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DIALLEL ANALYSIS AND RELATIONSHIP BETWEEN MOLECULAR POLYMORPHISMS AND YELLOW MAIZE HYPRID PERFORMANCE

BY

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ABSTRACT

A half diallel cross between 10 inbred lines of maize (*Zea mays* L.) was evaluated under two different sowing dates for ten quantitative characters. Sowing date, genotypes, parents and hybrids mean squares were significant for all traits under study. Significant genotypes x sowing date mean squares were obtained for all traits except ear height, ear husk and no. of rows/ear. Significant interaction between hybrids and sowing dates mean squares were obtained for all traits except ear height, ear husk and no. of rows/ ear. General and specific combing ability mean squares were significant for all traits. The magnitudes of the ratios of GCA/SCA revealed that the additive and additive x additive types of gene action were the most important expressions for ear husk, maturity date, no. of rows/ear, tasseling date and silking date. Plant height, ear height, no. of grain/row, 100-kernel weight and grain yield/plant showed GCA/SCA ratios less than unity. The mean squares of interaction between sowing dates and both types of combining ability were significant for tasseling date, silking date, plant height, no. of grains/row and grain yield/plant. The ratio for GCA x D/GCA was higher than ratio of SCA x D/SCA for tasseling date, plant height, no. of grains/row, and grain yield/ plant. The parental inbred line no. 4 seemed to be good combiner for; plant height, ear height, no. of grains/row, 100-kernel weight and grain yield/plant. The parental inbred line no. 10 appeared to be one of the good combiner for; ear husk, no. of rows/ ear, no. of grains/row and grain yield/plant. The cross P_1xP_8 had the highest values for both SCA and heterotic effects followed by crosses P_1xP_{10}, P_4xP_8, P_6xP_8 and P_6xP_{10} for grain yield. The five RAPD primers generated 143 scorable bands across 10 inbred lines. These primers produced a total of 32 reproducible fragments, from which 26 (73.06) were polymorphic. The mean of polymorphic bands per primer was 5.2. The lowest genetic similarity (0.333) was obtained between the two inbred lines P_2 and P_9, while, the highest genetic similarity (0.81) was scored between the two inbred lines P_{10} and P_9. The estimated value for correlation coefficient between genetic diversity (GD), and each of mean performance and heterosis relative to both checks varietes and SCA for grain yield/ plant were significant (r = 0.315, 0.332, 0.334, 0.401), respectively. The correlation coefficient between sub cluster1 (inbred lines P_1 and P_2) and main cluster 2 (inbred lines P_7, P_8, $P_9$and P_{10}) was higher (r = 0.56). In the same time the highest values of grain yield and heterosis were obtained from the crossing between inbred line P_1 (sub cluster 1) and inbred line P_8 (main cluster 2). Also crossing between inbred line P_1 (sub

and inbred line P_8 (main cluster 2). Also crossing between inbred line P_1 (su cluster 1) and inbred line P_{10} (main cluster 2) ranked the third for grain yiel specific combining ability and heterosis. While the crosses P_6xP_8 and P_6xP derived from inbred line P_6 (sub-sub cluster 2) and P_8 and P_{10} (main cluster 2) ha the fourth rank for grain yield and heterosis, The results indicated that RAP marker can be used as a tool for determining the extent of genetic diversi among maize inbred lines and classiting genotypes into different groups. Th study showed that GD can be used to precisely predict the yield performance a heterosis value for F_1 hybrids.

Key words: Combining ability, diallel analysis, heterosis, RAPD marke genetic distance

INTRODUCTION

The amount of heterosis expressed in F_1 hybrid is mainly affected by genetic diversity (Griffing and Lindstrom 1954; Moll *et al.*, 1965 and Hallauer *et* 1988). Previous studies have shown a positive relationship between genetic distan as measured by geographical distance and F_1 grain yield and grain yield heterosis maize. East (1936), Hayes and Johnson (1939) and Moll *et al.*, (1962) stated t heterosis in maize appeared to increase with genetic divergence of the pare Genetic diversity can be obtained from pedigree and heterosis data, fr morphological traits or using molecular marker which detect variation at the D sequence level (Smith and smith 1992). In particular, DNA-based polymorphism powerful tool in the assessment of the genetic similarity between breeding stocks (1995). Molecular techniques are now a valuable tool for advances in genome resea generating considerable interest in predicting hybrid performance. Molecular mar are of great value in genetic research and partial breeding programs since they re the genetic variation among individuals. Various PCR-based marker techniques h recently been successfully introduced in the fingerprinting of plant genomes (Ke *et al.*, 1994) and in genetic diversity studies (Tinker *et al.*, 1993 and Lanze *et* 1997). Among them random amplified polymorphic DNA (RAPD) analysis whic relatively simple rapid and cost effective. Our objectives were (1) to establish magnitude of both general combining ability GCA and specific combining ab SCA effects and their interaction with the two sowing dates. (2) To determine hy mean performance and heterosis for the ten selected inbred lines. (3) To determin genetic similarity among ten selected inbred lines by using RAPD marker. (4 obtain a RAPD fingerprint for each line. (5) To determine the relationship betw the RAPD-based distances of these inbred lines and mean performance of their si cross hybrids, SCA effects and heterosis for grain yield performance.

MATERIALS AND METHODS

Field experiments

Ten yellow inbred lines (*Zea mays* L.) were used as parents in this st Moshtohor P_1 (1012), P_2 (106), P_3 (103), P_4 (100), P_5 (161), P_6 (120B), P_7 (1(P_8 (L56), P_9 (313A), P_{10} (500) were obtained by Prof. Dr. A.A.M. El-Hosa the Department of Agronomy, Faculty of Agric. at Moshtohor, Benha Univ

the first season (summer 2005) the ten inbred lines were sown in 18th May, 28th May and 8th June to avoid differences in flowering time and to secure enough hybrid seed. All possible combinations without reciprocals were made between the ten inbred lines by hand method giving a total of 45 crosses. In the second season (summer 2006), two adjacent experiments were conducted at the two sowing dates: 28th May and 14th June. In each experiment the ten inbred lines and their 45 hybrids as well as two check hybrids (S.C. G.155 and S.C. Pioneer 3062) were grown in a randomized complete block design with three replications. Each plot consisted of two ridges of 5 m length and 70 cm width. Hills were spaced by 25 cm with two kernels per hill and later thinned to one plant per hill. The dry method of sowing was used. The first irrigation was given after about 21 days from sowing. The 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 silking and tasseling dates (days) in 50% of the plant silked or tasseled, plant height (cm), ear height (cm), maturity date (days) in phisyologacal matured, ear husk, no. of kernels/row, no. of rows/ear, 100-kernel weight and grain yield/plant which was adjusted for 15.5% moisture.

DNA extraction

Leaf tissue from each genotype was collected from 5-7 days old germinated seedlings. Equal quantities of leaf tissue from 10 seedlings of each line were bulked, lyophilized, and ground with a mortar. Genomic DNA was isolated and extracted using the mi-Plant Genomic DNA Isolation Kit.

RAPD-PCR analysis

Amplifications were conducted with 10-mer primers from Operon Technologies Inc. (Alameda, Calif., USA). 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 obtained data were statistically analyzed for analysis of variance by using computer statistical program MSTAT-C. General and specific combining ability estimates were estimated according to Griffing's (1956) diallel cross analysis designated as method 2 model I for each experiment. The combined analysis of the two experiments was carried out whenever homogeneity of variance was detected (Gomez and Gomez, 1984). Heterosis expressed as the percentage deviation of the F1 mean performance from each of S.C. G.155 and S.C. Pioneer 3062 was determined. The obtained data of RAPD analysis was 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

produced for the RAPD data using Nei and LI's formula (1979). A dendrogram tree was constructed by the UPGMA clustering algorithm from the SAHN option of NTSYS-PC version 2.1 (Rohlf, 2000).

