hybrids SC 10 and SC Pioneer 30K8, 3) to determine the genetic divergence for maize inbred lines and 4) Correlate single-cross performance to genetic divergence of the parental inbred lines.

MATERIALS AND METHODS

Plant materials: Seven white corn (*Zea mays* L.) inbred lines i.e. P$_1$ (82-s), P$_2$ (101pA), P$_3$ (317-2), P$_4$ (211-1), P$_5$ (83-s), P$_6$ (81-sp) and P$_7$ (202-f) were used as parents in this investigation. These parents were developed at the Department of Agronomy, Fac. of Agric., Benha Univ. by Prof. Dr. A.A. EL-Hosary.

Field experiments: In 2011 growing season, the seven parental inbred lines were crossed in a half diallel mating design according to Griffing's method 2 to generate 21 F$_1$ crosses. In order to overcome the differences of parental inbred lines in flowering time and to secure enough hybrid seeds, the parents were sown at various sowing datess i.e. May 10th, 20th and 30th. In 2012 season, two experiments were undertaken in two different sowing datess (29 April and 13 June, early and late sowing

dates, respectively) at the Agric. Res. and Experimental Station of the Fac. of Agric., Benha University. Each experiment included the 21 crosses along with two check varieties single cross Giza single cross 10 (SC 10) and SC Pioneer 30K8. A randomized complete block design with three replications was used. Each plot consisted of two ridges of six meters length and 70 cm width. Hills were spaced at 25 cm with two kernels hill^{-1} on one side of the ridge. The seedlings were thinned to one plant hill^{-1}. The other cultural practices were followed as usual for ordinary maize field in the area. Random sample of 20 guarded plants in each plot were taken to evaluate No. of kernels row^{-1}, No. of rows ear^{-1}, 100-kernel weight and grain yield plant^{-1} which was adjusted for 15.5% moisture.

DNA extraction: 15 seeds of parental inbred lines were sowing in pots. Leaf tissue was collected from 5-7 days old germinated seedlings. Equal quantities of leaf tissue from 10 seedlings of each inbred line were bulked, lyophilized and ground with a mortar. Genomic DNA was isolated and extracted using mi-plant genomic DNA Isolation Kit (Metabion).

RAPD-PCR: PCR-RAPD reactions were conducted using arbitrary 10-mer primers (Operon Technologies, Inc.). Eleven 10-bp oligonucleotide primers (QIAGEN Pharmacia Bioteach) were screened for the ability to provide a suitable band pattern with various parental inbred lines. Only five primers were applied because they give polymorphic results for parents understudy. All PCR reactions were performed as reported by Williams *et al.* (1990), with minor modifications, using 25 ng of DNA. Controls were made by replacing DNA with water. Reaction mixtures (25 µl) contained 0.2 µM of primer, 2.0 units of Taq DNA polymerase, 2.5 µl of 10 x supplied buffer, 0.2 mM of each dNTP, and 2.5 mM of MgCl2. The amplifications were carried out a PTC 200 DNA Thermal Cycler. DNA denaturation was done at 94°c for 4 min., followed by 36-cycle amplification (94°c, 30sec.; 36°c, 1 min.; 72°c, 2 min.) and by a final extension step at 72°c for 10 min. amplification products were

separated by electrophoresis on 1.2% agarose gels, stained with ethidium bromide, and photographed under uv light.

Data analysis: The experimental obtained data was statistically analysis of variance using Computer Statistical Program MSTAT-C. Heterosis expressed as the percentage deviation of F_1 mean performance from SC 10 and SC Pioneer 30k8. General and specific combining abilities were estimated according to Griffing (1956) diallel cross analysis designated as method 2 model 1 for each experiment. The combined analysis of the two experiments was carried out whenever homogeneity of variance was detected (Gomez and Gomez, 1984).

The obtained data of RAPD analysis were entered in a computer file as binary matrices where 0 stands for the absence of a band and 1 stands for the presence of a band in each individual sample. Similarity coefficients between a pair of inbred lines were calculated according to Jaccard (1908). A dendrogram tree was constructed by the UPGMA clustering algoritm from the SAHN option of NTSYS-PC version 2.1 (Rohlf, 2000).

RESULTS AND DISCUSSION

Analysis of variance: The analysis of variance for yield and its components at each sowing datess and the combined analysis is presented in Table 1. Significant differences were detected among sowing datess for all the traits studied i.e. No. of rows ear⁻, No. of kernels row, 100-kernel weight and grain yield'plant
with high mean performance of early sowing dates compared to those in late one. The increase in early sowing dates may be due to the prevailed favorable temperature and day length leading to better vegetative growth, yield and its components of corn plant. Therefore, early sowing dates seemed to be non-stress environment. Such results are in good agreement with those reported by EL-Hosary *et al.* (2006) and Hefny (2011).

Mean squares due to genotypes, parental inbred lines, crosses and parent *vs* crosses

were significant for all the traits studied at each and across sowing datess. This indicates the wide diversity between the genetic materials used in the present study. Significant genotype x sowing dates mean squares were obtained for all traits, except No. of rows ear $^{-1}$ (Tables 1), revealing that the performance of genotypes differed from sowing dates to another. On the other hand, insignificant interaction between genotypes and sowing datess was obtained for No. of rows ear^{-1}, revealing that the response of genotypes had nearly similar in magnitude at the two sowing datess.

Insignificant interaction mean squares between parental inbred lines and sowing datess were obtained for all traits. This result may reveal higher repeatability of performance of the parental inbred lines under different sowing datess.

Significant interaction mean squares between hybrids and sowing datess were obtained for all traits, indicating that, these hybrids behaved somewhat differently from sowing dates to another. Also, significant interaction mean squares between parents *vs.* crosses and sowing datess were obtained for all traits, except No. of kernel row^{-1}. This result indicates that the hetrotic effects were differed by sowing dates changes.

