DIALLEL CROSS ANALYSIS FOR YIELD AND GENETIC MARKERS FOR HETEROSIS AND COMBINING ABILITY IN MAIZE (Zea mays, L.)

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K. A. El-Shouny[1], K. I.M. Ibrahim[1], M.F. Ahmed[1], Rania. A. A. Younis[2] and W. S. Mohamed[1].

[1-] *Agronomy Dept. Faculty of Agric. Ain Shams Univ. Cairo, Egypt.*
[2-] *Genetics Dept. Faculty of Agric. Ain Shams Univ. Cairo, Egypt.*

ABSTRACT

A half diallel set of crosses involving ten maize inbred lines were evaluated in the field. Five maize inbred lines and their 10 F_1 hybrids were used for protein electrophoresis and PCR-RAPD study in a trail to predict of heterosis and combining ability. The obtained data revealed that the large variations have been detected among F_1 hybrids in all studied traits. Both general (GCA) and specific (SCA) combining ability variances were found to be highly significant for all studied traits. This would indicate the importance of additive and non–additive genetic variances in determining the performance of all studied characters. The ratios of GCA / SCA variances were found to be less than unity for all studied traits except ear height indicating that non-additive gene action was of greater importance in the inheritance of these traits. Heterosis over better parent and the check variety showed that, the best hybrids were P_3 x P_5 and P_6 x P_9 for grain yield per plant and most of the studied traits. The parental line P_6 appeared to be the best combiner for grain yield /plant and most yield attributes while, P_2 and P_7 lines seemed to be high combiners for days to 50% tasseling and silking. Meanwhile, each of P_1, P_3, P_4, P_5, P_8, P_9 and P_{10} showed high GCA for one or more of yield attributes. Seven crosses (P_1 x P_2, P_1 x P_8, P_3 x P_5, P_4 x P_5, P_4 x P_8, P_4 x P_9 and P_6 x P_9) exhibited significant SCA effects for grain yield per plant and most of the studied traits. The electrophoresis patterns and PCR-RAPD technique could be a useful tools for the identification and characterization of these inbred lines. Using soluble protein electrophoresis and PCR-RAPD technique could be effective in the identification of the highly heterotic hybrids and those having high specific combining ability effects as genetic markers associated with hybrid vigor and specific combining ability in maize.

Key words: *Diallel cross, Maize, Heterosis, Combining ability, Electrophoretic patterns*, *PCR-RAPD technique..*

INTRODUCTION

Maize, the most important cereal crop in the world, represents one of the major principal cereal crops in Egypt. High yield is one of the major goals of maize breeding. Combining ability is a concept developed to help the breeder in identifying and selecting useful parental inbred lines. The parents of the best potentiality to transmit desirable traits to their progenies are those exhibiting the highest value for general combining ability effects, whereas combinations of highest specific combining ability effects demonstrate exploitation of heterosis concept. General and specific combining ability effects and heterosis have been studied in maize by several investigators (El-Shouny *et al*, 2003; Abdel-Sattar and Ahmed, 2004; Ibrahim, 2005; Ojo *et al,* 2007; Aliu *et al*, 2008 and Bello and Olaoye, 2009).

The electrophoretic patterns (SDS-PAGE) for water soluble proteins in grains has been used as biochemical genetic makers associated with heterosis and combining ability. Several investigators (Abdel-Tawab et al, 1989; Abdel-Sattar and Ahmed, 2004 and Hosni *et al*, 2006) tried to identify and characterize the parental lines of maize using proteins electrophoresis. The randomly amplified polymorphic DNA (RAPD) assay, which detects nucleotide sequence polymorphisms by means of the polymerase chain reaction (PCR) has become extremely a useful tool for identifying maize genotypes and to asses genetic diversity. Therefore, development of a reliable method for developing of heterotic groups and predicting hybrid performance without testing thousands of single cross combinations was the goal of numerous studies, using molecular and phenotypic markers (El-Khishin *et al*, 2003; Mohammadi *et al,* 2008; Pabendon *et al,* 2009 and Xin Qi *et al,* 2010).

The present investigation aimed to; (1) evaluate ten maize inbred lines and their 45 F_1 hybrids in half diallel cross for heterosis and combining ability in agronomic traits to identify the high GCA lines that could be used as parental lines in breeding programe for specific traits and to identify promising hybrids with high SCA that could be used commercially and (2) studying the possibility of predicting heterosis and combining ability in maize via protein electrophoresis and PCR- RAPD technique.

