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COMBINING ABILITY IN MAIZE UNDER TWO SOWING DATES AND GENETIC DIVERSITY AS REVEALED BY RAPD MARKER

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ABSTRACT

A half diallel cross between 10 inbred lines of maize (Zea mays L.) was evaluated under two different planting dates for ealiness, yield and its components.. planting date, genotypes, parental inbred lines, crosses and parent vs crosses were significant for all studied traits at each and across planting dates except for, parental inbred lines for grain yield plant-1 at each and across planting dates. Significant interaction mean squares between parental inbred lines and planting dates were obtained for all traits except days to 50% silking.

Significant mean squares associated with general (GCA) and specific (SCA) combining abilities were detected for all traits under study. GCA/SCA ratio was computed. For, grain yield plant-1 at both and across planting date as well as No. of kernels row-1 at D2 and combined data 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 all remain cases, there 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

Significant interaction mean squares between planting dates and general combining ability were detected for all traits except GCA x D for days to 50% sillking and 100-Kernel weight. Meanwhile, Insignificant interaction mean squares between planting dates and specific combining ability were found for all studied traits except grain yield plant-1. the parental inbred lines P4 and P9 to be the best general combiners for earliness and grain yield plant-1, respectively.

The favorable ($\hat{S}_{ij}$) effects were observed in the crosses P1xP3, P1xP8, P3xP7 and P6xP8 for days to 50% silking and P1xP5, P1xP6, P1xP8, P1xP9, P5xP7, P6xP7 and P7xP9 for grain yield plant-1 in both sowing dates and the combined analysis.

The lowest genetic similarity (0.289) was detected between P3 and P8. While, the highest genetic similarity was (0.824) scoured between the two parental inbred lines P8 and P9.

The estimate value of correlation coefficient between GD, and mean performance for grain yield plant-1 found negative (r =-0.045). Therefore, the RAPD marker could not be predicted about the mean performance for grain yield plant-1 in this study.

Key wards: Maize, Combining ability, Genetic distance, RAPD Marker.

INTRODUCTION

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.

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).

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).

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 dates, 2) to estimate the relative superior of the investigated crosses than both check hybrids SC 122 and SC 124, 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: Ten white corn (Zea mays L.) inbred lines were diverse sources and provided by Maize Research Department, Field Crops Res. Inst. (FCRI) ARC, Giza, Egypt. The codes, names and pedigree of these inbred lines are presented in table (1)

Table (1). The code, names, pedigree of the parental inbred lines.

Parent code	Name	Pedigree
P1	SD-7	A.E.D
P2	SD-34	A.E.D
P3	SD-63	Tepalcinqo (Tep#5)
P4	SD-1108	GZ-2-EV-8
P5	SD-1157	Var-5
P6	SD-1159	KAH-1
P7	GZ-613	B-73xSD-7
P8	GZ-628	B-73(P-90 BSSS-1)xSD-62
P9	SK-8	Pop SK-1
P10	SK-9	SC10xSK-43

Field experiments: In 2011 growing season, the parental inbred lines were crossed in a half diallel mating design according to Griffing's method 2 to generate 45 F1 crosses. The ten parental inbred lines were grown at Sakha Experimental Stations, ARC in two planting dates with ten days intervals in order to overcome the differences of parental inbred lines in flowering time and to secure enough hybrid seeds.

In 2012 season two experiments were undertaken in two different planting dates (1st May and 15 June, early and late planting date, respectively) at Sakha Experimental Stations, ARC. Each experiment included the 45 crosses along with two check varieties single cross 122 (SC 122) and SC 124 (SC 124). A randomized complete block design with three replications was used. Each plot consisted of one 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 10 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, lnc.). 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 F1 mean performance from SC 122 and SC 124. General and specific combining ability 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 earliness, yield and its components at each planting dates and the combined analysis is presented in Table 2. Significant differences were detected among planting date for all the studied traits, with high mean performance of early planting date compared to those in late one. The increase

in early planting date 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 planting date 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 studied traits at each and across planting dates except for, parental inbred lines for grain yield plant-1 at each and across planting dates. This indicates the wide diversity between the genetic materials used in the present study. Significant genotype x planting date mean squares were obtained for No. of rows ear-1 and grain yield plant-1 (Tables 2), revealing that the performance of genotypes differed from planting date to another. On the other hand, insignificant interaction

Table 2: Mean squares for days to 50% tasseling, yield and its components of 45 maize F1 evaluated at two sowing dates as well as the combined across sowing date.

SOV	Df	Days to 50% sillking	No of rows ear-1	No of kernels row-1	100-kernel weight	Grain yield plant -1
Sowing date - 01/05/2012 (Early planting date)						
Rep	2	16.93**	3.59**	2.56	37.54**	2502.13**
Genotypes	54	32.35**	2.24**	123.09**	65.49**	10371.64**
Parent	9	30.40**	1.52**	46.96**	31.29**	840.63
Cross	44	12.78**	1.78**	35.77**	34.83**	4374.87**
Par.vs.cr.	1	911.12**	28.91**	4650.43**	1722.09**	360008.20**
Error	108	2.87	0.43	6.01	6.98	504.17
GCA	9	17.20**	1.88**	42.95**	35.67**	1907.49**
SCA	45	9.50**	0.52**	40.64**	19.06**	3767.16**
Error	108	0.96	0.14	2.00	2.33	168.06
GCA/SCA		1.81	3.62	1.06	1.87	0.51
Sowing date - 15/06/2012 (Late planting date)						
Rep	2	7.30**	2.78**	4.10	189.03**	4273.58**
Genotypes	54	35.61**	3.94**	137.69**	57.96**	9311.49**
Parent	9	33.00**	4.50**	39.58**	55.31**	840.04
Cross	44	18.92**	2.60**	39.60**	25.20**	3642.97**
Par.vs.cr.	1	793.34**	57.82**	5336.68**	1523.22**	334969.50**
Error	108	1.39	0.38	3.19	9.85	437.11
GCA	9	29.48**	4.08**	31.50**	21.48**	736.65**
SCA	45	8.35**	0.76**	48.78**	18.89**	3577.27**
Error	108	0.46	0.13	1.06	3.28	145.70
GCA/SCA		3.53	5.37	0.65	1.14	0.21
Combined over 2 sowing dates						
Sowing date (D)	1	6101.70*	3.71*	466.39*	683.57*	153459.25*
Rep/D	4	11.84**	3.18**	3.33	113.29**	3387.86**
Genotypes (G)	54	65.33**	5.53**	254.78**	113.04**	18745.43**
Parent (Par.)	9	60.67**	5.01**	74.08**	60.97**	713.83
Cross (Cr.)	44	29.08**	3.84**	70.82**	52.57**	7069.92**
Par.vs.cr.	1	1702.42*	84.24*	9975.31*	3242.26*	694752.10*
G x D	54	2.63	0.66*	6.00	10.41	937.70**
Par x D	9	2.73	1.01*	12.46**	25.63**	966.84*
Cr. xD	44	2.62	0.54	4.54	7.46	947.92**
Par.vs.cr.Vs.D	1	2.04	2.48*	11.80	3.05	225.60
Error	216	2.13	0.41	4.60	8.41	470.64
GCA	9	45.34**	5.49**	69.23**	53.39**	2153.43**
SCA	45	17.06**	1.11**	88.07**	34.54**	7067.49**
GCA x D	9	1.33	0.47**	5.23**	3.76	490.71**
SCA x D	45	0.79	0.17	1.35	3.41	276.94**
Error	216	0.71	0.14	1.53	2.80	156.88
GCA/SCA		2.66	4.94	0.79	1.55	0.30
GCA x D/GCA		0.03	----	---	0.07	0.23
SCA x D/SCA		0.05	---	---	0.10	0.04