Mean performances and heterosis: Mean performances of the tested seven parental inbred lines and their 21 hybrids and two check varieties at each and across sowing datess and heterosis relative to both checks /hybrids are presented in (Table 2).

Mean performance for parental inbred lines: The inbred line No. 4 and 7 gave the highest mean values for No. of rows ear^{-1} at both and across sowing datess. Meanwhile, the parental inbred lines No. 1 and 6 scored the highest mean values for No. of kernels row^{-1}. The parental inbred line No. 3 recorded heavier 100-kernel weight, but without superiority over those of No. 5 and 7. The parental inbred lines no. 7, 3 and 6 had the highest parental inbred lines mean values of grain yield plant^{-1} in both and across sowing datess. These inbred lines exhibited high mean values for two or more of the traits contributing to grain yield.

Table 1: Mean squares from analysis of variance and combining abilities for each and across sowing datess for yield and its components.

	Env.	d.f	No. of rows ear-1	No. of kernals row-1	100-kernel weight	Grain yield plant-1
Sowing datess (D)	Comb.	1	90.64**	4060.16**	2679.93**	343637.47**
	D1	2	0.35	2.11	6.33	315.86
Rep/D	D2	2	0.64	19.37	14.3	2.58
	Comb.	4	0.5	10.74	10.32	159.22
	D1	27	6.46**	33.09**	12.49*	240.62
Genotypes (G)	D2	27	7.35**	30.80*	10.49*	300.80**
	Comb.	27	13.73**	52.22**	22.48**	482.47*
	D1	6	3.85**	44.75**	35.74**	6972.93**
Parent (Par.)	D2	6	1.88**	37.57**	80.58**	2138.68**
	Comb.	6	4.08**	53.02**	62.64**	4278.55**
	D1	1	187.36**	1661.88**	4112.32**	343165.21**
Par.*vs*.cr.	D2	1	69.03**	1653.18**	644.48**	58059.99**
	Comb.	1	241.92**	3315.05**	4006.37**	341765.60**
GxD	Comb.	27	1.77	24.31**	67.67**	5795.35**
par.xD	Comb.	6	0.08	11.67	0.5	58.94
Cr.xD	Comb.	20	1.65**	29.31**	53.68**	4833.06**
Par.vs.cr.x D	Comb.	1	14.47**	0.01	750.42**	59459.60**
	D1	54	0.85	7.81	8	163.96
Error	D2	54	0.58	6.63	5.79	140.93
	Comb.	108	0.71	7.22	6.9	167.45
	D1	6	4.02**	5.37*	5.15**	2822.87**
GCA	D2	6	2.52**	9.58**	21.02**	343.38**
	Comb.	6	6.11**	7.39**	16.17**	1994.40**
	D1	21	3.66**	42.20**	76.34**	6877.08**
SCA	D2	21	1.67**	38.37**	30.81**	1531.07**
	Comb.	21	4.70**	72.31**	81.00**	6259.24**
GCA x D	Comb.	27	0.43	7.56**	10.00**	1171.85**
SCA x D	Comb.	21	0.64**	8.26**	26.15**	2148.91**
	D1	54	0.28	2.6	2.67	54.65
Error	D2	54	0.19	2.21	1.93	46.98
	Comb.	108	0.24	2.41	2.3	55.82
	D1	-	1.1	0.13	0.07	0.41
GCA/SCA	D2	-	1.5	0.25	0.68	0.22
	Comb.	-	1.3	0.1	0.19	0.32
GCA x D/GCA	Comb.	-	0.07	1.02	0.62	0.58
SCA x D/SCA	Comb.	-	0.14	0.11	0.32	0.34

* and ** indicate significance at 0.05 and 0.01 levels of probability, respectively.
S. refers to single sowing level, D1, D2 and Comb. Refer to early, late sowing dates and combined analysis across sowing dates, respectively.

Table 2: Mean performance of parents, crosses, check varieties and heterosis under each and across sowing datess for yield and its components.