MATERIALS AND METHODS

The genetic material used in this investigation included new ten white maize (*Zea mays*, L.) inbred lines (P_1, P_2, P_3, P_4, P_5, P_6, P_7, P_8, P_9 and P_{10}), representing a wide range of diversity for several agronomic characters. These inbred lines were developed by Prof. Dr. K.A. El-Shouny through a breeding program at Agronomy Department, Fac. of Agric., Ain Shams Univ. The first five inbred lines were derived from the open pollinated variety Giza 2 and the other five lines were derived from the three way cross (T.W.C 352). In 2007 season, all possible cross combinations excluding reciprocals were made among the ten inbred lines giving a total of 45 F_1 crosses.

In 2008 growing season, the ten inbred lines, their forty five crosses and the check variety (Ch.v.) single cross 10 were planted in 21^{st} of May at the Agric. Res. Stat. Fac. Of Agric., Ain Shams Univ., Shalakan, Kalubia Governorate, Egypt. The experiment was conducted in a randomized complete block design with three replications. The parental lines were randomly grown separately in each block. The experimental plot included one row of four meters long and 70 cm wide. Planting was in hills spaced at 25cm apart and hills were thinned at one plant per hill. The common agricultural practices of growing maize were applied properly as recommended in the district. Data were recorded on 10 guarded plants for; Days to 50% tasseling, Days to 50% sillking, Plant height (cm), Ear height (cm), Ear length (cm), Ear diameter (cm), Number of rows /ear, Number of kernels /row, 100-kernel weight (g) and Grain yield per plant (g).

General and specific combining ability variances and effects were obtained by employing Griffing's (1956) diallel cross analysis method 4 model I. Percentage of heterosis was estimated according to Wynne *et al* (1970). In 2009, based on field data; the five divergent inbred lines P_1,P_3,P_5,P_9 and P_{10} (as manifested from field study) and their 10 F_1"s were used for SDS-protein a nalysis. Sodium dodecylsulphate polyacrylamide gel electrophoresis (SDS-PAGE) was performed on water soluble protein fractions (albumin and globulin) according to the method of Laemmli (1970) as modified by Studier (1973). The SDS-protein gel was scanned and analyzed using Gel Doc 2000 Bio-Rad System.

PCR for RAPD analyses was performed in 25 µl volume containing 2.5 mM MgCl2, 0.2 mM dNTPs, 20µM primer, 50 ng genomic DNA and 1 unit Taq DNA polymerase (Bioron, Germany). All reactions were performed in a Perkin Elmer 2400 thermal cycler. RAPD Program was performed as 1 cycle of 94^0C for 4 min and 40 cycles of 94^0C for 1 min, 35^0C for 1 min, and 72^0C for 2 min. To visualize the PCR products, 15 µl of each reaction was loaded on 1.2% agarose gel. The gel was run at 90V for 1 h and visualized with UV Transilluminator and photographed using UVP gel documentation system (GelWorks 1D advanced software, UVP).

In the molecular genetic study, six random primers were used for RAPD analysis, provided by Operon Technology (USA), with the folloeing sequences:

Primer codes	Sequences
A0 2	GTGAGGCGTC
A08	GATGACCGCC
A 13	TCAACGGACC
C0 2	CAGTGCTGTG
C0 3	CCGCATCTAC
B 15	TCGGCGGTTC

Data of polymorphic and monomorphic bands for both analyses was scored using the UVP gel documentation system. Amplicon sizes were estimated using 100-bp and 1-kb DNA standards (Bioron, Germany).

RESULTS AND DISCUSSION

Analysis of variance

Mean squares estimates for all studied traits are presented in Table (1). Values show that the large variations have been detected among F_1 hybrids in all studied traits. The partitioning of genetic variations into general combining ability (GCA) and specific combining ability (SCA) show that both general and specific combining ability variances were found to be highly significant for all studied traits.

Table (1): Mean squares estimates for all studied traits in 10 x 10 maize diallel crosses.

Source of variance	D.f	Days to 50 % tasseling	Days to 50% silking	Plant height	Ear height	Ear length
Rep	2	1.266	6.89	361.09	422.46	4.01
Crosses	44	16.35**	21.26**	1062.34**	674.22**	6.65**
GCA	9	44.96**	62.79**	2072.95**	2104.47**	7.92**
SCA	35	8.98**	10.58**	802.47**	306.44**	6.33**
Error	88	0.80	1.30	131.53	144.90	1.06
GCA/SCA		0.06	0.83	0.36	1.74	0.16

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

Table (1): Cont.