* and ** refer to significant at p = 0.05 and 0.01, respectively.

between genotypes and planting dates was obtained for days to 50% silking, No of Kernel row-1 and 100-kernel weight revealing that the response of genotypes had nearly similar in magnitude at the two planting dates.

Significant interaction mean squares between parental inbred lines and planting dates were obtained for all traits except days to 50% silking. This result may reveal higher repeatability of performance of the parental inbred lines under different planting dates.

Insignificant interaction mean squares between hybrids and sowing dates were obtained for all traits except grain yield plant-1, indicating that, these hybrids behaved somewhat stability from planting date to another. Also, insignificant interaction mean squares between parent vs. crosses and planting date were obtained for all traits except days to 50% sillking. This result indicates that the hetrotic effects were not differed by planting date changes.

Mean performances and heterosis: Mean performances of the tested ten parental inbred lines and their 45 hybrids and two check varieties at each and across planting date and heterosis relative to both checks hybrids are presented in (Table 3 and 4).

Mean performance for parental inbred lines (Table 3): The inbred line No. 2 and 3 gave the earliest mean values for days to 50% silking at both and across planting dates. The inbred line No. 7 showed the highest mean value for No of rows ear-1 as well as No of kernel row-1. Meanwhile, the parental inbred lines No. 10 recorded heavier 100-kernel weight but without superiority over those of No. 2 and 4 and 10.

Mean performance for the studied traits at the combined over two planting dates and heterosis relative to SC 122 and 124 in both planting date and the combined data are presented in Table (4).

Mean performance in the combining data; of days to 50% silking ranged from 61.00 days (P4xP9) to 73.33 days for (P1xP3), No. of rows ear-1, mean randed from 37.05 (P3xP8) to 50.63 (P1xP9) for 100-kernel weight mean ranged from 30.93 (P1xP7) to 44.64 (P6xP9).

Also, mean values for grain yield plant -1 ranged from 161.21 (P1xP7) to 325.59 for (P7xP9) in early sowing date, from 92.78 for (P1xP7) to 248.26 for (P6xP7) to 276.31 for P6xP7 in the combined data. Also, the two crosses P1xP8 and P6xP7 had the highest values for both SCA and heterosis effects relative to SC 122 and /or 124 in both sowing dates and across over them. These hybrids surpassed significant than both check hybrids SC 122 and 124 with average 44.43 and 63.11, respectively. Hence, it could be concluded that both crosses offer good possibility for improving grain yield in maize. Also, the most considerable heterosis was generally detected from

Table 3: Mean performance of parents under each and across planting dates for earliness, yield and its components.

	Days to 50% silking			No of rows ear-1			No of kernel row-1			100-kernel weight			grain yield plant-1		
	D1	D2	Comb	D1	D2	Comb	D1	D2	Comb	D1	D2	Comb	D1	D2	Comb
p1	74.00	67.33	70.67	12.27	10.53	11.40	34.73	33.67	34.20	30.03	32.57	31.30	104.09	84.61	94.35
p2	66.33	59.67	63.00	14.13	13.33	13.73	35.13	32.07	33.60	33.87	32.21	33.04	142.20	70.39	106.30
p3	68.00	58.33	63.17	12.13	11.47	11.80	33.00	27.07	30.03	26.68	30.89	28.79	102.69	46.00	74.34
p4	69.33	59.67	64.50	13.60	11.87	12.73	29.80	28.27	29.03	28.49	40.87	34.68	104.89	106.89	105.89
p5	70.67	62.00	66.33	13.33	14.13	13.73	34.00	29.27	31.63	29.20	31.62	30.41	129.72	71.62	100.67
p6	71.67	62.67	67.17	12.80	12.13	12.47	23.47	20.67	22.07	32.39	35.07	33.73	150.13	76.16	113.15
p7	71.67	69.67	70.67	14.27	14.53	14.40	38.40	28.80	33.60	23.88	27.60	25.74	116.33	77.19	96.76
p8	77.00	66.67	71.83	12.87	12.67	12.77	33.40	31.20	32.30	27.80	33.61	30.71	111.07	78.11	94.59
P9	77.00	66.00	71.50	13.33	13.30	13.33	32.20	31.47	31.83	29.54	26.72	28.13	108.38	74.83	91.60
P10	72.33	63.00	67.67	13.47	12.40	12.93	31.13	31.00	31.07	34.27	37.86	36.06	113.11	100.56	106.84
Mean	71.80	63.50	67.65	13.22	12.64	12.93	32.53	29.35	30.94	29.62	32.90	31.26	118.26	78.64	98.45

combinations involving inbred line that are very diverse in origin and widely different in their diverse in origin and widely different in their mean performance.

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. For, grain yield plant-1 at both and across planting date as well as No. of kernels row-1 at D2 and combined data 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 all remain cases, there 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)

Table 4: Mean performance of crosses, check varieties and heterosis under each and across planting dates for yield and its components.