RESULTS AND DISCUSSION

The analysis of variance for ordinary analysis over the two experiments for all traits is given in Table (1). Sowing date mean squares for all traits under study were significant, with mean values in early sowing being higher than those in late sowing for all traits except ear husk. The increase in these traits at early sowing date may be due to the prevailing of favorable temperature and day length leading to greater vegetative growth, yield and its components of corn plants therefore, the first sowing date seemed to be non-stress environment.

Genotypes mean squares were significant for all traits (Table 1). This indicates wide diversity between the parental materials used in the present study. Significant genotypes x sowing date mean squares were obtained for all traits except ear height, ear husk and no. of rows/ear., revealing that the performance of genotypes differed from sowing date to another.

Significant parent's mean squares were obtained in all cases Table (1). Insignificant interaction mean squares between parental inbred lines and sowing dates were detected in all traits studied except tasseling date, silking dates and plant height. This result may reveal the high repeatability of the parental inbred lines under different sowing dates. For the exceptional traits on the contrarily, significant interaction was obtained revealing that the parental inbred lines varied in their response to sowing dates.

Hybrids mean squares were significant for all traits. Significant interaction between hybrids sowing dates mean squares were obtained for all traits except ear height, ear husk and no. of rows/ear Table (1). Such results indicate that, these hybrids behaved some what differently from sowing date to another. For the exceptional traits, insignificant interaction was obtained, reflecting that the hybrids were suspected to environmental changes by nearly similar magnitudes.

Mean performances of parental inbred lines and their F_1 hybrids, S.C. G.155 and S.C. pioneer 3062 are presented in Table (2). For tasseling date, the inbred lines no. 6, 7, 8 and 2 gave the earliest ones. Also, the inbred lines no. 6, 7, 1 and 2 exhibited significant earliest for silking date. As for maturity date, the inbred line no. 2, 5, 6, 8 and 10 behaved as the earliest inbred lines. The parental inbred lines no.1, 4 and 7 gave the lowest mean values for ear and plant heights. The parental inbred lines no. 3 and 9 had the highest mean values for ear husk. The parental inbred line no. 5 gave the highest number of rows/ear. The parental inbred lines no. 4, 7 and 5 gave the highest no. of kernels/row. The inbred line no. 4 recorded heavier 100-kernel weight but without superiority than those of no. 1, 3, 5, 6, 7 and 9. These inbred lines exhibited high mean values for two or more of traits contributing grain yield.

Table (1): Observed mean squares from ordinary analysis and combining ability for the studied traits over the two sowing dates.

S.O.V.	d.f	Tasseling date	Silking date	Plant height	Ear height	maturity date	Ear husk	No of rows/ear	no of Kernels/ row	100-kernel weight	Grain yield/plant
Sowing dates	1	3221.09**	3066.78**	4933.87**	7593.60**	1597.20**	20.38**	5.71**	65.48**	98.18**	12121.21**
Rep/D	4	0.97	1.55	60.63	42.32	1.55	1.06**	1.46	6.07	9.39	193.93
Genotypes	54	28.92**	35.54**	8139.04**	2213.27**	21.95**	8.83**	9.92**	350.75**	134.91**	16724.51**
parent	9	15.60**	23.94**	2709.57**	786.35**	35.08**	8.65**	2.68**	149.78**	48.34**	1734.78**
Cross	44	10.11**	10.56**	949.17**	393.45**	16.42**	8.82**	5.90**	72.57**	37.15**	2431.50**
Par.vs.cr.	1	976.17**	1239.12**	373358.70**	95128.02**	147.18**	11.12**	251.89**	14399.17**	5215.55**	780524.31*
G/D	54	5.22**	7.84**	85.47**	37.92	2.11**	0.14	1.01	12.24*	15.91**	460.75**
par./D	9	12.96**	20.16**	59.38*	52.75	0.16	0.08	1.19	10.41	16.33	137.69
Cr./D	44	3.75**	5.48**	92.72**	35.4	2.36**	0.15	0.95	12.84*	15.63**	476.53**
Par.vs.cr.Vs.D	1	0.42	0.76	1.00	15.05	8.98**	0.0002	1.61	2.39	24.57	2674.08**
Error	216	0.58	0.75	25.49	30.72	1.17	0.34	0.79	7.98	9.05	104.61
GCA	9	11.53**	15.25**	951.11**	269.89**	12.62**	11.60**	5.05**	56.87**	20.90**	1077.65**
SCA	45	9.26**	11.17**	3065.39**	831.33**	6.26**	1.21**	2.96**	128.92**	49.79**	6474.27**
GCA x D	9	2.44**	3.03**	22.20**	11.76	0.29	0.04	0.23	5.18*	3.7	134.00**
SCA x D	45	1.60**	2.53**	29.75**	12.82	0.79**	0.05	0.36	3.86*	5.62**	157.50**
Error	216	0.19	0.25	8.5	10.24	0.39	0.11	0.26	2.66	3.02	34.87
GCA/SCA		1.24	1.37	0.31	0.32	2.02	9.56	1.71	0.44	0.42	0.17
GCA x D/GCA		0.21	0.2	0.02	0.04	0.02	0	0.05	0.09	0.18	0.12
SCA x D/SCA		0.17	0.23	0.01	0.02	0.13	0.04	0.12	0.03	0.11	0.02

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

Table (2): Mean performance of the genotype for all the studied traits over the two sowing dates and heterosis relative to both checks varieties for grain yield/ plant.