	Trait								
	No. of rows ear^{-1}			No. of kernels row^{-1}			100-kernel weight		
Genotype	D1	D2	Comb	D1	D2	Comb	D1	D2	Comb
Parental inbred line									
P$_1$	9.75	9	9.38	29.88	23.33	26.61	22	21	21.5
P$_2$	10.17	9.67	9.92	30.13	18.3	24.22	19.33	19.33	19.33
P$_3$	10.6	10.33	10.47	31.5	19.9	25.7	24.67	24	24.34
P$_4$	13.5	13	13.25	24.4	14.7	19.55	22.67	22.67	22.67
P$_5$	9.73	9	9.37	29.5	17.6	23.55	25.33	24	24.67
P$_6$	10.35	10.17	10.26	35.03	23.21	29.12	22.33	21	21.67
P$_7$	12.5	12.27	12.39	27.2	21.9	24.55	24.33	24	24.17
mean of parents	10.94	10.49	10.72	29.66	19.85	24.76	22.95	22.29	22.62
Crosses									
P$_1$xP$_2$	13.6	12.93	13.27	35.53	29	32.27	38	31.67	34.84
P$_1$xP$_3$	14.18	12.27	13.23	40.18	31.8	35.99	40.67	24.33	32.5
P$_1$xP$_4$	13.33	12.33	12.83	39.33	31	35.17	40	36.33	38.17
P$_1$xP$_5$	12.46	11.12	11.79	38.35	28.49	33.42	31.67	22.33	27
P$_1$xP$_6$	13.07	12.2	12.64	41.05	30.78	35.92	45.33	22	33.67
P$_1$xP$_7$	12.95	11.89	12.42	39.58	29.54	34.56	38.33	34	36.17
P$_2$xP$_3$	13.47	12.67	13.07	38.13	31.04	34.59	39.67	24	31.84
P$_2$x P$_4$	15.24	12.25	13.75	41.26	30.45	35.86	40	34.67	37.34
P$_2$xP$_5$	14.33	12.4	13.37	40.57	25.47	33.02	44	23.33	33.67
P$_2$xP$_6$	13.33	12.44	12.89	43.4	28.99	36.2	36.33	34.33	35.33
P$_2$xP$_7$	14.27	12.37	13.32	39	28.3	33.65	43	38	40.5
P$_3$xP$_4$	14.29	12.4	13.35	40.23	27.59	33.91	41.33	33.67	37.5
P$_3$xP$_5$	15.78	12.4	14.09	45.67	28.29	36.98	41.33	25	33.17
P$_3$xP$_6$	14.67	12.53	13.6	30.53	26.77	28.65	32.67	22.67	27.67
P$_3$xP$_7$	14.93	12.45	13.69	38.87	27.55	33.21	41.33	31	36.17
P$_4$xP$_5$	16.09	12.46	14.28	36.6	27.54	32.07	36.67	28.67	32.67
P$_4$xP$_6$	15.23	13.93	14.58	41.33	34.47	37.9	35.33	27.33	31.33
P$_4$xP$_7$	15.76	15.03	15.4	42.63	37.82	40.23	39	30.67	34.84
P$_5$xP$_6$	13.87	13.47	13.67	42.27	40	41.14	36	30.33	33.17
P$_5$xP$_7$	16.73	12.84	14.79	49.08	28.7	38.89	41.33	23.67	32.5
P$_6$xP$_7$	14.67	11.87	13.27	35	28.4	31.7	39.33	24.33	31.83
SC10	12	11.6	11.8	41.6	33	37.3	38	32	35
SC Pionner 30k8	14	13.8	13.9	42	32.8	37.4	39.5	30.2	34.85
mean of crosses	14.27	12.6	13.44	40.1	30.34	35.22	39.08	28.89	33.99
mean of genotypes	13.49	12.11	12.8	37.66	27.89	32.78	35.32	27.35	31.34
LSD 5%	1.5	1.25	0.97	4.56	4.2	3.07	4.62	3.93	3
LSD 1%	2	1.66	1.28	6.07	5.59	4.07	6.14	5.23	3.98

* and **** indicate significance at 0.05 and 0.01 levels of probability, respectively.

S. refers to single sowing level, D1, D2 and Comb. Refer to early, late sowing dates and combined analysis across sowing dates, respectively.

Table 2: Continue

	Trait			Heterosis					
	grain yield plant^{-1}			Relative to SC 10			Relative to SC Pioneer 30k8		
Genotype	D1	D2	Comb	D1	D2	Comb.	D1	D2	Comb.
Parental inbred line									
P$_1$	63.06	44.32	53.69						
P$_2$	59.23	34.24	46.74						
P$_3$	82.51	48.92	65.72						
P$_4$	74.3	43.61	58.96						
P$_5$	69.06	40.11	54.59						
P$_6$	76.44	52.86	64.65						
P$_7$	81.74	65.29	73.52						
mean of parents	72.33	47.05	59.70						
Crosses									
P$_1$xP$_2$	171.53	118.84	145.19	-19.77**	-2.98	-13.66**	-24.34**	-13.06	-20.10**
P$_1$xP$_3$	173.96	98.87	136.42	-18.63**	-19.29*	-18.87**	-23.26**	-27.67**	-24.92**
P$_1$xP$_4$	205.13	138.67	171.9	-4.06	13.2	2.23	-9.51	1.44	-5.39
P$_1$xP$_5$	151.36	61.54	106.45	-29.20**	-49.76**	-36.69**	-33.23**	-54.98**	-41.41**
P$_1$xP$_6$	218.85	73.73	146.29	2.36	-39.81**	-13.00**	-3.46	-46.06**	-19.49**
P$_1$xP$_7$	196.32	119.32	157.82	-8.18	-2.59	-6.14	-13.40**	-12.71	-13.14**
P$_2$xP$_3$	198.8	101.7	150.25	-7.02	-16.98*	-10.64*	-12.31*	-25.60**	-17.31**
P$_2$x P$_4$	232.1	129.2	180.65	8.56	5.47	7.44	2.38	-5.48	-0.58
P$_2$xP$_5$	228.25	84.87	156.56	6.76	-30.72**	-6.89	0.68	-37.91**	-13.84**
P$_2$xP$_6$	178.8	123.71	151.26	-16.37**	0.99	-10.05*	-21.13**	-9.5	-16.76**
P$_2$xP$_7$	227.93	132.83	180.38	6.61	8.44	7.27	0.54	-2.83	-0.73
P$_3$xP$_4$	236.22	114.79	175.51	10.49*	-6.29	4.38	4.2	-16.03*	-3.41
P$_3$xP$_5$	280.11	87.61	183.86	31.01**	-28.48**	9.34*	23.56**	-35.91**	1.19
P$_3$xP$_6$	135.73	84.2	109.97	-36.52**	-31.26**	-34.60**	-40.13**	-38.40**	-39.48**
P$_3$xP$_7$	234.6	106.3	170.45	9.73	-13.22	1.37	3.48	-22.24**	-6.19
P$_4$xP$_5$	304.95	98.32	201.64	42.63**	-19.74*	19.92**	34.52**	-28.07**	10.97**
P$_4$xP$_6$	222.01	115.57	168.79	3.84	-5.65	0.38	-2.07	-15.46*	-7.1
P$_4$xP$_7$	257.85	140.3	199.08	20.60**	14.53	18.39**	13.74**	2.64	9.56*
P$_5$xP$_6$	189.77	170.6	180.19	-11.24*	39.27**	7.16	-16.29**	24.80**	-0.83
P$_5$xP$_7$	307.58	90.4	198.99	43.86**	-26.20**	18.34**	35.68**	-33.87**	9.52*
P$_6$xP$_7$	279	71.73	175.37	30.50**	-41.44**	4.29	23.07**	-47.53**	-3.49
SC10	213.8	122.5	168.15						
SC Pionner 30k8	226.7	136.7	181.7						
mean of crosses	220.49	109.66	165.08						
mean of genotypes	185.92	95.06	140.49						
LSD 5%	21.86	19.39	14.46						
LSD 1%	29.07	25.78	19.17						

* and ** indicate significance at 0.05 and 0.01 levels of probability, respectively.