	Silking			No of rows			No of kernel			100-kernel weight		
	D-1	**D-2**	**Comb.**	**D-1**	**D-2**	**Comb.**	**D-1**	**D-2**	**Comb.**	**D-1**	**D-2**	**Comb.**
P1xP2	75.00	68.00	71.50	13.07	14.00	13.53	50.07	48.87	49.47	38.61	39.26	38.94
P1xP3	78.00	68.67	73.33	12.80	12.53	12.67	51.27	47.87	49.57	37.31	42.84	40.07
P1xP4	69.00	61.67	65.33	14.00	13.20	13.60	45.60	43.40	44.50	41.60	45.41	43.51
P1xP5	70.00	61.33	65.67	14.40	14.00	14.20	50.07	47.73	48.90	38.10	39.65	38.88
P1xP6	68.00	59.67	63.83	13.47	13.33	13.40	47.27	44.87	46.07	36.62	38.32	37.47
P1xP7	68.33	61.00	64.67	13.20	12.13	12.67	41.47	35.27	38.37	29.81	32.05	30.93
P1xP8	68.67	61.00	64.83	14.13	13.33	13.73	48.53	46.33	47.43	39.62	40.24	39.93
P1xP9	77.33	68.00	72.67	14.27	14.00	14.13	51.87	49.40	50.63	42.37	45.66	44.02
P1xP10	68.67	60.00	64.33	13.47	13.07	13.27	46.57	43.53	45.05	38.17	39.05	38.61
P2xP3	69.67	62.33	66.00	13.73	13.87	13.80	49.07	48.40	48.73	36.82	40.83	38.83
P2xP4	69.33	61.33	65.33	14.13	14.53	14.33	47.33	44.53	45.93	41.46	40.62	41.04
P2xP5	66.33	56.33	61.33	13.87	14.40	14.13	45.53	41.67	43.60	38.67	41.98	40.33
P2xP6	69.00	61.33	65.17	13.47	14.13	13.80	45.27	44.20	44.73	36.83	39.76	38.30
P2xP7	66.67	59.00	62.83	14.53	14.53	14.53	51.13	50.80	50.97	34.63	40.58	37.60
P2xP8	69.00	62.00	65.50	14.40	14.67	14.53	48.87	46.13	47.50	37.53	39.82	38.68
P2xP9	68.67	61.00	64.83	14.40	14.40	14.40	46.27	45.00	45.63	39.06	41.53	40.29
P2xP10	70.00	60.00	65.00	14.13	15.20	14.67	45.73	44.80	45.27	39.83	42.74	41.28
P3xP4	67.33	59.33	63.33	14.67	13.73	14.20	42.33	41.13	41.73	42.19	43.95	43.07
P3xP5	69.33	61.00	65.17	15.07	14.53	14.80	47.00	43.07	45.03	37.81	37.57	37.69
P3xP6	68.67	60.00	64.33	14.53	13.60	14.07	44.60	41.47	43.03	37.17	41.07	39.12
P3xP7	69.67	60.00	64.83	13.73	13.87	13.80	51.73	47.47	49.60	35.78	38.92	37.35
P3xP8	70.00	65.00	67.50	12.53	12.40	12.47	39.30	34.80	37.05	28.43	36.72	32.58
P3xP9	70.00	61.33	65.67	14.13	13.33	13.73	49.07	49.07	49.07	40.18	42.64	41.41
P3xP10	71.00	61.33	66.17	13.73	13.87	13.80	44.93	43.67	44.30	36.31	39.91	38.11
P4xP5	65.67	57.33	61.50	15.33	15.20	15.27	43.00	43.67	43.33	39.20	44.32	41.76
P4xP6	65.00	55.33	60.17	13.87	13.73	13.80	40.53	39.80	40.17	41.24	44.18	42.71
P4xP7	68.67	60.67	64.67	14.67	15.07	14.87	49.87	43.80	46.83	39.02	41.47	40.24
P4xP8	67.33	59.33	63.33	14.93	14.40	14.67	44.27	39.33	41.80	39.44	40.11	39.78
P4xP9	66.00	56.00	61.00	15.20	14.00	14.60	44.60	42.67	43.63	41.34	38.40	39.87
P4xP10	65.67	55.33	60.50	14.27	14.27	14.27	39.70	40.27	39.98	45.23	42.97	44.10
P5xP6	69.00	59.67	64.33	14.93	14.27	14.60	40.53	38.53	39.53	34.41	38.93	36.67
P5xP7	69.00	61.67	65.33	15.47	16.13	15.80	52.07	48.07	50.07	36.26	40.39	38.32
P5xP8	68.67	59.33	64.00	14.80	14.27	14.53	45.93	44.93	45.43	35.69	42.03	38.86
P5xP9	66.33	59.33	62.83	15.73	16.27	16.00	47.53	44.73	46.13	37.99	40.71	39.35
P5xP10	68.00	57.33	62.67	15.33	16.67	16.00	41.67	40.33	41.00	40.40	44.85	42.63
P6xP7	68.33	58.00	63.17	14.67	13.87	14.27	46.40	44.13	45.27	31.48	36.10	33.79
P6xP8	66.00	55.33	60.67	14.13	13.60	13.87	41.40	39.47	40.43	36.60	38.43	37.52
P6xP9	66.00	57.00	61.50	14.40	14.00	14.20	43.73	41.93	42.83	43.92	45.37	44.64
P6xP10	65.33	55.00	60.17	14.00	13.60	13.80	44.67	42.00	43.33	42.87	44.61	43.74
P7xP8	68.33	60.33	64.33	13.47	14.13	13.80	50.20	46.27	48.23	33.64	39.83	36.73
P7xP9	69.33	61.00	65.17	15.60	15.87	15.73	50.20	49.00	49.60	38.50	39.90	39.20
P7xP10	65.67	60.67	63.17	14.40	14.13	14.27	47.67	43.00	45.33	35.11	39.32	37.21
P8xP9	68.00	59.33	63.67	15.87	15.07	15.47	46.33	48.60	47.47	38.40	40.66	39.53
P8xP10	67.67	58.33	63.00	13.73	14.13	13.93	46.07	45.73	45.90	34.30	35.45	34.87
P9xP10	66.33	57.33	61.83	15.07	14.53	14.80	45.87	44.40	45.13	39.63	45.87	42.75
Sc122	69.33	59.70	64.52	13.50	13.80	13.65	47.67	45.60	46.64	35.30	40.98	38.14
SC 124	67.70	58.67	63.18	13.40	14.00	13.70	47.85	46.40	47.13	36.53	42.82	39.68
Mean of crosses	68.62	60.06	64.34	14.27	14.16	14.22	46.35	44.17	45.26	37.90	40.83	39.36
Mean of genotype	69.18	60.66	64.92	14.08	13.90	13.99	43.93	41.57	42.75	36.45	39.44	37.94
LSD 5%	2.76	1.89	1.67	1.05	0.98	0.72	3.92	2.86	2.43	4.23	5.02	3.28

* indicate significance at 0.05 levels of probability.