Genotype	Tasseling date	Silking date	plant height	Ear height	Maturity date	Ear husk
P1	61.17 EG	63.67 CD	158.7 Z	70.50 Z	100.3 UZ	6.833 EH
P2	61.33 EF	62.83 DE	196.5 X	92.50 WX	98.00 Z	5.500 LP
P3	63.00 C	67.67 A	184.5 Y	97.17 VW	101.2 PW	8.333 A
P4	65.83 A	67.50 A	160.7 Z	81.00 Y	102.5 IQ	5.500 LP
P5	62.83 CD	66.17 B	218.0 W	110.5 U	99.83 WZ	5.167 NP
P6	60.83 EH	63.00 CE	215.0 W	103.2 V	99.00 YZ	6.000 IM
P7	61.33 EF	62.50 EF	166.5 Z	91.00 WX	103.8 DJ	5.500 LP
P8	61.83 DE	64.00 C	170.0 Z	86.17 XY	97.67 Z	7.167 DG
P9	63.00 C	65.83 B	187.5 Y	88.67 X	104.7 CE	8.500 A
P10	64.50 B	66.67 AB	194.2 X	99.50 V	98.83 Z	6.667 FI
$\bar{P}$	62.57	64.98	185.15	92.02	100.58	6.52
1x2	55.00 W	56.83 V	246.8 U	124.0 T	101.8 MU	5.000 OP
1x3	57.17 QU	58.33 RU	259.5 ST	130.2 NT	103.8 DJ	7.167 DG
1x4	59.33 IL	60.67 HM	260.5 RT	125.7 RT	104.3 DG	6.833 EH
1x5	56.50 TV	58.00 TU	267.3 MR	137.7 GN	99.17 XZ	5.833 JN
1x6	59.17 JM	60.67 HM	258.2 T	124.7 ST	100.5 TY	6.667 FI
1x7	56.67 SV	58.83 PT	263.3 PT	144.2 CG	102.2 KS	8.167 AB
1x8	55.83 VW	58.17 SU	269.3 LP	132.2 LS	101.2 PW	7.833 AD
1x9	58.33 LQ	59.83 LQ	286.7 CD	147.0 CF	102.3 JR	7.833 AD
1x10	59.67 HK	61.17 HK	274.0 GM	142.8 CI	104.0 DI	8.000 AC
2x3	56.17 UW	58.67 QT	264.0 PT	126.5 RT	100.5 TY	6.333 HK
2x4	56.50 TV	58.00 TU	261.3 QT	125.8 RT	101.0 QW	3.833 R
2x5	57.83 NS	59.33 NR	273.5 HN	143.5 CH	102.2 KS	3.833 R
2x6	59.17 JM	61.17 HK	273.8 GM	139.7 FL	100.3 UZ	4.167 QR
2x7	55.83 VW	57.33 UV	232.3 V	113.8 U	99.83 WZ	3.500 R
2x8	55.17 W	56.83 V	269.5 LP	135.8 HP	100.2 VZ	4.000 R
2x9	58.17 LQ	60.00 KP	284.2 CE	134.7 JQ	101.5 NV	6.167 HL
2x10	56.83 RV	60.17 JO	279.0 EK	137.0 GN	102.0 LT	6.500 GJ
3x4	59.00 JN	60.00 KP	283.2 CE	141.3 EJ	102.2 KS	6.833 EH
3x5	58.17 LQ	59.50 MQ	296.8 A	154.5 AB	104.5 DF	6.833 EH
3x6	58.17 LQ	60.50 HN	269.5 LP	128.5 PT	103.8 DJ	6.500 GJ
3x7	58.17 LQ	59.83 LQ	245.7 U	128.7 PT	103.0 FN	7.167 DG
3x8	59.17 JM	60.33 IO	272.5 KO	129.2 OT	103.0 FN	7.167 DG
3x9	60.00 GJ	61.33 GJ	272.2 KO	133.3 KR	103.5 DL	7.167 DG
3x10	59.00 JN	60.67 HM	261.3 QT	132.8 KR	103.7 DK	7.500 BE
4x5	58.17 LQ	60.00 KP	275.7 FL	144.2 CG	103.5 DL	4.833 PQ
4x6	60.67 EH	62.50 EF	266.0 OS	127.8 QT	100.8 RW	6.167 HL
4x7	58.17 LQ	60.17 JO	288.5 BC	149.7 BC	101.8 MU	4.833 PQ
4x8	58.00 MR	59.83 LQ	280.5 DG	132.7 KR	101.3 OW	6.167 HL
4x9	58.83 JO	61.17 HK	271.3 LO	138.3 GM	102.8 GO	6.833 EH
4x10	58.33 LQ	60.83 HL	286.7 CD	131.5 MT	103.3 EM	5.833 JN
5x6	58.17 LQ	60.33 IO	273.3 IN	138.2 GM	100.3 UZ	4.833 PQ
5x7	56.83 RV	59.17 OS	283.3 CE	146.3 CF	102.8 GO	4.167 QR
5x8	58.83 JO	60.33 IO	266.7 NR	134.8 JQ	104.2 DH	6.833 EH
5x9	59.00 JN	61.17 HK	272.7 JO	134.8 JQ	101.0 QW	5.167 NP
5x10	59.00 JN	60.83 HL	281.8 CF	134.7 JQ	103.0 FN	5.500 LP
6x7	58.83 JO	60.67 HM	264.2 PT	135.3 IQ	102.7 HP	5.167NP
6x8	58.50 KP	60.00 KP	285.0 CE	131.5 MT	103.3 EM	6.333 HK
6x9	59.83 HJ	61.67 FH	288.5 BC	131.0 MT	101.3 OW	5.667 KO
6x10	58.33 LQ	61.50 FI	288.7 BC	137.7 GN	104.8 CE	5.333 MP
7x8	57.33 PU	58.83 PT	280.3 DH	148.8 BD	101.3 OW	5.833 JN
7x9	57.83 NS	59.67 LQ	267.5 MQ	141.3 EJ	100.7 SX	7.333CF
7x10	58.17 LQ	59.67 LQ	268.0 MQ	140.0 FK	105.0 BD	6.000 IM
8x9	58.17 LQ	59.83 LQ	279.5 EJ	147.8 BE	99.00 YZ	5.167 NP
8x10	60.00 GJ	62.33 EG	284.7 CE	140.2 FK	104.5 DF	6.167 HL
9x10	58.83 JO	61.50 FI	278.8 EK	141.5 DJ	106.0 BC	6.833 EH
G155	57.67 OT	59.33 NR	294.0 AB	157.8 A	107.7 A	6.667 FI
3062	60.50 FI	62.33 EG	279.7 DI	136.5 GO	106.3 AB	6.167 HL
$\bar{C}$	58.11	59.96	272.36	136.04	102.31	6.04
$\bar{X}$	58.92	60.87	256.50	128.03	102.00	6.13

Table (2): Cont.