S. refers to single sowing level, D1, D2 and Comb. Refer to early, late sowing dates and combined analysis across sowing dates, respectively.

Mean performance for crosses as well as check hybrids:

Regarding mean performance of F_1 hybrids, SC 10 and SC Pioneer 30k8 at each and across sowing datess, the four crosses P_3xP_5, P_4xP_5, P_4xP_7 and P_5xP_7 showed superiority over the two check hybrids for No. of rows ear^{-1} in early sowing dates. Also, the hybrid P_4xP_7 had the highest No. of rows ear^{-1} in late sowing dates as well as the combined analysis. The crosses P_3xP_5, P_4xP_5, P_4xP_6, P_4xP_7 and P_5xP_7 gave the highest mean values for this trait.

The hybrid P_5xP_7 had the highest No. of kernels row^{-1} followed by cross P_3xP_5 and then by SC Pioneer 30k8 in early sowing dates. While the two hybrids, P_4xP_7 and P_5xP_6 had significant superiority over the best check hybrid (SC Pioneer 30k8) in late sowing dates as well as the combined data.

The six crosses i.e. P_1xP_4, P_2xP_4, P_2xP_7, P_3xP_4, P_3xP_7, SC 10 and SC Pioneer 30k8 gave the highest mean values for 100-kernel weight in the both and across sowing datess.

Concerning grain yield plant^{-1} the crosses P_4xP_5, P_4xP_7 and P_5xP_7 in the combined analysis, P_3xP_5, P_4xP_5, P_4xP_7, P_5xP_7 and P_6xP_7 in early sowing dates and P_5xP_7 in late sowing dates had significant superiority over the best check hybrid (SC Pioneer 30k8). These hybrids exhibited significant increase of one or more of traits contributing to grain yield (Table 2). The fluctuation of hybrids from sowing dates to another was detected for most traits. These results would be due to significant interaction between hybrids and sowing datess. Several investigators recorded the variability among maize hybrids. Among those were: EL-Hosary *et al.* 2006. Hefny (2011) and EL-Badawy 2013.

Heterosis:

Heterosis expressed as the percentage deviation of F_1 mean performance from each of SC 10 and SC Pioneer 30k8 values for grain yield plant^{-1} at both and across sowing datess (Table 2). Six, one and four parental combinations expressed significant positive heterotic

effects relative to SC 10 in early, late sowing datess and the combined analysis, respectively. Also, the crosses P_3xP_5, P_4xP_5, P_4xP_7, P_5xP_7 and P_6xP_7 in early sowing dates, P_5xP_7 in late sowing dates and P_4xP_5, P_4xP_7 and P_5xP_7 in the combined analysis had significant out yielded than the best check hybrid (SC Pioneer 30k8). In addition, the crosses P_2xP_4, P_2xP_5, P_2xP_7, P_3xP_4 and P_3xP_7 in early sowing dates, P_1xP_4 and P_4xP_7 in late sowing dates and P_3xP_5 in the combined analysis gave insignificant out yielded the best check hybrid SC Pioneer 30k8. Hence it could be concluded that these crosses offer possibility for improving grain yield of maize. Several investigators reported high heterosis for yield of maize among them El-Zeir (1998), Nawar *et al.* (1998), Abdel-Sattar *et al.* (1999), El-Bagoury *et al.* (2004), Nawar *et al.* (2002) El-Hosary *et al.* (2006) and EL-Badawy (2013).

Combining ability:

Significant mean squares associated with general and specific combining abilities were detected for all traits under study. Revealing that, both additive and non-additive types of gene action were involved in determining the performance of single-cross progeny. To determine the genetic effects of greatest importance, GCA/SCA ratio was computed. With the exception of No. of rows ear^{-1}, low values which less the unity were detected, indicating that the largest part of the total genetic variability associated with these traits was a result of non-additive type of gene action. For No. of rows ear^{-1}, it showed the highest GCA/SCA ratio, indicating that greatest role of the additive and additive x additive types of gene action in the expression of this trait (Table 1). Several investigators reported similar results (EL-Hosary *et al.* 2006, Sedhom *et al.* 2007 and El-Badawy 2013). On the other hand, Akbar *et al.* (2008) and Hefny (2010) reported that both additive and non-additive were important in genetic expression of the yield and its components traits in maize.

Significant interaction mean squares between sowing datess and both types of combining abilities were detected for all

traits, except GCA x D for No. of rows ear^{-1}. Such results showed that, the magnitude of all types of gene action varied from sowing dates to another. It is fairly evident that the ratio for GCA x D/ GCA was higher than ratio of SCA x D/ SCA for No. of kernels row^{-1}, 100-kernel weight and grain yield plant^{-1}. This result indicated that additive effects were more influenced by the environmental conditions than non-additive. *Vice reverse*, for No. of rows ear^{-1} the non- additive effects were more influenced by change in sowing dates. This conclusion is in well agreement with those reported by Gilbert (1958).