Table 4: Continue

	grain yield / plant			Heterosis relative to SC 122						Heterosis relative to SC 124					
	D-1	D-2	Comb.	D-1		D-2		Comb.		D-1		D-2		Comb.	
P1xP2	260.68	197.39	229.03	46.72	*	-7.23		19.75		30.07		-6.24		11.91	
P1xP3	205.20	230.36	217.78	-8.75		25.74		8.50		-25.40		26.73		0.66	
P1xP4	253.24	193.24	223.24	39.29	*	-11.38		13.95		22.63		-10.40		6.12	
P1xP5	257.99	238.45	248.22	44.04	*	33.83	*	38.93	*	27.39		34.81	*	31.10	*
P1xP6	282.07	227.27	254.67	68.12	*	22.65		45.38	*	51.46	*	23.63		37.55	*
P1xP7	161.21	92.78	127.00	-52.74	*	-111.84	*	-82.29	*	-69.39	*	-110.86	*	-90.12	*
P1xP8	271.48	243.79	257.64	57.52	*	39.17	*	48.35	*	40.87	*	40.16	*	40.51	*
P1xP9	300.17	224.97	262.57	86.22	*	20.35		53.28	*	69.57	*	21.33		45.45	*
P1xP10	195.27	150.63	172.95	-18.68		-53.99	*	-36.34	*	-35.34		-53.01	*	-44.17	*
P2xP3	244.62	204.68	224.65	30.67		0.06		15.37		14.02		1.05		7.53	
P2xP4	286.95	214.26	250.61	73.00	*	9.64		41.32	*	56.35	*	10.62		33.48	*
P2xP5	203.35	209.17	206.26	-10.60		4.55		-3.03		-27.26		5.53		-10.86	
P2xP6	239.77	199.53	219.65	25.82		-5.09		10.37		9.17		-4.10		2.53	
P2xP7	267.69	189.60	228.65	53.74	*	-15.02		19.36		37.08	*	-14.04		11.52	
P2xP8	258.50	194.41	226.46	44.55	*	-10.21		17.17		27.90		-9.22		9.34	
P2xP9	223.94	187.94	205.94	9.99		-16.68		-3.35		-6.67		-15.69		-11.18	
P2xP10	220.01	201.01	210.51	6.06		-3.62		1.22		-10.59		-2.63		-6.61	
P3xP4	214.30	207.39	210.85	0.35		2.77		1.56		-16.30		3.76		-6.27	
P3xP5	213.26	165.64	189.45	-0.69		-38.98	*	-19.84		-17.35		-38.00	*	-27.67	*
P3xP6	238.25	179.57	208.91	24.30		-25.05		-0.38		7.64		-24.07		-8.21	
P3xP7	260.07	213.77	236.92	46.12	*	9.14		27.63	*	29.46		10.13		19.80	
P3xP8	126.82	69.97	98.40	-87.13	*	-134.65	*	-110.89	*	-103.79	*	-133.66	*	-118.72	*
P3xP9	255.51	206.16	230.83	41.56	*	1.54		21.55		24.90		2.52		13.71	
P3xP10	200.65	158.69	179.67	-13.31		-45.93	*	-29.62	*	-29.96		-44.95	*	-37.45	*
P4xP5	243.17	191.14	217.16	29.22		-13.48		7.87		12.57		-12.49		0.04	
P4xP6	227.23	162.33	194.78	13.28		-42.29	*	-14.51		-3.38		-41.31	*	-22.34	
P4xP7	257.56	207.10	232.33	43.61	*	2.48		23.04		26.96		3.46		15.21	
P4xP8	208.12	170.94	189.53	-5.83		-33.68	*	-19.76		-22.49		-32.70		-27.59	*
P4xP9	235.33	197.62	216.47	21.38		-7.00		7.19		4.72		-6.02		-0.65	
P4xP10	255.58	214.49	235.03	41.63	*	9.87		25.75	*	24.97		10.86		17.91	
P5xP6	191.66	136.37	164.01	-22.29		-68.26	*	-45.27	*	-38.95	*	-67.27	*	-53.11	*
P5xP7	308.00	210.65	259.32	94.05	*	6.03		50.04	*	77.39	*	7.01		42.20	*
P5xP8	231.93	172.13	202.03	17.98		-32.49		-7.26		1.32		-31.51		-15.09	
P5xP9	268.26	222.81	245.53	54.31	*	18.18		36.25	*	37.65	*	19.17		28.41	*
P5xP10	227.93	204.77	216.35	13.98		0.15		7.06		-2.68		1.13		-0.77	
P6xP7	304.36	248.26	276.31	90.41	*	43.64	*	67.02	*	73.75	*	44.62	*	59.19	*
P6xP8	214.33	190.75	202.54	0.37		-13.87		-6.75		-16.28		-12.89		-14.58	
P6xP9	258.50	201.66	230.08	44.54	*	-2.96		20.79		27.89		-1.98		12.96	
P6xP10	242.34	220.87	231.61	28.39		16.25		22.32		11.74		17.24		14.49	
P7xP8	252.03	215.62	233.83	38.08	*	11.00		24.54		21.43		11.99		16.71	
P7xP9	325.59	224.92	275.26	111.64	*	20.30		65.97	*	94.99	*	21.28		58.14	*
P7xP10	218.72	199.33	209.02	4.77		-5.30		-0.26		-11.88		-4.31		-8.10	
P8xP9	236.92	190.59	213.75	22.97		-14.04		4.47		6.31		-13.05		-3.37	
P8xP10	186.00	177.84	181.92	-27.95		-26.79		-27.37	*	-44.61	*	-25.80		-35.20	*
P9xP10	236.97	234.76	235.87	23.02		30.14		26.58	*	6.36		31.13		18.75	
Sc122	213.95	204.62	209.29												
SC 124	230.60	203.64	217.12												
Mean of crosses	238.64	195.83	217.23												
Mean of genotype	217.52	175.27	196.39												
LSD 5%	35.93	33.46	24.55												

* indicate significance at 0.05 levels of probability.

Significant interaction mean squares between planting dates and general combining ability were detected for all traits except GCA x D for days to 50% sillking and 100-Kernel weight. Meanwhile, Insignificant interaction mean squares between planting dates and specific combining ability were found for all studied traits except grain yield plant-1. Such results showed the significant type of combining ability refer to magnitude of type of gene action varied from planting date to another. It is fairly evident that the ratio for GCA x D/ GCA was higher or significant than ratio of SCA x D/ SCA for No of rows ear-1, No. of kernels row-1, and grain yield plant-1. This result indicated that additive effects were more influenced by the environmental condition than non-additive. Vice reverse, for days to 50% tasseling and 100-Kernel weight the non- additive effects were more influenced by change in planting date. This conclusion is in well agreement with those reported by Gilbert (1958).

General combining ability effect ($\hat{g}_i$): Estimation of general combining ability effects ($\hat{g}_i$) for individual inbred lines under both and across planting dates were presented in Table 5. High positive values would be of interest for all studied traits in question except silking date where high negative would be useful from the breeder point of view. The parental inbred line P1 exhibited significant positive ($\hat{g}_i$) effects for No of kernel row-1 under both and across planting date. However, it gave significant undesirable or insignificant ($\hat{g}_i$) effects for other traits. The parental line (P2) expressed significant positive ($\hat{g}_i$) effects for No. of Kernel row-1 at both and across planting date, Also, it gave desirable significant positive for 100-kernel and grain yield plant-1 in the first planting date and No o f rows ear-1 at late planting date. The parental line (P4) expressed significant negative ($\hat{g}_i$) effects and seemed to be the best combiner for days to 50% silking and positive for 100-kernel weight at both and across planting date. Also, it gave desirable significant positive for No of rows ear-1under early planting. On the contrarily, it expressed significant undesirable or insignificant ($\hat{g}_i$) effects for the rest traits.

The parental line (P5) showed significant negative ($\hat{g}_i$) effects for days to 50% silking, and showed significant positive effect for No of rows ear-1at early, late planting date and the combined analysis; however, it gave either significant negative or insignificant ($\hat{g}_i$) effects for other traits. The parental line (P6) showed significant negative ($\hat{g}_i$) effects for days to 50% silking, and showed significant positive effect for

Table 5: General combining ability effects for all studied traits under each and across planting dates for yield and its components.