Genotype	No of rows / ear	no of Kernels/ row	100- kernel weight	Grain yield /plant	H% relative SC. 155	H% relative SC. 3062
P1	12.00 QT	17.87V	24.00 MN	36.53 Y		
P2	11.43 ST	24.23 U	18.33 O	47.39 XY		
P3	11.12 T	17.47 V	27.33 LM	50.68 X		
P4	11.93 RT	28.12 RT	28.00 KM	82.61 V		
P5	13.45 IO	24.90 TU	25.50 MN	78.73 V		
P6	12.38 NS	23.08 U	26.33 MN	64.69 W		
P7	12.23 OT	26.32 SU	26.33 MN	73.82 VW		
P8	11.33 ST	17.75 V	23.00 N	40.83 XY		
P9	11.90 RT	14.45 V	24.33 MN	45.57 XY		
P10	12.08 PT	14.67 V	22.50 N	43.13 XY		
$\bar{P}$	11.99	20.89	24.57	56.40		
1x2	14.33EK	29.50 QS	36.00 BG	157.6 RT	-27.17*	-25.17*
1x3	13.27JP	34.13 LP	34.83 CJ	152.7 TU	-32.13*	-30.13*
1x4	13.02 LR	34.53KP	35.50 BH	156.9 RT	-27.92*	-25.92*
1x5	14.60 DI	42.00 AD	32.83 FJ	196.2 EG	11.40	13.40
1x6	14.60DI	38.50DJ	35.33 BI	195.3 EH	10.53	12.53
1x7	13.47IO	40.03CH	35.33 BI	186.1GK	1.33	3.33
1x8	15.22 AF	40.83BG	38.67 AC	231.0 A	46.23**	48.23**
1x9	15.50 AE	36.57HN	34.00 DJ	201.3 DF	16.47	18.47
1x10	15.67 AD	44.30 AB	31.50 HK	218.0 BC	33.23**	35.23**
2x3	12.25 OT	36.77 HN	37.00 BF	159.5 QT	-25.33*	-23.33*
2x4	13.53 IN	40.47CH	38.00 AD	194.9 EH	10.06	12.06
2x5	13.73 IM	37.87EL	34.67 CJ	182.0 GM	-2.76	-0.76
2x6	13.47 IO	39.50CI	34.17 DJ	172.8 KQ	-12.00	-10.00
2x7	13.30 JP	31.05PR	35.33 BI	143.7 U	-41.13**	-39.13**
2x8	14.53DJ	33.77MP	36.67 BF	188.8 FJ	3.99	5.99
2x9	15.33 AE	39.37CI	37.17 BF	203.5 DE	18.67	20.67
2x10	13.93 GL	41.07AG	36.33 BF	194.5 EH	9.70	11.70
3x4	12.97 LR	40.03CH	33.00 FJ	171.4 LQ	-13.40	-11.40
3x5	13.47 IO	38.60CJ	33.17 EJ	166.0 OS	-18.78	-16.78
3x6	13.25JP	41.82AE	36.83 BF	182.9 GL	-1.87	0.13
3x7	12.33NS	37.60FM	35.33 BI	153.6 SU	-31.23**	-29.23**
3x8	14.52DJ	37.17GN	35.83 BH	179.8 IN	-5.05	-3.05
3x9	13.97FL	32.45OQ	33.33 EJ	150.2 TU	-34.63**	-32.63**
3x10	14.50DJ	44.73 A	31.83 GK	194.5 EH	9.67	11.67
4x5	14.00FL	41.50 AF	34.17 DJ	192.0 EI	7.20	9.20
4x6	13.98FL	41.15 AG	34.17 DJ	184.7 GL	-0.07	1.93
4x7	12.93LR	38.30 DK	35.50 BH	181.5 HM	-3.32	-1.32
4x8	15.02BH	39.32CI	41.67 A	223.5 AB	38.66**	40.66**
4x9	15.12AG	37.68FL	35.33 BI	190.7 EI	5.88	7.88
4x10	13.17KQ	40.07CH	36.00 BG	185.9 GK	1.06	3.06
5x6	14.43DK	41.93 AD	33.50 EJ	201.4 DF	16.65	18.65
5x7	12.53MS	35.28 JO	39.33 AB	162.5 PT	-22.27*	-20.27
5x8	15.88AC	35.15JO	34.83 CJ	187.9 FJ	3.14	5.14
5x9	15.07AH	33.57 NP	33.83 DJ	175.9JP	-8.94	-6.94
5x10	14.42DK	38.12DK	34.50 CJ	184.9GL	0.15	2.15
6x7	13.97FL	40.20 CH	31.83 GK	178.3 IO	-6.54	-4.54
6x8	14.62DI	39.38 CI	39.33 AB	209.9 CD	25.04*	27.04*
6x9	16.27 A	36.67 HN	31.00 IL	189.7 EJ	4.87	6.87
6x10	15.12 AG	42.58 AC	31.83 GK	209.8 CD	25.00*	27.00*
7x8	13.80 HL	33.62 NP	39.33 AB	173.8 KP	-11.03	-9.03
7x9	15.20 AG	35.27 JO	31.67 GK	168.5 MR	-16.33	-14.33
7x10	14.40 DK	40.37 CH	34.00 DJ	188.9 FJ	4.07	6.07
8x9	14.70 CI	32.00 OQ	31.50 HK	149.2 TU	-35.63**	-33.63**
8x10	14.33 EK	36.73HN	32.83 FJ	167.8 NR	-17.05	-15.05
9x10	16.13 AB	39.00 CJ	30.50 JL	172.5 KQ	-12.27	-10.27
G155	14.38 EK	35.77 IO	37.50 BE	184.8 GL	-	-
3062	13.83 HL	38.68 CJ	36.50 BF	182.8 GL	-	-
$\bar{C}$	14.21	38.01	34.87	182.49	-	-
$\bar{X}$	13.67	34.90	33.00	159.57	-	-

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

It is favorable if the single crosses were earlier in flowering than parents to develop early maturity hybrids to avoid damage by borers or other environmental adverse conditions. The parental combinations that incorporated earliness in silking and tasseling dates are plants of those F_1 hybrids 1x2, 1x8, 2x7, and 2x8. The cross 2x7 gave the lowest mean values of plant and ear heights. The three crosses 8x9, 1x5 and 2x7 had earliness in maturity date.

The cross 1x7 gave the highest mean value of ear husk, but without superiority than those of hybrids 1x8, 1x9 and 1x10. The higher value for ear husk is the most important trait for insect resistance in maize. The cross 6x9 gave the highest mean value for no. of rows/ear. Nine hybrids gave significant highest number of kernels/row. The cross 3x10 recorded the highest number of kernels/row, but without significantly differed from the hybrids 1x5, 1x10, 2x10,3x6, 4x5, 4x6, 5x6 and 6x10. Six cross; 4x8, 1x8, 2x4, 5x7, 6x8 and 7x8 gave the highest mean values for 100-kernel weight. In addition, grain yield/plant, eight crosses 1x8, 1x9, 1x10, 2x9, 4x8, 5x6, 6x8 and 6x10 had significant superiority over the best check hybrids. These hybrids exhibited significant increased of two or more of traits contributing grain yield.

Heterosis:

Mean squares for parents vs. hybrids as an indication to average heterosis over all crosses, was significant for all traits Table (1). Insignificant interaction between mean squares parent vs. crosses and sowing date were obtained revealing that grand means of parental inbred lines and their F_1 hybrids not differed from sowing date to another.

Heterosis expressed as the percentage deviation of F_1 mean performance from each of S.C. G.155 and S.C. Pioneer 3062 values for grain yield/plant are presented in Table (2). Concerning grain yield/plant the cross 1x8, 4x8, 1x10, 6x8 and 6x10, out yielded the two checks hybrids. The useful heterotic effects relative to S.C. G.155 ranged from 25.0 to 46.23 and S.C. Pioneer 3062 ranged from 27 to 48.23%. Also, thirty one and thirty two hybrids had insignificant heterotic effects relative to S.C. G.155 and S.C. Pioneer 3062, respectively. Hence, it could be concluded that these crosses offer possibility for improving grain yield in maize. Many investigators reported high heterosis for yield of maize; i.e. El-Bagoury *et al.*, (2004), Nawar *et al.*, (2002), Shafey *et al.*, (2003), Singh *et al.*, (2004) and El-Hosary *et al.*, (2006).

Combining ability

The analysis of variance for combining ability at the combined analysis for all the studied traits is presented in Table (1). The variance of general combining ability includes the additive and additive x additive genetic portion while specific combining ability represents the non additive genetic portion of the total variance arising largely from dominance and epistatic deviations. The mean squares due to general and specific combing ability 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 general and specific combing ability mean squares which were highly significant. Hence, GCA/SCA ratio was used as measure to reveal the nature of genetic variance involved

For ear husk, maturity date, no. of rows/ear, tasseling date and silking date, high ratios which largely exceeded the unity were obtained, indicating that a large part of the total genetic variability associated with theses traits was a result of additive and additive by additive gene action.

Plant height, ear height, no. of grains/row, 100-kernel weight and grain yield/plant, showed GCA/SCA ratios less than unity. Therefore, it could be concluded that the large portion of the total genetic variability for these traits was due to non-additive gene action. The largest heterotic magnitude expressed in the previous traits as the deviation of particular F_1 mean performance from both checks (S.C. G155 and S.C. pioneer 3062), may strengthened the conclusion about the importance of non-additive gene effects in the inheritance of these traits. The genetic variance was previously reported to be mostly due to non-additive for Plant, ear height, no. of grains/row by (Amer 2003 and Shafey *et al.*, 2003) and grain yield/ plant by (Amer 2003; Mosa 2003; Shafey *et al.*, 2003; EL-Hosary and EL-Badawy 2005 and El-Hosary *et al.*, 2006). On the other hand, the additive genetic variance was previously reported to be most prevalent for earliness and no. of rows/ear by (Amer, 2003; Mosa, 2003; EL-Hosary and EL-Badawy 2005); ear husk by (EL-Hosary and EL-Badawy 2005) and 100-kernel weight by (Dubey *et al.*, 2001; Shafey *et al.*, 2003; EL-Hosary and EL-Badawy 2005).