General combining ability effects

($\hat{g}_i$): Estimates of general combining ability effects ($\hat{g}_i$) for individual inbred lines under both and across sowing datess were presented in Table 3. High positive values would be of interest for all the studied traits in question. The parental inbred line P_2 exhibited significant positive ($\hat{g}_i$) effects for 100-kernel weight under late sowing dates. However, it gave significant undesirable or insignificant ($\hat{g}_i$) effects for the other traits. The parental line (P_4) expressed significant positive ($\hat{g}_i$) effects for No. of rows ear^{-1} and grain yield plant^{-1} in both and across sowing dates. Also, it gave desirable significant positive for 100-kernel weight under late sowing dates as well as the combined data. The parental line (P_5) expressed significant positive ($\hat{g}_i$) effects for No. of kernels row^{-1} and grain yield plant^{-1} under early sowing dates. On the contrarily, it expressed significant undesirable or insignificant ($\hat{g}_i$) effects for the rest traits.

The parental line (P_6) showed significant positive ($\hat{g}_i$) effects for No. of kernels row^{-1} at late sowing dates and the combined analysis; however, it gave either significant negative or insignificant ($\hat{g}_i$) effects for the other traits. The parental line (P_7) seemed to be the best combiner for; no of rows ear^{-1}, 100-kernel weight and grain yield plant^{-1} in both and across sowing datess. While, it expressed insignificant "$\hat{g}_i$" effects for the most other traits.

It is worthnoting 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. In most traits, the values of ($\hat{g}_i$) effects mostly differed from sowing dates to another. This finding coincided with that reached above where significant GCA by sowing dates mean squares were detected Table (1). From the previous results, it could be concluded that the parental inbred lines P_4 and P_7 seemed to be the best general combiners for grain yield plant^{-1} and some of its components in the combined analysis of both sowing datess. El-Badawy (2013) found that the parents M9 and M120 were good general combiners for yield and its components. These inbred lines may be attained if they are used in hybridization program because they contain favorable genes to improvement of yield.

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

Specific combining ability effects were only estimated whenever significant SCA variances were obtained, (Table 4).

As for No. of rows ear^{-1}; nine, eight and seven crosses expressed significant positive $\hat{S}_{ij}$ effects at early, late sowing datess as well as the combined analysis, respectively. The results indicated that, the crosses P_1xP_2 and P_5xP_7 gave the highest desirable $\hat{S}_{ij}$ effects for this trait. With regard to No. of kernels row^{-1}, eleven, seven and seven crosses expressed significant positive $\hat{S}_{ij}$ effects at early, late sowing datess as well as the combined analysis, respectively. The results indicated that, crosses P_4xP_7, P_5xP_6 and P_5xP_7 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. As for 100-kernel weight, fourteen, nine and ten crosses expressed significant positive $\hat{S}_{ij}$ effects at early, late sowing datess and the combined

Table 3: General combining ability effects for all the traits studied under each and across sowing datess for yield and its components.

Inbred line		No. of rows ear-1	No of kernel row-1	100-kernel weight	Grain yield plant-1
		Traits			
P_1	D1	-1.02**	-0.57	-0.29	-24.56**
	D2	-0.64**	0.78	-0.44	-4.57*
	Comb.	-0.83**	0.1	-0.37	-14.56**
P_2	D1	-0.41*	-0.09	-0.1	-11.94**
	D2	-0.23	-1.16*	0.89*	2.1
	Comb.	-0.32**	-0.62**	0.39	-4.92**
P_3	D1	0.03	-0.26	0.64	-5.73*
	D2	-0.12	-0.83	-0.89*	-5.49*
	Comb.	-0.05	-0.54*	-0.12	-5.61**
P_4	D1	0.97**	-0.97	-0.32	15.84**
	D2	0.88**	-0.22	2.22**	9.26**
	Comb.	0.92**	-0.60**	0.95**	12.55**
P_5	D1	0.05	1.40**	0.12	15.02**
	D2	-0.42**	-0.73	-1.70**	-7.46**
	Comb.	-0.18**	0.34	-0.79**	3.78**
P_6	D1	-0.3	0.52	-1.21*	-11.08**
	D2	0.03	1.73**	-1.52**	0.51
	Comb.	-0.13*	1.13**	-1.37**	-5.28**
P_7	D1	0.67**	-0.04	1.16*	22.46**
	D2	0.50**	0.43	1.44**	5.64**
	Comb.	0.59**	0.19	1.30**	14.05**
L.S.D 5% $\hat{g}i$	D1	0.33	1	1.01	4.96
	D2	0.27	0.92	0.86	4.23
	Comb.	0.13	0.41	0.4	1.96
L.S.D1% $\hat{g}i$	D1	0.44	1.32	1.34	6.6
	D2	0.36	1.22	1.14	5.63
	Comb.	0.17	0.55	0.54	2.66
L.S.D1% $\hat{g}i$ - $\hat{g}i$	D1	0.5	1.52	1.54	7.58
	D2	0.42	1.4	1.31	6.46
	Comb.	0.23	0.72	0.7	3.45
L.S.D1% $\hat{g}i$ - $\hat{g}i$	D1	0.67	2.02	2.05	10.08
	D2	0.55	1.86	1.74	8.59
	Comb.	0.31	0.97	0.95	4.68

* and ** indicate significance at 0.05 and 0.01 levels of probability, respectively.
D1, D2 and Comb. Refer to early, late sowing dates and combined analysis across sowing dates, respectively.

Table 4: Estimates of specific combining ability effects "$\hat{S}_{ij}$" for the twenty one crosses studied at early, late sowing datess as well as the combined data for the traits studied.