Parent		Days to 50% silking	no of rows/ear	no of kernels/row	100 kernel weight	grain yield/plant
P1	D-1	1.07**	-0.65**	1.71**	0.09	0.39
	D-2	1.79**	-1.02**	1.59**	-0.43	4.31
	Comb	1.43**	-0.83**	1.65**	-0.17	2.35
P2	D-1	0.40	-0.10	1.49**	0.84*	8.26*
	D-2	0.76**	0.30**	1.92**	-0.10	1.87
	Comb	0.58*	0.10	1.70**	0.37	5.06
P3	D-1	1.68**	-0.50**	0.30	-1.31**	-18.90**
	D-2	1.68**	-0.68**	-0.37	-0.55	-15.68**
	Comb	1.68**	-0.59**	-0.03	-0.93*	-17.29**
P4	D-1	-1.88**	0.26*	-2.07**	2.21**	0.04
	D-2	-2.43**	-0.08	-1.70**	2.53**	4.66
	Comb	-2.16**	0.09	-1.88**	2.37**	2.35
P5	D-1	-0.54*	0.53**	-0.03	-0.35	1.18
	D-2	-0.49**	0.93**	-0.35	0.07	-1.84
	Comb	-0.52*	0.73**	-0.19	-0.14	-0.33
P6	D-1	-1.18**	-0.18	-3.36**	0.40	8.99*
	D-2	-1.85**	-0.37**	-3.15**	0.34	0.21
	Comb	-1.52**	-0.27**	-3.26**	0.37	4.60
P7	D-1	0.62*	0.26*	2.99**	-3.26**	16.42**
	D-2	1.98**	0.50**	0.82**	-2.42**	3.33
	Comb	1.30**	0.38**	1.91**	-2.84**	9.88**
P8	D-1	0.51**	-0.12	-0.33	-1.82**	-15.21**
	D-2	0.29	-0.13	-0.13	-1.02*	-11.18**
	Comb	0.40	-0.12	-0.23	-1.42**	-13.20**
P9	D-1	0.09	0.51**	0.68	1.61**	13.92**
	D-2	-0.41*	0.44**	1.85**	0.12	10.39**
	Comb	-0.16	0.48**	1.27**	0.86	12.16**
P10	D-1	-0.77**	-0.01	-1.38**	1.60**	-15.10**
	D-2	-1.32**	0.12	-0.48	1.47**	3.93
	Comb	-1.04**	0.05	-0.93**	1.54**	-5.58
L.S.D gi 0.05	D-1	0.54	0.20	0.76	0.82	6.99
	D-2	0.37	0.19	0.56	0.98	6.51
	Comb	0.46	0.20	0.66	0.90	6.72
L.S.D gi 0.01	D-1	0.71	0.27	1.00	1.08	9.20
	D-2	0.48	0.25	0.73	1.28	8.56
	Comb	0.60	0.26	0.87	1.18	8.82
L.S.D gi-gj 0.05	D-1	0.80	0.31	1.14	1.23	10.43
	D-2	0.55	0.29	0.83	1.46	9.71
	Comb	0.68	0.29	0.99	1.34	10.02
L.S.D gi-gj 0.01	D-1	1.05	0.40	1.50	1.61	13.71
	D-2	0.72	0.38	1.09	1.92	12.76
	Comb	0.89	0.39	1.30	1.76	13.14

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

D1, D2 and Comb. Refer to early, late planting date and combined analysis across planting date, respectively.

grain yield plant-1 at late planting date; however, it gave either significant negative or insignificant ($\hat{g}_i$) effects for other traits. The parental line (P7) showed significant positive ($\hat{g}_i$) effects for No of rows ear-1 and No of kernel row-1 in both and across planting date also, grain yield plant-1 at early planting date and the combined data; however, it gave either significant negative or insignificant ($\hat{g}_i$) effects for other traits. The parental line (P9) seemed to be the best combiner for; grain yield plant-1 and No of rows ear-1 in both and across planting date and 100-Kernel weight in early planting date also, it gave significant desirable ($\hat{g}_i$) effects for days to 50% tasseling as well as No of kernels row-1 date at late planting date . While, it expressed insignificant "$\hat{g}_i$" effects for the most other traits. The parental line (P10) showed significant negative ($\hat{g}_i$) effects for days to 50% silking, and showed significant positive effect for 100-kernel weight at late planting date; however, it gave either significant negative or insignificant ($\hat{g}_i$) effects for other traits.

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. In most traits, the values of ($\hat{g}_i$) effects mostly differed from planting date to another. This finding coincided with that reached above where significant GCA by sowing date mean squares were detected Table (2). From the previous result, it could be concluded that the parental inbred lines P4 and P9 to be the best general combiners for earliness and grain yield plant-1, respectively. Also, these parental inbred lines exhibited a best some of its components in the combined analysis of both planting dates. El-Badawy (2013) found that the parents M9 and M120 were good general combiner 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 (6). Results showed that the favorable ($\hat{S}_{ij}$) effects were observed in the crosses P1xP3, P1xP8, P3xP7 and P6xP8 for days to 50% silking in both planting dates and the combined data. Eight, twelve and nine; twenty six, twenty nine and twenty eight;

Table 6: Estimate of specific combining ability effects " $\hat{S}_{ij}$ " for the twenty one crosses studied at early, late planting dates as well as the combined data for the traits studied.