The mean squares of interaction between sowing dates and both types of combining ability were significant for tasseling date, silking date, plant height, no. of grains/row and grain yield/plant. Such results showed that the magnitude of all types of gene action varied from sowing date to another. It is fairly evident that the ratio for GCA x D/GCA was higher than ratio of SCA x D/SCA for tasseling date, plant height, no. of grains/row, and grain yield/ plant. This result indicated that additive effects were more influenced by the environmental conditions than non- additive genetic effects of these traits. Such results indicated that non-additive effects are influenced by seasonal changes (Mosa and Motawei 2005 and El-Hosary *et al.*, 2006). For silking date, the ratio of SCA x D/SCA was higher than GCA x D/GCA. This result indicated that non- additive effects were more influenced by sowing date than additive genetic effects of this trait. This conclusion is in well agreement with those reported by (Gilbert 1958).

For maturity date and 100-kernel weight, the mean squares of interaction between sowing date and SCA was significant. However, insignificant GCA by sowing date mean squares was detected. Such results indicated that non-additive effects were more influenced by sowing date than additive genetic one.

On the other hand, insignificant mean squares of interaction between sowing date and both combining abilities were obtained for ear height, ear husk and no. of rows/ ear revealing that all types of gene action were not appreciably fluctuated in magnitude from sowing date to another. This finding confirms those obtained above from the ordinary analysis of variance. Such results indicated that additive effects are influenced by environmental changes (Amer 2005 and El-Hosary *et al.*, 2006).

General combining ability effects:

Estimations of GCA effects ($\hat{g}_i$) for individual parental inbred lines for each trait in the combined analysis are presented in Table (3) General combining ability effects estimated herein differ significantly from zero. High positive values would be of interest under all traits in question except silking, tassling and maturity dates as well as plant and ear heights where high negative effects would be useful from the breeder's point of view.

The parental inbred line no. 1 exhibited significant negative ($\hat{g}_i$) effects for; tasseling, silking dates, plant and ear heights, indicating that this inbred line could be considered as good combiner for developing early and short genotypes. Also, it gave significant ($\hat{g}_i$) effects for ear husk. Earliness is required for early maturing season to escape corn pests. The parental inbred line no. 2 showed significant negative ($\hat{g}_i$) effects for tasseling, silking and maturity dates and plant and ear heights, indicating that this line could be considered as good combiner for developing early and short genotypes. Shortest plant and ear heights are required for lodging resistance. The parental inbred line no. 3 was poor combiner for tassling, silking, maturity dates, no. of rows/ear and grain yield/ plant. The parental inbred line no. 4 seemed to be good combiner for; plant height, ear height, no. of grains/row, 100-kernel weight and grain yield/plant. The parental inbred line no. 5 ranked the third for grain yield/plant. However, it gave undesirable ($\hat{g}_i$) effects for other traits. The parental inbred line no. 6 seemed to be good combiner for maturity date, no. of grains/ear, and grain yield/plant. The parental inbred line no. 7 seemed to be best combiner for; tasseling and silking dates and plant height. It seemed to be poor combiner for other traits. The parental inbred line no. 8 seemed to be best combiner for; tasseling, silking and maturity dates, ear husk, no. of rows/ear and 100-kernel weight. The parental inbred line no. 9 behaved as the best combiner for ear husk and no. of rows/ear. The parental inbred line no. 10 seemed to be good combiner for; ear husk, no. of rows/ear, no. of grains/row and grain yield/plant. It seemed to be poor combiner for tasseling, silking, maturity date plant height and100-kernel weight.

It is worth noting that the inbred line which possessed high ($\hat{g}_i$) effects for grain yield per plant might show the same for one or more of the traits contributing grain yield. In most traits, the values of ($\hat{g}_i$) effects was mostly differed from sowing date to another. This finding coincided with that reached above where significant GCA by sowing date mean squares were detected Table (1).

Table (3): General combining ability effects for all the studied traits over the two sowing date.

Parent	Tasseling date	Silking date	Plant height	Ear height	Maturity date	Ear husk	No. of Rows/ ear	no of Kernels/ row	100 Kernels weight	Grain yield/Plant
P1	-0.68**	-0.81**	-9.88**	-4.92**	-0.17	0.80**	0.15	-0.65	-0.08	1.09
P2	-1.23**	-1.30**	-3.67**	-3.54**	-1.39**	-1.09**	-0.38**	-0.50	-0.08	-5.27**
P3	0.24*	0.41**	-2.32**	-0.75	0.69**	0.99**	-0.76**	-0.47	0.24	-11.95**
P4	0.88**	0.71**	-2.21**	-2.45**	0.35*	-0.35**	-0.36*	2.12**	1.36**	7.61**
P5	0.01	0.12	8.80**	6.78**	-0.14	-0.77**	0.26	0.83	-0.10	4.27**
P6	0.37**	0.45**	6.30**	-0.64	-0.50**	-0.38**	0.22	2.00**	-0.19	8.25**
P7	-0.63**	-0.87**	-7.95**	1.82*	0.42*	-0.35**	-0.46**	0.04	0.61	-5.90**
P8	-0.29*	-0.43**	0.54	-0.25	-0.72**	0.20*	0.28*	-1.70**	1.14*	3.16
P9	0.58**	0.69**	4.57**	1.57	0.46**	0.65**	0.71**	-2.70**	-1.33**	-5.24**
P10	0.76**	1.03**	5.82**	2.40**	1.00**	0.30**	0.33*	1.03*	-1.56**	3.98*
L.S.D(0.05) gi	0.24	0.27	1.56	1.72	0.34	0.18	0.28	0.88	0.93	3.17
L.S.D(0.01) gi	0.31	0.35	2.05	2.25	0.44	0.24	0.36	1.15	1.22	4.16
L.S.D(0.05) gi-gj	0.35	0.40	2.33	2.56	0.50	0.27	0.41	1.30	1.39	4.73
L.S.D(0.01) gi-gj	0.46	0.52	3.06	3.36	0.66	0.35	0.54	1.71	1.82	6.20

Specific combining ability:

Estimation of SCA effects in 45 crosses for the studied traits over the two sowing date are presented in Table (4). The most desirable inter and intra allelic interactions were presented by P_2xP_7 for ear height P_1xP_7, P_1xP_8, P_1xP_{10}, P_2xP_{10} P_4xP_6, P_5xP_8 and P_7xP_9, for ear husk, with the exception of P_1xP_2, P_1xP_3, P_1xP_4, P_2xP_6, P_2xP_7, P_3xP_9, P_4xP_6, P_5xP_7, P_8xP_9 and P_8xP_{10} all hybrids exhibited significant positive $\hat{S}_{ij}$ effects for grain yield/plant and one or more of yield components. However, the most desirable SCA effects for grain yield/plant were detected for the crosses P_1xP_8, P_2xP_9 and P_1xP_{10} being 67.22, 54.41 and 53.40, respectively. These crosses may be prime importance in breeding programmes either towards hybrid maize production or synthetic varieties composed of hybrids which involved the good combiners for the traits in view.

RAPD-PCR marker

In this investigation the genetic variability among ten maize inbred lines was studied using RAPD marker Fig (1-5). Twenty random primers were tested. Five primers gave polymorphic amplification products. The five RAPD primers generated 143 scorable bands across 10 inbred lines (Table 5). These primers produced a total of 32 reproducible fragments, from which 26 (73.06%) were polymorphic. The mean of polymorphic bands per primer was 5.2. The size of fragments ranged from 144.72 bp to 16778.08 bp (Table 5). The least number of polymorphic bands was detected for primer B12 (1 out of 3 amplified bands), while the largest number of polymorphic bands was detected for primers A13 and B3 (8 out of 9 amplified bands) (Table 5).