	Traits					
	No. of rows ear-1			No. of kernels row-1		
Crosses	D1	D2	D3	D1	D2	D3
P_1xP_2	1.49**	1.74**	1.62**	-1.17	1.84	0.34
P_1xP_3	1.63**	0.97*	1.30*	3.64*	4.31**	3.98*
P_1xP_4	-0.15	0.03	-0.06	3.51*	2.91*	3.21
P_1xP_5	-0.11	0.12	0.01	0.15	0.91	0.53
P_1xP_6	0.85	0.75	0.8	3.73*	0.74	2.24
P_1xP_7	-0.23	-0.04	-0.14	2.82	0.8	1.81
P_2xP_3	0.32	0.97*	0.64	1.11	5.49**	3.3
$P_2x P_4$	1.15*	-0.46	0.35	4.95**	4.30**	4.63**
P_2xP_5	1.16*	0.99*	1.07*	1.89	-0.18	0.85
P_2xP_6	0.51	0.58	0.55	5.60**	0.88	3.24
P_2xP_7	0.47	0.04	0.25	1.76	1.5	1.63
P_3xP_4	-0.24	-0.42	-0.33	4.09**	1.1	2.6
P_3xP_5	2.16**	0.88*	1.52**	7.16**	2.32	4.74**
P_3xP_6	1.41**	0.56	0.99	-7.10**	-1.67	-4.39*
P_3xP_7	0.69	0.01	0.35	1.8	0.41	1.11
P_4xP_5	1.54**	-0.06	0.74	-1.2	0.96	-0.12
P_4xP_6	1.03*	0.96*	0.99	4.42**	5.43**	4.92**
P_4xP_7	0.59	1.59**	1.09*	6.28**	10.08**	8.18**
P_5xP_6	0.58	1.79**	1.19*	2.98*	11.47**	7.22**
P_5xP_7	2.48**	0.71	1.59**	10.36**	1.47	5.91**
P_6xP_7	0.76	-0.72	0.02	-2.85	-1.29	-2.07
LSD5% (sij)	0.95	0.79	1.05	2.9	2.67	3.34
LSD1% (sij)	1.27	1.05	1.43	3.85	3.55	4.54
LSD5% (sij-sik)	1.42	1.18	0.9	4.3	3.96	2.87
LSD1% (sij-sik)	1.88	1.56	1.22	5.72	5.27	3.89
LSD5% (sij-skl)	1.32	1.1	0.32	4.02	3.71	1.01
LSD1% (sij-skl)	1.76	1.46	0.43	5.35	4.93	1.38

* and ** indicate significance at 0.05 and 0.01 levels of probability, respectively.
D1, D2 and Comb. Refer to early, late sowing dates and combined analysis across sowing dates, respectively.

Table 4: Continue

Crosses	No. of rows ear-1			No. of kernels row-1		
	D1	D2	D3	D1	D2	D3
P_1xP_2	1.49**	1.74**	1.62**	-1.17	1.84	0.34
P_1xP_3	1.63**	0.97*	1.30*	3.64*	4.31**	3.98*
P_1xP_4	-0.15	0.03	-0.06	3.51*	2.91*	3.21
P_1xP_5	-0.11	0.12	0.01	0.15	0.91	0.53
P_1xP_6	0.85	0.75	0.8	3.73*	0.74	2.24
P_1xP_7	-0.23	-0.04	-0.14	2.82	0.8	1.81
P_2xP_3	0.32	0.97*	0.64	1.11	5.49**	3.3
$P_2x P_4$	1.15*	-0.46	0.35	4.95**	4.30**	4.63**
P_2xP_5	1.16*	0.99*	1.07*	1.89	-0.18	0.85
P_2xP_6	0.51	0.58	0.55	5.60**	0.88	3.24
P_2xP_7	0.47	0.04	0.25	1.76	1.5	1.63
P_3xP_4	-0.24	-0.42	-0.33	4.09**	1.1	2.6
P_3xP_5	2.16**	0.88*	1.52**	7.16**	2.32	4.74**
P_3xP_6	1.41**	0.56	0.99	-7.10**	-1.67	-4.39*
P_3xP_7	0.69	0.01	0.35	1.8	0.41	1.11
P_4xP_5	1.54**	-0.06	0.74	-1.2	0.96	-0.12
P_4xP_6	1.03*	0.96*	0.99	4.42**	5.43**	4.92**
P_4xP_7	0.59	1.59**	1.09*	6.28**	10.08**	8.18**
P_5xP_6	0.58	1.79**	1.19*	2.98*	11.47**	7.22**
P_5xP_7	2.48**	0.71	1.59**	10.36**	1.47	5.91**
P_6xP_7	0.76	-0.72	0.02	-2.85	-1.29	-2.07
LSD5% (sij)	0.95	0.79	1.05	2.9	2.67	3.34
LSD1% (sij)	1.27	1.05	1.43	3.85	3.55	4.54
LSD5% (sij-sik)	1.42	1.18	0.9	4.3	3.96	2.87
LSD1% (sij-sik)	1.88	1.56	1.22	5.72	5.27	3.89
LSD5% (sij-skl)	1.32	1.1	0.32	4.02	3.71	1.01
LSD1% (sij-skl)	1.76	1.46	0.43	5.35	4.93	1.38

* and ** indicate significance at 0.05 and 0.01 levels of probability, respectively.
D1, D2 and Comb. Refer to early, late sowing dates and combined analysis across sowing dates, respectively.

analysis, respectively. The other hybrids had insignificant $\hat{S}_{ij}$ effects. With regard to grain yield plant^{-1}, eighteen, thirteen and nineteen crosses showed significantly positive $\hat{S}_{ij}$ effects at early, late sowing datess and the combined analysis, respectively. In conclusion, the best combinations were P_3xP_5, P_4xP_5, P_4xP_6, P_5xP_6, P_5xP_7, P_1xP_4 and P_2xP_4 for grain yield plant^{-1} in 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^{-1} as well as most of the yield components over the two sowing datess.