	Days to 50% silking			no of rows/ear			no of kernels/row		
crosses	D-1	D-2	Comb	D-1	D-2	Comb	D-1	D-2	Comb.sk
P1xP2	-1.67	-1.60*	-1.63*	-0.29	0.82*	0.27	3.08*	3.95**	3.51**
P1xP3	-1.94*	-2.85**	-2.40**	-0.15	0.34	0.09	5.47**	5.24**	5.35**
P1xP4	-0.39	-0.40	-0.40	0.29	0.40	0.35	2.17	2.10*	2.14
P1xP5	-1.39	-1.02	-1.20	0.41	0.19	0.30	4.60**	5.09**	4.84**
P1xP6	-0.42	0.35	-0.04	0.19	0.82*	0.51	5.13**	5.01**	5.07**
P1xP7	6.44**	3.51**	4.98**	-0.51	-1.24**	-0.88**	-7.02**	-8.56**	-7.79**
P1xP8	-2.11*	-2.79**	-2.45**	0.80*	0.58	0.69*	3.37*	3.46**	3.41**
P1xP9	-4.03**	-2.43**	-3.23**	0.30	0.68*	0.49	5.69**	4.55**	5.12**
P1xP10	0.17	1.15	0.66	0.02	0.07	0.05	2.45	1.01	1.73
P2xP3	-1.94*	-1.82**	-1.88*	0.22	0.36	0.29	3.49**	5.44**	4.47**
P2xP4	-1.39	-2.71**	-2.05**	-0.13	0.42	0.15	4.13**	2.90**	3.52**
P2xP5	-0.06	0.35	0.15	-0.68	-0.72*	-0.70*	0.28	-1.31	-0.51
P2xP6	-1.75	-0.63	-1.19	-0.37	0.31	-0.03	3.35*	4.02**	3.69**
P2xP7	-1.22	-1.46*	-1.34	0.27	-0.15	0.06	2.87*	6.65**	4.76**
P2xP8	-1.44	-0.77	-1.10	0.51	0.60	0.56	3.92**	2.93**	3.43**
P2xP9	0.31	-1.07	-0.38	-0.12	-0.23	-0.18	0.31	-0.18	0.06
P2xP10	-0.83	-1.82**	-1.33	0.13	0.89**	0.51	1.83	1.95*	1.89
P3xP4	-1.67	-0.63	-1.15	0.80*	0.60	0.70*	0.31	1.79	1.05
P3xP5	-1.00	-0.90	-0.95	0.92**	0.39	0.66	2.94*	2.38*	2.66*
P3xP6	-1.03	-0.54	-0.79	1.10**	0.76*	0.93**	3.87**	3.58**	3.72**
P3xP7	-1.83*	-4.38**	-3.10**	-0.13	0.16	0.01	4.65**	5.60**	5.13**
P3xP8	-1.39	2.32**	0.46	-0.95**	-0.69*	-0.82*	-4.46**	-6.11**	-5.29**
P3xP9	-0.97	-0.65	-0.81	0.01	-0.32	-0.15	4.29**	6.18**	5.23**
P3xP10	0.89	0.26	0.58	0.13	0.54	0.33	2.22	3.11**	2.66*
P4xP5	-1.11	-0.46	-0.79	0.43	0.46	0.45	1.31	4.31**	2.81*
P4xP6	-1.14	-1.10	-1.12	-0.32	0.29	-0.02	2.18	3.24**	2.71*
P4xP7	0.72	0.40	0.56	0.05	0.76*	0.40	5.16**	3.26**	4.21**
P4xP8	-0.50	0.76	0.13	0.69*	0.71*	0.70*	2.88*	-0.25	1.31
P4xP9	-1.42	-1.88**	-1.65*	0.32	-0.25	0.03	2.20	1.10	1.65
P4xP10	-0.89	-1.63**	-1.26	-0.09	0.34	0.12	-0.64	1.04	0.20
P5xP6	1.53	1.29*	1.41	0.47	-0.19	0.14	0.13	0.63	0.38
P5xP7	-0.28	-0.54	-0.41	0.57	0.81*	0.69*	5.32**	6.19**	5.75**
P5xP8	-0.50	-1.18	-0.84	0.28	-0.43	-0.08	2.50	4.00**	3.25**
P5xP9	-2.42**	-0.49	-1.45	0.58	1.00**	0.79*	3.09*	1.83	2.46*
P5xP10	0.11	-1.57*	-0.73	0.70*	1.72**	1.21**	-0.72	-0.24	-0.48
P6xP7	-0.31	-2.85**	-1.58*	0.48	-0.15	0.16	2.98*	5.05**	4.02**
P6xP8	-2.53**	-3.82**	-3.17**	0.32	0.20	0.26	1.30	1.33	1.32
P6xP9	-2.11*	-1.46*	-1.79*	-0.04	0.04	0.00	2.62*	1.82	2.22
P6xP10	-1.92*	-2.54**	-2.23**	0.08	-0.04	0.02	5.62**	4.22**	4.92**
P7xP8	-2.00*	-2.65**	-2.33**	-0.78*	-0.13	-0.45	3.75**	4.16**	3.96**
P7xP9	-0.58	-1.29*	-0.94	0.72*	1.04**	0.88**	2.74*	4.91**	3.83**
P7xP10	-3.39**	-0.71	-2.05**	0.05	-0.38	-0.17	2.27	1.25	1.76
P8xP9	-1.81*	-1.27*	-1.54*	1.37**	0.86**	1.11**	2.19	5.46**	3.83**
P8xP10	-1.28	-1.35*	-1.31	-0.24	0.25	0.00	3.99**	4.93**	4.46**
P9xP10	-2.19*	-1.65**	-1.92*	0.46	0.08	0.27	2.77*	1.62	2.20
LSD5%(sij)	1.81	1.23	1.53	0.69	0.64	0.66	2.57	1.87	2.22
LSD1%(sij)	2.37	1.62	2.02	0.91	0.85	0.87	3.38	2.46	2.93
LSD5%(sij-sik)	2.65	1.82	2.25	1.01	0.95	0.97	3.78	2.75	3.27
LSD1%(sij-sik)	3.49	2.39	2.97	1.33	1.24	1.28	4.97	3.62	4.31
LSD5%(sij-ski)	2.53	1.73	2.15	0.97	0.90	0.93	3.60	2.62	3.12
LSD1%(sij-ski)	3.33	2.28	2.83	1.27	1.19	1.22	4.73	3.45	4.11