Genetic similarity

The genetic similarity matrix was produced for the RABD data using Nei and LI's formula (1979) Genetic similarity coefficient presented in (Table 6). The lowest genetic similarity (0.333) was obtained between the two inbred lines P_2 and P_9, while, the highest genetic similarity (0.81) was scored between the two inbred lines P_{10} and P_9. The overall mean for genetic similarity among all inbred lines under study was (0.522)

Cluster analysis

The dendrogram constructed from cluster analysis based an RAPD data is represented in Fig. (6). The data collectively distinguished two main clusters. The first main cluster consist of six inbred lines P_1, P_2, P_3, P_5, P_6 and P_4 and this cluster separated into two sub clusters: the first sub cluster was contained two inbred lines P_1 and P_2. Meanwhile, the second sub cluster contained the other four inbred lines i.e. P_3, P_5, P_6 and P_4. In addition, the second sub cluster divided to sub-sub cluster the first sub-sub cluster was contained P_4. While, the inbred lines P_3, P_5 and P_6 were belonging to the second sub- sub cluster as well as inbred lines 3 and 5 were closely related.

The second main cluster contained four inbred lines P7, P_8, P_9 and P_{10}, except inbred 7 all remain inbred lines belonging to sub cluster as well as inbred 9 and 10 were closely related. 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 are successful in confirming hypothesized relationship.

Table (4): Specific combining ability effects for all the studied traits and heterosis relative to S. C. G155 and S. C. Pioneer 3062 over the two sowing date.

Crosses	Tasseling date	Silking date	Plant height	Ear height	Maturity date	Ear husk	No. of Rows/ Ear	no of Kernels/ row	100 - Kernel weight	Grain yield/plant
P1xP2	-2.01**	-1.93**	3.88**	4.43**	1.39**	-0.84**	0.76**	-4.25**	3.17**	2.25**
P1xP3	-1.32**	-2.13**	15.20**	7.81**	1.31**	-0.76**	0.07	0.35	1.68**	3.97**
P1xP4	0.21	-0.11	16.09**	5.00**	2.15**	0.26**	-0.58**	-1.84**	1.22**	-11.38**
P1xP5	-1.75**	-2.18**	11.91**	7.78**	-2.53**	-0.32**	0.38**	6.92**	0.01	31.28**
P1xP6	0.56**	0.16	5.24**	2.19**	-0.83**	0.12**	0.43**	2.25**	2.61**	26.43**
P1xP7	-0.94**	-0.36**	24.66**	19.24**	-0.08**	1.59**	-0.03	5.74**	1.81**	31.39**
P1xP8	-2.12**	-1.47**	22.17**	9.31**	0.06**	0.70**	0.98**	8.28**	4.61**	67.22**
P1xP9	-0.48**	-0.91**	35.47**	22.32**	0.04**	0.26**	0.83**	5.02**	2.42**	45.85**
P1xP10	0.67**	0.07	21.56**	17.32**	1.17**	0.77**	1.38**	9.01**	0.14	53.40**
P2xP3	-1.76**	-1.31**	13.49**	2.76**	-0.81**	0.30**	-0.41**	2.84**	3.85**	17.12**
P2xP4	-2.07**	-2.29**	10.71**	3.79**	0.04**	-0.85**	0.47**	3.96**	3.72**	32.95**
P2xP5	0.14	-0.36**	11.86**	12.24**	1.69**	-0.44**	0.05	2.65**	1.85**	23.47**
P2xP6	1.11**	1.14**	14.70**	15.82**	0.22**	-0.49**	-0.17**	3.10**	1.44**	10.25**
P2xP7	-1.22**	-1.37**	12.55**	-12.47**	-1.19**	-1.19**	0.33**	-3.38**	1.81**	-4.73**
P2xP8	-2.23**	-2.31**	16.13**	11.60**	0.28**	-1.24**	0.83**	1.07**	2.61**	31.33**
P2xP9	-0.10**	-0.26**	26.77**	8.61**	0.43**	0.48**	1.20**	7.68**	5.58**	54.41**
P2xP10	-1.61**	-0.44**	20.35**	10.11**	0.39**	1.16**	0.18**	5.64**	4.97**	36.22**
P3xP4	-1.04**	-1.99**	31.20**	16.50**	-0.88**	0.06**	0.28**	3.49**	-1.60**	16.17**
P3xP5	-1.00**	-1.90**	33.85**	20.44**	1.94**	0.48**	0.16**	3.34**	0.03	14.14**
P3xP6	-1.36**	-1.23**	9.02**	1.86**	1.64**	-0.24**	-0.01	5.39**	3.79**	27.07**
P3xP7	-0.36**	-0.58**	-0.57**	-0.43**	-0.11**	0.40**	-0.26**	3.13**	1.49**	11.86**
P3xP8	0.29**	-0.52**	17.78**	2.14**	1.03**	-0.16**	1.19**	4.44**	1.46**	28.97**
P3xP9	0.27**	-0.63**	13.42**	4.49**	0.35**	-0.60**	0.21**	0.72**	1.43**	7.79**
P3xP10	-0.92**	-1.65**	1.34**	3.15**	-0.03**	0.08**	1.12**	9.27**	0.15	42.87**
P4xP5	-1.64**	-1.70**	12.57**	11.81**	1.29**	-0.17**	0.29**	3.66**	-0.10**	20.55**
P4xP6	0.50**	0.46**	5.41**	2.89**	-1.01**	0.77**	0.32**	2.13**	0.00	9.31**
P4xP7	-1.00**	-0.55**	42.16**	22.26**	-0.93**	-0.59**	-0.06**	1.25**	0.53**	20.21**
P4xP8	-1.51**	-1.33**	25.67**	7.33**	-0.29**	0.19**	1.28**	4.00**	6.17**	53.12**
P4xP9	-1.54**	-1.11**	12.47**	11.18**	0.03**	0.41**	0.95**	3.37**	2.31**	28.74**
P4xP10	-2.22**	-1.79**	26.56**	3.51**	-0.01**	-0.24**	-0.61**	2.01**	3.19**	14.70**
P5xP6	-1.12**	-1.11**	1.72**	4.00**	-1.03**	-0.14**	0.15**	4.20**	0.79**	29.37**
P5xP7	-1.46**	-0.95**	25.97**	9.71**	0.56**	-0.84**	-1.08**	-0.48**	5.82**	4.60**
P5xP8	0.20**	-0.23**	0.82**	0.28**	3.03**	1.27**	1.53**	1.12**	0.79**	20.95**
P5xP9	-0.50**	-0.51**	2.79**	-1.54**	-1.32**	-0.84**	0.28**	0.54**	2.26**	17.26**
P5xP10	-0.68**	-1.19**	10.71**	-2.54**	0.14**	-0.16**	0.02**	1.36**	3.15**	17.13**
P6xP7	0.18**	0.21**	9.31**	6.12**	0.75**	-0.23**	0.40**	3.26**	-1.58**	16.35**
P6xP8	-0.50**	-0.90**	21.66**	4.36**	2.56**	0.38**	0.31**	4.18**	5.39**	38.87**
P6xP9	-0.03**	-0.34**	21.13**	2.04**	-0.63**	-0.73**	1.53**	2.47**	-0.47**	27.09**
P6xP10	-1.71**	-0.86**	20.04**	7.87**	2.33**	-0.71**	0.76**	4.65**	0.58**	38.00**
P7xP8	-0.67**	-0.74**	31.24**	19.24**	-0.36**	-0.14**	0.17**	0.38**	4.58**	16.94**
P7xP9	-1.03**	-1.02**	14.38**	9.92**	-2.21**	0.91**	1.14**	3.03**	-0.61**	20.04**
P7xP10	-0.87**	-1.37**	13.63**	7.75**	1.58**	-0.07**	0.72**	4.40**	1.94**	31.22**
P8xP9	-1.04**	-1.30**	17.89**	18.49**	-2.74**	-1.81**	-0.10**	1.50**	-1.31**	-8.33**
P8xP10	0.61**	0.85**	21.81**	9.99**	2.22**	-0.46**	-0.09**	2.50**	0.25**	1.04**
P9xP10	-1.42**	-1.09**	11.95**	9.50**	2.54**	-0.24**	1.28**	5.76**	0.39**	14.22**
LSD5% (sij)	0.79	0.90	5.24	5.75	1.12	0.61	0.92	2.93	3.12	10.61
LSD1% (sij)	1.04	1.18	6.90	7.58	1.48	0.80	1.21	3.86	4.11	13.98
LSD5% (sij-sik)	1.16	1.32	7.70	8.45	1.65	0.89	1.35	4.31	4.58	15.59
LSD1% (sij-sik)	1.54	1.74	10.14	11.14	2.17	1.17	1.78	5.68	6.04	20.55
LSD5% (sij-ski)	1.11	1.26	7.34	8.06	1.57	0.85	1.29	4.11	4.37	14.87
LSD1% (sij-ski)	1.46	1.65	9.67	10.62	2.07	1.12	1.70	5.41	5.76	19.59