Source of variance	D.f	Ear diameter	Number of rows/ ear	Number of kernels / row	100 - kernel weight	Grain yield per plant
Rep	2	0.03	0.93	11.11	19.54	1390.42
Crosses	44	0.24**	4.78**	62.69**	10.37**	1995.956**
GCA	9	0.34**	14.53**	55.14**	21.06**	1748.56 **
SCA	35	0.22**	2.28**	64.63**	7.62**	2059.57**
Error	88	0.02	0.24	8.67	0.94	185.97
GCA/SCA		0.20	0.88	0.10	0.38	0.10

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

This would indicate the importance of additive and non - additive genetic variances in determining the performance of all studied characters.

The ratio of GCA/SCA variances was found to be greater than unity for ear height indicating that, additive and additive x additive types of gene action were of greater importance in the inheritance of this trait. These results are in harmony with those obtained by Amer, 2003; El- Shouny *et al*, 2003 and Soliman *et al*, 2005. Meantime, the ratio of GCA / SCA variances was found to be less than unity for other studied characters, indicating that non-additive gene action was of greater importance in the inheritance of these traits. These results are in agreement with those reported by Shafey *et al*, 2003; Abdel – Sattar and Ahmed, 2004; El-Shenawy, 2005 and Ibrahim, 2005.

Mean performance and heterosis over better parent and check variety

Mean values of all studied traits are presented in Table (2). Mean values for these traits exhibited the parental diversity and the hybrid differential response.The parental lines P_7 and P_2 were the best values for days to 50% tasseling and silking while, the parental lines P_1, P_2 and P_7 appeared to be the best for grain yield per plant and most yield attributes.

The hybrids P_3 x P_5, P_5 x P_6 and P_6 x P_9 exceeded their better parents and the ch.v. for grain yield per plant and most yield attributes (Table 3).

Table (2): Mean performance for all studied traits in10 x 10 maize diallel crosses