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

Table 6: Continue

	100-kernel weight			grain yield/plant		
Crosses	D-1	D-2	Comb.sk	D-1	D-2	Comb.sk
P1xP2	1.21	0.45	0.83	34.68**	17.00	25.84*
P1xP3	2.06	4.47**	3.27*	6.36	67.52**	36.94**
P1xP4	2.83*	3.97*	3.40*	35.46**	10.06	22.76*
P1xP5	1.89	0.67	1.28	39.07**	61.76**	50.41**
P1xP6	-0.34	-0.94	-0.64	55.34**	48.53**	51.93**
P1xP7	-3.49*	-4.44**	-3.97**	-72.95**	-89.08**	-81.01**
P1xP8	4.88**	2.35	3.62*	68.95**	76.45**	72.70**
P1xP9	4.20**	6.63**	5.42**	68.51**	36.05**	52.28**
P1xP10	0.01	-1.34	-0.67	-7.37	-31.83**	-19.60
P2xP3	0.83	2.14	1.48	37.92**	44.28**	41.10**
P2xP4	1.94	-1.15	0.39	61.31**	33.52**	47.41**
P2xP5	1.71	2.67	2.19	-23.44	34.92**	5.74
P2xP6	-0.87	0.18	-0.34	5.17	23.24*	14.21
P2xP7	0.59	3.76*	2.17	25.66*	10.18	17.92
P2xP8	2.05	1.61	1.83	48.11**	29.51**	38.81**
P2xP9	0.14	2.17	1.16	-15.59	1.47	-7.06
P2xP10	0.92	2.02	1.47	9.50	21.00	15.25
P3xP4	4.82**	2.62	3.72*	15.82	44.20**	30.01**
P3xP5	3.01*	-1.30	0.85	13.63	8.94	11.28
P3xP6	1.62	1.93	1.77	30.80*	20.82	25.81*
P3xP7	3.89**	2.55	3.22*	45.19**	51.89**	48.54**
P3xP8	-4.90**	-1.05	-2.97	-56.42**	-77.39**	-66.90**
P3xP9	3.42*	3.73*	3.57*	43.13**	37.23**	40.18**
P3xP10	-0.45	-0.36	-0.40	17.29	-3.78	6.76
P4xP5	0.87	2.37	1.62	24.61*	14.10	19.36
P4xP6	2.16	1.96	2.06	0.85	-16.76	-7.95
P4xP7	3.60*	2.01	2.81	23.75*	24.89*	24.32*
P4xP8	2.59	-0.74	0.92	5.95	3.24	4.59
P4xP9	1.05	-3.59*	-1.27	4.02	8.35	6.19
P4xP10	4.94**	-0.38	2.28	53.29**	31.69**	42.49**
P5xP6	-2.10	-0.83	-1.47	-35.86**	-36.23**	-36.05**
P5xP7	3.41*	3.39*	3.40*	73.05**	34.93**	53.99**
P5xP8	1.40	3.64*	2.52	28.61*	10.92	19.77
P5xP9	0.26	1.18	0.72	35.81**	40.03**	37.92**
P5xP10	2.68	3.96*	3.32*	24.50*	28.46*	26.48*
P6xP7	-2.12	-1.17	-1.64	61.59**	70.49**	66.04**
P6xP8	1.56	-0.23	0.66	3.20	27.50*	15.35
P6xP9	5.44**	5.57**	5.50**	18.23	16.84	17.53
P6xP10	4.40**	3.45*	3.92*	31.09**	42.52**	36.81**
P7xP8	2.26	3.93*	3.09*	33.47**	49.25**	41.36**
P7xP9	3.68**	2.86	3.27*	77.90**	36.98**	57.44**
P7xP10	0.30	0.92	0.61	0.05	17.85	8.95
P8xP9	2.14	2.22	2.18	20.86	17.15	19.01
P8xP10	-1.95	-4.35**	-3.15*	-1.04	10.87	4.91
P9xP10	-0.05	4.94**	2.45	20.79	46.23**	33.51**
LSD5%(sij)	2.77	3.29	3.01	23.52	21.90	22.50
LSD1%(sij)	3.64	4.32	3.96	30.93	28.80	29.65
LSD5%(sij-sik)	4.07	4.83	4.42	34.58	32.20	33.07
LSD1%(sij-sik)	5.35	6.35	5.83	45.46	42.33	43.58
LSD5%(sij-ski)	3.88	4.61	4.22	32.97	30.70	31.53
LSD1%(sij-ski)	5.10	6.06	5.56	43.35	40.36	41.56

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

thirteen, twelve and thirteen; and twenty fore, twenty three and twenty four parental combinations showed significant positive ($\hat{S}_{ij}$) effects for No. of row ear -1, No of kernel row-1, 100-kernel weight and grain yield plant-1 at first, second planting dates and across planting dates, respectively. The most desirable inter and intra-allelic interactions were represented by crosses; P3xP6, P5xP10 and P8xP9 for no of rows ear-1, by p1xP3, P1xP6, P1xP9, P3xP7, P3xP9, P5xP7 for no of kernels row-1, P1xP9 and P6xP9 for 100-kernel weight, and P1xP5, P1xP6, P1xP8, P1xP9, P5xP7, P6xP7 and P7xP9 for grain yield plant-1 in both sowing dates and 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 dates.

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 sowing date to another. This finding coincided with that reached above where significant SCA by sowing date mean squares were detected Table (2). 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 ten parental inbred lines. A total of 55 amplification products, among which 49 were found polymorphic (Table 7). This resulted in 89 % polymorphism. The number of amplification products per locus where 10 for primer A03, B09 for B11, 11 for B16 and 14 for B05, with and average number of 11 bands per locus (Table 7). All the primer produced polymorphic amplification products, however, the extent of percent polymorphism varied with each primer (80-100%). The number of polymorphic band per locus ranged from 8 (primer A03 and B11) to 13 (primer B05) with an average number of 9.8 bands per locus (Table 7). Genetic similarity for RAPD marker: Jaccard's pair-wise similarity estimates between genotypes were calculated and have been presented in Table 8. The lowest genetic similarity (0.289) was detected between P3 and P8. While, the highest genetic similarity was (0.824) scoured between the two parental inbred lines P8 and P9. The average for genetic similarity between all parents was 0.451.

Table (7): 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 ten maize inbred lines.

primer name and sequence	Molecular weight (bp)	P1	P2	P3	P4	P5	P6	P7	P8	P9	P10	TSB	TF	NPF	PPf
primer A03 AGTCAGCCAC	1300	0	0	0	0	0	0	1	0	0	0	50	10	8	80
	1200	0	1	0	1	0	0	1	0	0	0				
	1015	0	1	0	1	0	0	1	1	1	1				
	720	0	1	0	1	1	1	1	1	1	1				
	590	1	1	1	1	1	1	1	1	1	1				
	470	0	0	0	1	1	1	1	1	1	1				
	405	1	1	1	1	1	1	1	1	1	1				
	350	0	0	0	1	0	0	0	0	0	0				
	290	0	0	0	0	0	0	0	1	1	0				
	245	0	0	0	0	0	0	0	1	1	0				
B05 TGCGCCCTTC	2050	0	0	0	0	0	0	0	1	1	0	61	14	13	93
	1480	0	0	0	0	1	0	0	0	0	0				
	1440	1	1	0	0	0	0	0	0	0	0				
	1285	1	1	0	0	0	0	0	1	1	0				
	1015	1	1	1	1	1	0	1	0	0	0				
	795	1	0	0	0	0	0	1	0	0	0				
	670	1	1	0	0	1	0	1	0	0	0				
	590	1	1	1	1	0	0	1	1	1	1				
	530	1	1	1	0	1	1	1	1	1	1				
	450	1	1	0	0	1	0	1	1	1	1				
	400	0	0	0	0	0	0	0	1	1	0				
	345	0	0	0	0	1	0	0	1	1	0				
	295	1	1	1	1	1	1	1	1	1	1				
	245	0	0	0	0	0	0	0	1	0	0				
B09 TGGGGGACTC	1510	0	0	1	1	0	0	0	0	0	0	57	10	9	90
	1040	1	1	1	1	1	1	1	0	0	0				
	905	1	1	1	1	1	1	1	1	1	1				
	760	0	0	0	0	0	1	1	1	1	1				
	610	0	0	0	0	1	1	0	1	1	1				
	540	1	0	1	1	1	1	1	0	0	0				
	475	0	0	1	1	1	1	1	1	1	1				
	420	0	0	1	1	1	1	1	0	0	0				
	340	0	0	1	1	1	1	0	1	1	1				
	290	0	0	0	0	1	1	0	0	0	0				
B11 GTAGACCCGT	2600	0	0	0	0	0	0	0	0	0	1	50	10	8	80
	1630	0	0	0	1	0	0	1	0	1	0				
	1370	1	1	1	1	1	1	1	1	1	1				
	1205	0	1	0	0	0	0	1	1	0	0				
	1030	0	0	0	0	0	0	0	0	1	0				
	714	1	1	1	1	1	1	1	1	1	1				
	600	0	0	0	1	0	1	1	1	1	1				
	490	1	0	1	0	1	0	1	1	1	1				
	390	0	0	0	0	1	0	1	1	1	1				
	270	0	0	0	1	0	0	0	1	1	1				
B16 TTTGCCCGGA	1760	0	1	1	1	0	0	0	0	0	0	32	11	11	100
	1460	0	1	0	0	0	0	1	0	0	0				
	1350	1	0	0	1	0	0	0	0	0	0				
	1180	0	0	0	1	0	0	0	0	0	0				
	1000	1	1	1	1	1	1	1	0	0	1				
	790	0	0	0	0	0	0	0	1	1	1				
	705	1	0	0	0	1	0	0	0	0	1				
	520	0	0	0	1	0	0	0	0	0	0				
	400	1	0	0	0	1	0	1	1	1	1				
	330	0	0	0	0	0	0	0	0	0	1				
	300	1	0	0	0	1	0	0	0	0	0				
Total		22	21	18	27	27	19	30	30	30	26	250	55	49	89