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

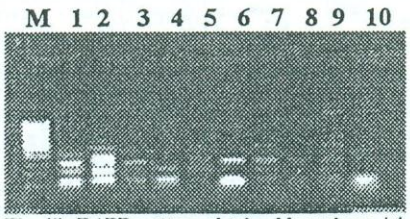

Fig. (1): RAPD pattern obtained by primer A4.

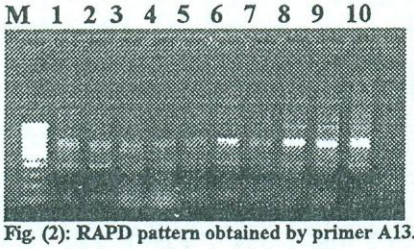

Fig. (2): RAPD pattern obtained by primer A13.

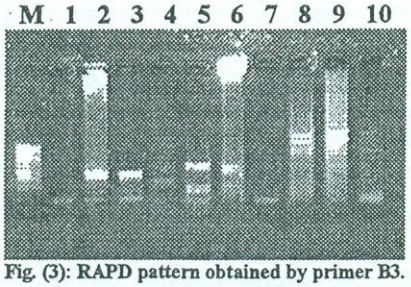

Fig. (3): RAPD pattern obtained by primer B3.

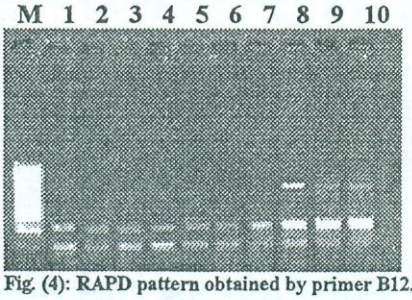

Fig. (4): RAPD pattern obtained by primer B12.

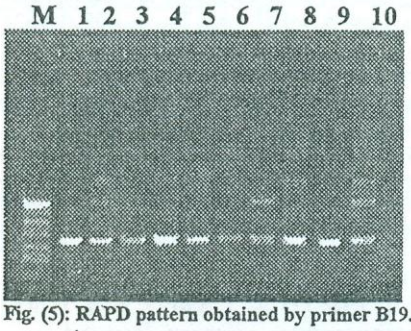

Fig. (5): RAPD pattern obtained by primer B19.

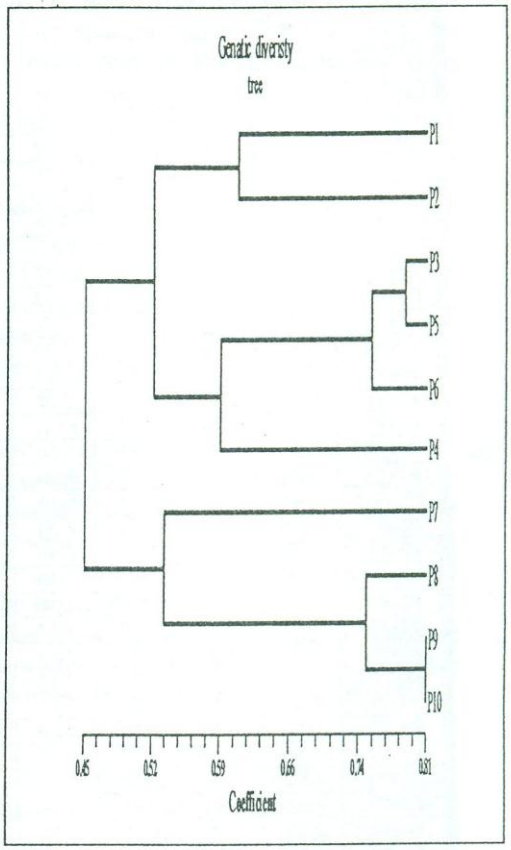

Fig. (6): Dendrogram of the genetic distance among the ten maize inbred lines based on RAPD analysis.

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

Primer	Sequence	Molecular weigh (bp)	P1	P2	P3	P4	P5	P6	P7	P8	P9	P10	TSB	TF	NPF	PPF
A4	5`AATCGGGCTG3`	1678.08	0	0	0	0	0	0	0	0	1	1	30	8	7	87.50
		720.81	0	0	0	0	0	0	0	0	1	1				
		528.76	0	0	0	0	0	0	1	0	1	0				
		472.42	0	1	0	0	0	0	0	0	0	0				
		387.88	1	0	0	0	0	0	0	0	0	0				
		292.66	1	1	1	0	1	1	1	1	1	1				
		220.82	1	1	0	1	0	0	0	0	0	0				
		144.72	1	1	1	1	1	1	1	1	1	1				
A13	5`CAGCACCCAC3`	1038.24	0	1	1	0	0	1	1	1	1	1	45	9	8	88.89
		679.27	1	1	1	1	1	1	1	1	1	1				
		511.92	1	1	1	1	1	1	0	1	1	1				
		414.07	0	0	0	0	0	0	1	0	1	1				
		404.43	0	1	0	0	0	0	0	0	0	0				
		351.09	1	1	0	0	0	0	0	0	0	0				
		342.92	0	0	1	1	1	1	1	1	1	1				
		290.76	0	0	1	0	0	0	0	0	0	0				
		246.53	1	1	0	1	1	0	0	0	0	0				
B3	5`CATCCCCCTG3`	1358.14	0	0	0	0	0	0	0	1	1	1	29	9	8	88.89
		1202.93	0	0	0	0	0	0	0	1	1	1				
		888.14	0	0	0	0	0	0	0	1	1	1				
		546.6	0	0	0	0	0	0	0	0	1	0				
		499.04	0	1	1	1	1	0	0	0	0	0				
		484.13	0	0	0	0	0	1	0	0	0	0				
		391.5	0	0	0	1	0	0	0	0	0	0				
		326.34	0	0	1	0	1	1	0	0	0	0				
		240.94	1	1	1	1	1	1	1	1	1	1				
B12	5`CCTTGACGCA3`	703.21	0	0	0	0	0	0	0	1	1	1	23	3	1	3.33
		277.72	1	1	1	1	1	1	1	1	1	1				
		177.81	1	1	1	1	1	1	1	1	1	1				
B19	5`ACCCCCGAAG3`	1353.17	0	1	0	0	0	0	0	1	0	1	16	3	2	66.67
		1030.51	0	1	0	0	0	0	1	0	0	1				
		633.58	1	1	1	1	1	1	1	1	1	1				
Total													143	32	26	
Mean													28.6	6.4	5.2	73.06

TSB = Total number of scorble bands, TF = Total number of fragments, NPF = Number of polymorphic fragments. And PPF = fragments percentage.