Genotypes	Days to 50 % tasseling (day)	Days to 50% Silking (day)	Plant height (cm)	Ear height (cm)	Ear length (cm)	Ear Diameter (cm)	Number of rows / ear	Number of kernels / row	100 kernel Weight (g)	Grain yield per plant (g)
				Parents						
P_1	66.67	68.00	171.13	88.20	14.70	3.77	11.13	26.00	28.53	86.70
P_2	61.00	62.67	183.33	96.67	14.70	3.70	11.87	24.80	27.32	81.39
P_3	64.00	66.00	163.23	76.13	13.03	3.72	9.73	24.33	24.97	58.73
P_4	64.00	65.00	186.67	96.00	13.67	3.60	10.27	25.20	25.30	65.06
P_5	66.00	68.67	172.80	95.00	13.53	3.73	11.33	26.27	25.60	75.76
P_6	66.00	68.33	166.17	79.17	14.67	3.17	11.07	25.00	26.07	74.36
P_7	58.00	60.67	184.17	90.00	13.70	3.63	12.67	25.00	26.60	84.70
P_8	61.33	63.33	147.57	64.90	12.73	2.87	10.80	22.33	24.90	59.38
P_9	64.00	65.00	182.27	85.67	13.87	3.87	12.00	22.93	27.23	74.70
P_{10}	65.00	66.67	151.77	66.67	10.67	3.17	10.00	23.40	24.87	57.71
mean	63.60	65.43	171.11	83.84	13.53	3.58	11.15	24.55	26.27	71.85
LSD 0.05%	3.39	3.12	35.27	21.72	0.54	0.26	0.74	1.82	1.38	7.91
				Hybrids						
P_1 x P_2	59.33	61.67	246.67	141.00	18.63	4.07	13.20	41.40	29.30	164.50
P_1 x P_3	61.00	63.33	233.33	112.67	18.03	3.10	11.27	33.37	27.00	102.21
P_1 x P_4	65.33	67.00	236.33	127.33	17.30	2.90	11.20	28.20	25.90	86.12
P_1 x P_5	61.67	63.00	265.33	151.60	17.43	3.70	13.00	34.20	32.13	145.44
P_1 x P_6	58.33	59.67	277.33	153.33	17.77	3.90	12.67	39.13	30.73	153.63
P_1 x P_7	59.33	60.33	261.00	146.33	17.77	3.90	12.93	42.40	28.27	154.39
P_1 x P_8	59.67	61.00	260.00	122.00	18.03	4.27	13.93	38.63	27.13	149.50
P_1 x P_9	60.33	62.33	279.33	143.33	19.80	3.67	13.73	39.30	26.43	142.98
P_1 x P_{10}	60.67	62.67	247.33	141.13	16.90	3.77	13.47	34.60	24.90	118.84
P_2 x P_3	56.33	58.00	244.00	130.67	17.20	3.93	13.47	40.97	26.30	143.85
P_2 x P_4	59.33	60.67	255.33	139.33	16.57	4.00	13.33	37.20	28.37	135.65
P_2 x P_5	59.33	61.33	248.67	142.67	16.00	4.00	13.40	34.73	28.67	133.15
P_2 x P_6	61.67	64.00	234.33	139.67	15.00	4.07	14.40	32.17	24.87	124.34
P_2 x P_7	60.00	61.33	216.00	108.00	16.83	3.97	12.93	31.93	28.13	112.48
P_2 x P_8	54.33	55.67	237.00	117.27	16.97	3.97	13.87	37.63	27.60	143.98
P_2 x P_9	57.67	59.33	244.67	128.00	17.40	4.03	14.20	36.77	27.53	142.11
P_2 x P_{10}	58.33	60.00	252.67	132.33	16.77	3.67	13.27	32.50	26.30	159.99
P_3 x P_4	60.00	62.00	260.67	122.67	19.50	3.73	12.90	40.53	26.13	102.66
P_3 x P_5	58.67	60.00	272.00	130.00	19.90	4.07	13.67	44.27	31.67	177.58
P_3 x P_6	55.00	55.33	255.33	120.00	16.73	3.87	14.13	38.53	27.63	150.30
P_3 x P_7	56.33	55.67	258.67	131.67	16.87	3.90	14.13	34.97	27.67	131.38
P_3 x p_8	58.67	58.67	252.00	103.67	18.87	3.87	13.60	36.83	25.77	131.36
P_3 x P_9	60.00	61.67	248.00	117.00	17.80	3.57	13.80	35.03	24.17	117.13
P_3 x P_{10}	60.67	62.00	246.00	133.67	16.77	3.83	14.67	32.87	27.27	131.67
P_4 x P_5	62.00	64.67	267.33	144.67	19.43	4.00	12.87	39.83	29.27	152.84
P_4 x P_6	64.00	66.33	287.33	166.00	18.00	3.93	13.87	39.10	26.27	139.90
P_4 x P_7	59.33	61.67	270.00	149.00	17.90	4.00	13.33	41.93	26.43	150.49
P_4 x P_8	56.67	62.33	256.67	131.33	17.80	3.93	12.67	42.27	27.60	150.37
P_4 x P_9	62.00	64.33	277.67	135.33	19.03	3.67	14.07	41.07	26.37	146.83
P_4 x P_{10}	61.67	63.67	279.00	146.33	17.43	3.67	14.33	34.73	26.07	132.12
P_5 x P_6	62.00	65.67	288.67	158.33	19.50	4.13	14.67	39.40	30.30	170.88
P_5 x P_7	59.67	62.00	261.33	138.67	16.13	3.80	12.60	32.23	29.50	113.59
P_5 x P_8	61.67	63.67	213.33	101.67	14.30	3.37	12.30	26.70	25.27	79.28
P_5 x P_9	63.67	65.67	224.00	115.33	14.03	3.03	11.03	25.57	26.10	57.85
P_5 x P_{10}	61.00	63.33	264.33	146.00	18.50	4.27	14.07	39.53	28.93	153.26
P_6 x P_7	59.33	61.00	284.33	126.67	15.90	4.17	15.47	39.13	27.13	161.62
P_6 x P_8	57.67	60.00	235.33	121.33	17.57	3.97	14.27	38.50	27.47	146.30
P_6 x P_9	60.00	62.00	272.00	136.67	19.83	3.90	16.17	43.10	30.57	172.33
P_6 x P_{10}	62.33	63.33	252.00	145.67	17.17	3.83	17.13	33.50	26.13	148.04
P_7 x P_8	55.67	58.33	258.33	120.47	18.03	4.03	14.67	39.70	29.13	150.93
P_7 x P_9	56.67	58.67	234.00	124.00	17.57	3.97	13.87	40.20	25.87	148.39
P_7 x P_{10}	58.33	60.33	253.00	127.67	16.03	3.83	16.13	38.13	27.00	152.17
P_8 x P_9	58.33	60.33	215.33	98.00	13.43	3.70	13.50	26.77	24.97	78.68
P_8 x P_{10}	58.00	59.00	240.67	126.33	16.00	3.70	14.33	32.53	25.43	118.07
P_9 x P_{10}	60.00	59.67	240.67	124.67	16.13	3.77	16.77	32.23	25.77	129.54
Mean	59.60	61.39	253.27	133.77	17.35	3.83	13.76	36.54	27.12	135.75
LSD 0.05%	2.52	3.21	32.23	36.31	2.89	0.42	1.38	8.28	2.73	38.33
C.h.v	65.00	66.00	273.00	134.33	19.23	3.90	13.07	34.97	29.37	140.50

Table (3): Percentage of heterosis over better- parent (B.P.) and check variety (Ch.v.) for all studied traits in 10x10 maize diallel cross.