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

	P1	P2	P3	P4	P5	P6	P7	P8	P9	P10
P1	1									
P2	0.536	1								
P3	0.481	0.444	1							
P4	0.324	0.412	0.552	1						
P5	0.531	0.371	0.500	0.385	1					
P6	0.323	0.333	0.542	0.484	0.586	1				
P7	0.486	0.545	0.455	0.500	0.541	0.485	1			
P8	0.293	0.300	0.289	0.349	0.415	0.389	0.452	1		
P9	0.359	0.333	0.324	0.349	0.487	0.429	0.452	0.824	1	
P10	0.371	0.343	0.375	0.395	0.514	0.500	0.514	0.629	0.781	1

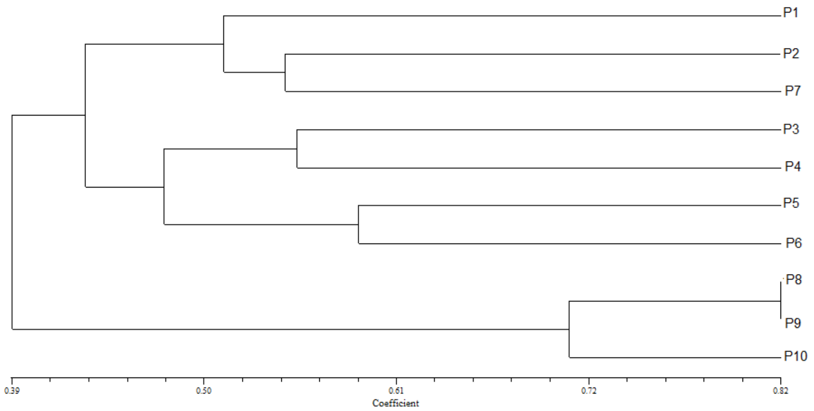

Figure (1): Dendrogram generated based on UPGM clustering method and Jacquard's coefficient using RAPD analysis among the parental inbred lines.

Cluster analysis: On the basis of Jaccard's coefficient, the ten parental inbred lines can be distinguished into 3 major main clusters (Fig.1). The first main cluster consists of the inbred line No. 1, 2 and 7. The second main cluster includes four inbred lines P3, P4, P5 and P6 and this cluster separated into two sub-clusters: the first sub-cluster contained P3 and P4. Meanwhile, the second sub cluster contained two inbred lines P5 and P6. In addition, P8, P9 and P10 were belonged in third cluster also, P8 and P9 were closely related. 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 as well as heterosis for grain yield plant-1: The estimate value of correlation coefficient between GD, and mean performance for grain yield plant-1 found negative (r =-0.045). Therefore, the RAPD marker could not be predicted about the mean performance 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 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 F1 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).

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تقدير القدره على التآلف فى الذرة الشامية تحت ميعادين زراعة و تقدير التباعد الوراثى بأستخدام المعلمات الجزيئية RAPD

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2- قسم بحوث الذرة الشامية – معهد المحاصيل الحقلية – مركز البحوث الزراعية.

قيمت 10 سلالات مرباة داخليا والهجن النصف دائرية بينهم فى ميعادين زراعة مختلفين للتبكير و المحصول ومكوناتة. اظهر التباين الراجع الى ميعاد الزراعة، التراكيب الوراثية ، الاباء، الهجن والاباء x الهجن معنوية فى كل صفات الدراسة لكل ميعاد على حدى والتحليل التجميعى لهم عدا تباين الاباء لصفة محصول النبات الفردى. كما ظهرت معنوية لتفاعل الاباء مع ميعاد الزراعة لكل الصفات ماعدا عدد الايام حتى ظهور 50% حريرة.

كانت هناك معنوية لتباين القدرة العامة والخاصة على الائتلاف لكل الصفات المدروسة. كانت النسبة بين GCA/SCA لصفة محصول النبات الفردى فى الميعادين والتجميعى ولصفة عدد الحبوب فى الصف للميعاد الثانى اقل من الواحد الصحيح مما يشير الى الدور الاكبر للتباين الوراثى راجع الى التباين غير مضيف اما باقى الحالات اظهرت نسبة اعلى من الواحد مما يشير الى الدور الاكبر للفعل المضيف فى تباين هذه الصفات.

اظهر تباين التفاعل بين ميعاد الزراعة والقدرة الائتلافية العامة معنوية لكل الصفات ماعدا صفة عدد الايام حتى ظهور 50% حريرة ووزن 100 حبة . بينما كان هناك تفاعل غير معنوى بين ميعاد الزراعة والقدرة الائتلافية الخاصة لكل صفات الدراسة ماعدا محصول الحبوب للنبات الفردى. كانت السلالة الابوية P4 والسلالة الابوية P9 الافضل فى قدرتهم الائتلافية العامة لصفتى التبكير ومحصول النبات الفردى على التوالى.

ظهرت افضل قدرة ائتلافية خاصة فى الهجن P1 x P3و P1 x P8 و P3 x P7 و P6 x P8 لصفة عدد الايام حتى ظهور 50%حريرة والهجن P1 x P5و P1 x P6 و P1 x P8 و P1 x P9 و P5 x P7و P6 x P7 و P7 x P9 لصفة محصول الحبوب للنبات الفردى فى كلا الميعادين والتحليل التجميعى بينهم.

كان اقل تشابة وراثى (0,289) بين الاب الثالث والاب الثامن بينما اعلى تشابة وراثى (0.824) ظهر بين الاب الثامن والاب التاسع.

ظهر معامل الارتباط بين التباعد الوراثى GD ومتوسط الاداء لمحصول الحبوب للنبات الفردى سالبا و غير معنوى . لذلك لايمكن الاعتماد على طريقة المعلمات الجزيئية (RAPD) فى التنبؤ بمحصول الحبوب للنبات الفردى للهجن المتكونة من الاباء فى هذه الدراسة.