Table (6): Genetic similarity based on Nei and LI's coefficient for ten inbred lines in maize revealed by RAPD.

Inbred line	P1	P2	P3	P4	P5	P6	P7	P8	P9	P10
P1	1.000									
P2	0.611	1.000								
P3	0.471	0.500	1.000							
P4	0.600	0.526	0.563	1.000						
P5	0.600	0.526	0.786	0.714	1.000					
P6	0.500	0.450	0.786	0.500	0.714	1.000				
P7	0.412	0.450	0.563	0.412	0.500	0.600	1.000			
P8	0.421	0.455	0.556	0.421	0.500	0.588	0.500	1.000		
P9	0.348	0.333	0.455	0.348	0.409	0.476	0.550	0.700	0.100	
P10	0.348	0.440	0.455	0.348	0.409	0.476	0.550	0.789	0.810	1.000

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

The correlation between genetic distance and each of mean performance, SCA and heterosis for grain yield/plant.

The correlation of GD and each of SCA and heterosis for grain yield which computed for 45 hybrids combination studied are estimated. The estimate value of correlation coefficient between GD, and each of mean performance and heterosis relative to both checks variety and SCA for grain yield/plant found highly significant (r = 0.315, 0.332, 0.334, 0.401), respectively. Therefore, this specified tendency could be predicted about the relationship of GD and heterosis for grain yield/plant in this study. A similar finding was obtained by Lanza *et al.*, (1997). The correlation coefficient between sup cluster1 (P_1 and P_2) and main cluster 2 (P_7, P_8, P_9 and P_{10}) was higher (r = 0.56). In the same time, the highest values of grain yield and heterosis produced from the cross between P_1 (sub cluster 1) and P_8 (main cluster 2). Also the cross between P_1 (sub cluster 1) and P_{10} (main cluster 2) was the best third each of grain yield, specific combining ability and heterosis. While the crosses P_6xP_8 and P_6xP_{10} derived from P_6 (sub-sub cluster 2) and P_8 and P_{10} (main cluster 2) had the fourth rank for grain yield and heterosis. On the other hand, most crosses had derived from inbred lines in the same (within) cluster group (low genetic distances) lower grain yield and heterosis Table (2). Melchinger (1999) 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 each pair parents and SCA for the F_1 was moderate, low and positive. The higher correlation between marker distance, mean performance and heterosis has been reported by Lee *et al.*, (1989) and Melchinger (1993). The results indicated that RAPD marker can be used as a tool for determining the extent of genetic diversity among maize inbred lines and for genotypes into different groups. This study showed that GD can be used to precisely predict the yield performance and heterosis value for F1 hybrids.

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التحليل التبادلى والعلاقة بين المعلمات الجزيئية المتعددة المظهر وآداء الهجن الصفراء فى الذرة الشامية

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أجرى تقييم الهجن الناتجة من التهجين النصف دائرى لعشرة سلالات من الذرة الصفراء وذلك فى ميعادين مختلفين لعشرة صفات كمية. كانت متوسطات التباين لكل من مواعيد الزراعة والتراكيب الوراثية والآباء والهجن معنوية فى كل الصفات تحت الدراسة. كما كان متوسط التباين للتفاعل بين التراكيب الوراثية ومواعيد الزراعة معنوي لكل الصفات تحت الدراسة ما عدا ارتفاع الكوز ودرجة انفتاح الكوز وعدد الصفوف للكوز. كما أظهر متوسط التباين للتفاعل بين السلالات الأبوية ومواعيد الزراعة معنوية لكل الصفات تحت الدراسة ما عدا ميعاد التزهير للنورة المذكرة والمؤنثة وارتفاع النبات. كما كان متوسط التباين للتفاعل بين الهجن ومواعيد الزراعة معنوى لكل الصفات ما عدا صفة ارتفاع الكوز وانفتاح الكوز وعدد الصفوف للكوز. وكانت التباينات للقدرة العامة والخاصة معنوية لكل الصفات تحت الدراسة. وكانت النسبة بين القدرة العامة والقدرة الخاصة أكبر من الوحدة لكل من صفة انفتاح الكوز وميعاد النضج وعدد الصفوف للكوز وميعاد التزهير للنورة المذكرة والمؤنثة.

وكان متوسط التباين للتفاعل بين مواعيد الزراعة والقدرة العامة والخاصة معنويا لكل من مواعيد التزهير وطول النبات وعدد الحبوب للصف ومتوسط محصول الحبوب للنبات وكانت النسبة بين التفاعل فى القدرة العامة والمواعيد للقدرة العامة عالية عن النسبة بين التفاعل للقدرة الخاصة والمواعيد بالنسبة للقدرة الخاصة لصفات ميعاد التزهير للنورة المذكرة وطول النبات وعدد الحبوب للصف ومتوسط محصول الحبوب للنبات.

أظهرت السلالة الأبوية رقم ٤ قدرة جيدة عامة على التوافق لصفة طول النبات وارتفاع الكوز وعدد الحبوب للصف ووزن المائة حبة ومتوسط محصول الحبوب للنبات. كما أظهرت السلالة رقم ١٠ قدرة جيدة على التآلف لصفة انفتاح الكوز وعدد الصفوف للكوز وعدد الحبوب للصف ومتوسط محصول الحبوب للنبات. أظهر الهجين $P_8 \times P_1$ أنه أعلى الهجن لقيم القدرة الخاصة على التآلف وتبعه الهجن P_1xP_{10} و P_6xP_{10} و P_6xP_8 و P_8xP_4 لصفة متوسط محصول النبات.

كان معدل عدد شظايا الـ DNA الناتجة من خمس بادئات من RAPD لعشر سلالات أبوية هى ١٤٣ شظية.

وكان عدد المعلمات ٣٢ شظية حققت ٢٦ منهم عدد متباين من الإختلافات بنسبة ٧٣,٠٦ % وكان متوسط التباين أو الإختلاف للبادئ الواحد هى ٥,٢. وكان أقل درجة تشابة بين السلالات الأبوية هى ٣٣ ,٠ بين السلالات الأبوية (p_2, p_9) وأعلى درجة تشابة ٨١ بين السلالات الأبوية p_9, p_{10} . وكان الإرتباط معنوى بين التباعد الوراثى وكل من متوسط آداء وقوة الهجين وتأثير القدرة الخاصة على التآلف لكل الهجن تحت الدراسة وهى٣١٥, ٠، ٣٣٢, ٠، ٤٠١, ٠ على التوالى. وكان الإرتباط بين التباعد

الوراثى ومجموعة الهجن الناتجة من تهجين السلالات تحت المجموعة الأولى من الدندوجرام والمجموعة الرئيسية الثانية للدندو جرام معنوى بمقدار ٥٦, . وفى نفس الوقت كانت قوة الهجين الناتجة من التهجين بين السلالات المتباعدة وراثيا عالية حيث حقق الهجين الناتج من تهجين السلالة P_1 تحت المجموعة الأولى والسلالة P_8من المجموعة الرئيسية الثانية أعلى قيمة فى قوة الهجين وحقق الهجين الناتج من التهجين من P_1 تحت المجموعة و P_{10}من المجموعة الرئيسية أعلى ثالث قيمة فى قوة الهجين. وكانت قيمة الإرتباط بين التباعد الوراثى للهجن الناتجة من المجاميع القريبة وقوة الهجين منخفضا .

من خلال هذه الدراسة RAPD كتكنيك من المعلمات الجزيئية يمكن أن يستخدم فى تحديد التباعد الوراثى بين سلالات الذرة الشامية وتقسيمها الى مجموعات واستخدام هذا التباعد فى التنبؤ بالمحصول وقوة الهجين للهجن الناتجة بين هذه السلالات.