In these crosses showing high specific combining a`bility 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 sowing dates to another. This finding coincided with that reached above where significant SCA by sowing dates mean squares were detected Table (1). In briefly: the crosses which gave high specific combining ability effects may be importance either towards for hybrid maize production or development good inbred lines.

RAPD Polymorphism: Five RAPD markers were used to characterize and evaluate the genetic diversity of the seven parental inbred lines. A total of 32 amplification products, among which 20 were found polymorphic (Table 5). This resulted in 62.5 % polymorphism. The number of amplification products per locus where 4 for primer A17, 3 for A15, 9 for A19 and 8 for A18, with and average number of 6.4 bands per locus (Table 5). All the primer

produced polymorphic amplification products, however, the extent of percent polymorphism varied with each primer (33.3-75%). The number of polymorphic band per locus ranged from 2 (primer A15) to 6 (primer A14 and A18) with an average number of 4 bands per locus (Table 5).

Genetic similarity for RAPD marker: Jaccard's pair-wise similarity estimates between genotypes were calculated and have been presented in Table 6. The lowest genetic similarity (0.59) was detected between P_1 and P_6. While, the highest genetic similarity was (0.81) scoured between the two parental inbred lines P_3 and P_7. The average for genetic similarity between all parents was 0.69.

Cluster analysis: On the basis of Jaccard's coefficient, the seven parental inbred lines can be distinguished into 3 major main clusters (Fig.1). The first main cluster consists of the inbred line No. 1. The second main cluster includes four inbred lines P_2, P_3, P_7 and P_4 and this cluster separated into two sub-clusters: the first sub-cluster contained P_2. Meanwhile, the second sub cluster contained three inbred lines P_3, P_7 and P_4. In addition, P_3 and P_7 were closely related. The inbred lines P_5 and P_6 were belonging to the third main cluster. In this concern, Lanza et al. (1997) and Zhang et al. (1998) indicated that RAPD technique can be used as a tool for determining the extent of genetic diversity among maize inbred lines, for allocating genotypes into different groups and is successful in confirming hypothesized relationship.

The correlation between genetic distance (GD) and mean performance for grain yield plant^{-1}: The estimate value of correlation coefficient between GD and mean performance for grain yield plant^{-1} found positive (r = 0.07). Therefore, this specified tendency could be predicted about the relationship of GD for grain yield plant^{-1} in this study. A similar finding was obtained by EL-Hosary et al. (2006) showed that the correlation between marker-estimated

Table (5): Name of primers, the nucleotides sequences of the applied primers, molecular weight for RAPD loci found and total fragments detected by each primer and number of polymorphic fragments in seven maize inbred lines.

primer name and sequence	Molecular weight (bp)	P_1	P_2	P_3	P_4	P_5	P_6	P_7	TSB	TF	NPF	PPf
	984	1	1	1	1	0	0	1				
	432	1	1	1	1	1	1	1				
A17	365	1	1	1	1	1	0	1				
GAC CGC TTG T	178	1	1	1	1	0	0	1	23	4	3	75
	610.5	1	0	1	0	1	1	0				
A15	546.6	1	1	0	0	1	0	1	15	3	2	66.7
TTCCGAACC	391.5	1	1	1	1	1	1	1				
	998	1	1	1	1	1	1	1				
	856	1	0	1	1	1	1	1				
	690	1	1	1	1	1	1	1	53	9	3	33.3
	578	1	1	1	1	1	1	1				
	398	1	1	1	1	1	1	1				
	381	0	1	0	1	0	1	0				
	174	1	1	1	1	1	1	1				
A19	152	1	0	0	0	0	0	1				
CAA ACG TCG G	143	1	1	1	1	1	1	1				
	1150.9	0	1	1	1	0	0	1				
	710.5	1	0	0	0	0	0	0	37	8	6	75
	690.1	1	1	1	1	1	1	1				
	680.4	1	1	1	1	1	1	0				
	595.2	1	1	1	1	1	1	1				
	419.5	0	1	1	0	1	0	1				
A18	356.3	0	1	1	1	1	1	1				
AGGTGACCGT	325.4	1	0	0	1	0	0	0				
	1050.7	1	0	0	0	0	0	0				
	810.4	1	0	1	1	0	1	1				
	605.7	0	0	0	1	0	0	0	33	8	6	75
	470.4	0	0	0	1	0	1	1				
	460.2	0	1	1	1	1	1	1				
	300	1	1	1	1	1	1	1				
A14	200	1	1	1	1	1	1	1				
TCTGTGCTGG	135.5	1	1	0	0	0	1	0				
Total									161	32	20	62.5

TSB, TF, NPF and PPF refers to Total number of scorble bands, Total number of fragment and Number of polymorphic fragments and fragments percentage, respectively.

Table 6: Genetic similarity based on Jaccard coefficient for seven inbred lines in maize revealed by RAPD.

Inbred lines	P_1	P_2	P_3	P_4	P_5	P_6	P_7
P_1	1						
P_2	0.60	1					
P_3	0.66	0.77	1				
P_4	0.61	0.71	0.78	1			
P_5	0.61	0.72	0.79	0.61	1		
P_6	0.59	0.63	0.69	0.70	0.71	1	
P_7	0.63	0.74	0.81	0.75	0.69	0.61	1
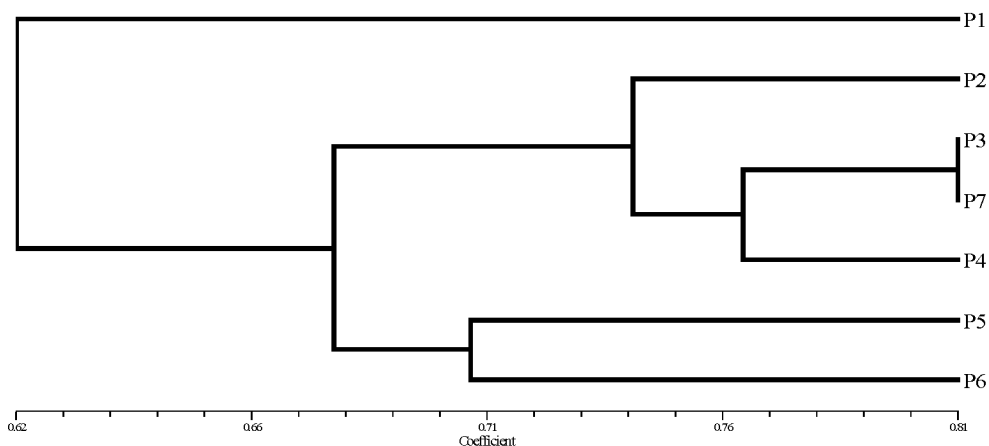
Figure (1): Dendrogram generated based on UPGM clustering method and Jacquard's coefficient using RAPD analysis among the parental inbred lines

genetic distance and heterosis in general is low or not high enough to be of predictive value. Parentoni *et al.* 2001 and Salama *et al.*, (2001) found that the correlation between marker genetic distance for pair parents was moderate, low and positive. The higher correlation between marker distance, mean performance and heterosis has been reported by Sedhom *et al.*, (2007). The results assess that GD can be used to precisely predict the yield performance for F_1 hybrids. The results indicated that RAPD marker can be used as a tool for determining fingerprint for each line and the extent of genetic diversity among maize inbred lines and for genotypes into different

groups but when used a large number of primers to detect the variation over all DNA or used a new marker like SSR or AFLP. Several investigators reported similar results (Ezzat *et al.* 2010 and Patra *et al.* 2011).

Recommendation

The results indicated that P_5xP_7 had significant out yielded than the best check hybrid. RAPD marker can be used as a tool for determining fingerprint for each line and the extent of genetic diversity among maize inbred lines and for genotypes into different groups but when used a large number of primers to detect the variation over all DNA or used a new marker like SSR or AFLP.

Conclusion

Mean squares for sowing datess, genotypes, parental inbred lines, crosses, parent *vs* crosses GCA and SCA were found to be significant. The cross P_5xP_7 in both and across sowing datess had highly heterotic effect.

The parental inbred lines P4 and P7 seemed to be the best general combiners for grain yield plant^{-1} and some of its components in the combined analysis of both sowing datess. The correlation of GD and each of mean performance for grain yield which computed for 21 hybrid combinations found positive (r = 0.07). Therefore, this specified tendency could be predicted about the relationship of GD for grain yield plant^{-1} in this study.

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القدرة على التآلف والتفوق و تقدير التباعد الوراثى بأستخدام تكنيك ال RAPD فى الذرة الشامية

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الملخص العربي

تم تقييم الهجن التبادلية بين ٧ سلالات مرباه داخليا من الذرة الشامية تحت ميعادى زراعة   هما ٢٩ ابريل ، ١٣ يونيه لصفات عدد الاسطر بالكوز ، عدد الحبوب فى السطر ، وزن ١٠٠ حبة و محصول الحبوب للنبات.

- كان التباين الراجع الى ميعادى الزراعة ، التراكيب الوراثية، الأباء، الهجن وقوة الهجين عالى المعنوية لكل الصفات تحت الدراسة.

- أظهرت الهجن ٥x٣، ٥x٤ ،٧x٤ ،٧x٥ و ٧x٦ فى الميعاد المبكر، ٧x٥ فى الميعاد المتأخر ، ٥x٤ ، ٧x٤ و ٧x٥ فى التحليل المشترك تفوقا معنويا فى المحصول بالمقارنة بالهجين الكشاف فردى بيونير 30k8.

- كان التباين الراجع لكل من القدرة العامة و الخاصة على التآلف معنويا لكل الصفات المدروسة.

- كانت نسبة القدرة العامة / الخاصة على التآلف اقل من الوحدة لكل الصفات تحت الدراسة ماعدا عدد الصفوف / كوز. و يشير ذلك الى الفعل الجينى غير مضيف له تأثير كبير فى أظهار هذه الصفات.

- أظهرت السلالتين الأبويتين ٤ و ٧ قدرة عامة عالية للمحصول و بعض مكوناته فى التحليل المشترك.

- أعطت الهجن ٥x٣، ٥x٤ ،٦x٤ ،٧x٥ ٤x١ و ٤x٢ قدره عالية خاصة و معنوية على التآلف لمحصول الحبوب/ نبات فى التحليل المشترك.

- كانت قيمة التباعد الوراثى المقدرة بأستخدام تكنيك ال RAPD بين السبع سلالات الابوية تراوحت بين ٠.١٩ الى ٠.٤٩ و كانت قيمة الأرتباط بين التباعد الوراثى و متوسط أداء الهجن لمحصول الحبوب/ نبات كانت موجبة و لكن منخفظة جدا (٠.٠٧).

- التوصية: يمكن استخدام الهجين $P_5 \times P7$ فى برامج انتاج هجن الذرة حيث انه تفوق معنويا عن الهجين الكشاف فى صفة المحصول ، كما يمكن استخدام تكنيك RAPD كأداة لتحديد البصمة الوراثية لكل سلالة ودرجة التباعد الوراثى بين سلالات الذرة والتراكيب الوراثية فى المجموعات المختلفة ولكن عند استخدام عدد كبير من البرايمر لتحديد الاختلافات على مستوى DNA كاملا او استخدام التكنيكات الحديثة مثل SSR أو AFLP.