Crosses	Days to 50% tasseling		Days to 50% silking		Plant height		Ear height		Ear length	
	B.P	C.hv.	B.P	C.hv.	B.P	C.hv.	B.P	C.hv.	B.P	C.hv.
P_1 x P_2	-2.74	-8.72**	-1.60	-6.56**	34.55**	-9.64	59.86**	4.97	26.76**	-3.12
P_1 x P_3	-4.69**	-6.15**	-4.05	-4.05	36.35**	-14.53*	48.00*	-16.12	22.68*	-6.24
P_1 x P_4	2.08	0.51	3.08	1.52	26.61**	-13.43*	44.37*	-5.21	17.69	-10.04
P_1 x P_5	-6.56**	-5.12**	-7.35**	-4.55	53.55**	-2.81	71.88**	12.86	18.59	-9.36
P_1 x P_6	-11.62**	-10.26**	-12.25**	-9.59**	56.21**	1.59	93.67**	14.14	20.86*	-7.59
P1 x P7	2.29	-8.72**	-0.56	-8.59**	41.72**	-4.40	65.91**	8.93	20.86*	-7.59
P_1 x P_8	-2.71	-8.20**	-3.68	-7.58**	51.93**	-4.76	87.98**	-9.18	22.68*	-6.24
P_1 x P_9	-5.73**	-7.18**	-4.11	-5.56*	53.26**	2.32	67.30**	6.70	34.69**	2.96
P_1 x P_{10}	-6.66**	-6.66**	-6.00*	-5.05*	44.53**	-9.40	111.68**	5.06	14.97	-12.12
P_2 x P_3	-7.66**	-13.34**	-7.45**	-12.12**	33.09**	-10.62	71.64**	-2.72	17.01	-10.56
P_2 x P_4	-2.74	-8.72**	-3.19	-8.08**	36.79**	-6.47	45.14*	3.72	12.70	-13.83
P_2 x P_5	-2.74	-8.72**	-2.14	-7.08**	35.64**	-8.91	50.18**	6.21	8.84	-16.80*
P_2 x P_6	1.10	-5.12**	2.12	-3.03	27.82**	-14.16*	76.42*	3.98	2.04	-22.00**
P2 x P7	3.45	-7.69**	-2.14	-7.08**	17.29*	-20.88**	20.00	-19.60	14.51	-12.48
P_2 x P_8	-10.93**	-16.42**	-11.17**	-15.65**	29.27**	-13.19*	80.69**	-12.70	15.42	-11.75
P_2 x P_9	-5.46**	-11.28**	-5.33*	-10.11**	33.45**	-10.38	49.41*	-4.71	18.37	-9.52
P_2 x P_{10}	-4.38*	-10.26**	-4.26	-9.09**	37.82**	-7.45	98.49**	-1.49	14.06	-12.79
P_3 x P_4	-6.25**	-7.69**	-4.62	-6.06*	39.64**	-4.52	61.13**	-8.68	42.68**	1.40
P_3 x P_5	-8.33**	-9.74**	-9.09**	-9.09**	57.41**	-0.37	70.76**	-3.22	47.04**	3.48
P_3 x P_6	-16.67**	-15.38**	-16.17**	-16.17**	53.66**	-6.47	57.63*	-10.67	14.09	-13.00
P_3 x P_7	-2.88	-13.34**	-8.24**	-15.65**	40.45**	-5.25	72.95**	-1.98	23.11*	-12.27
P_3 x p_8	-4.34*	-9.74**	-7.36**	-11.11**	52.51**	-7.69	59.74*	-22.82*	44.76**	-1.87
P_3 x P_9	-6.25**	-7.69**	-5.12*	-6.56**	36.06**	-9.16	53.68*	-12.90	28.37**	-7.44
P_3 x P_{10}	-5.20**	-6.66**	-6.06*	-6.06*	48.88**	-9.89	100.49**	-0.49	28.64*	-12.79
P_4 x P_5	-3.13	-4.62*	-0.51	-2.02	43.21**	-2.08	52.28**	7.70	42.20**	1.04
P_4 x P_6	0.01	-1.54	2.05	0.50	58.26**	5.25	109.68**	23.58*	22.73*	-6.40
P_4 x P_7	2.29	-8.72**	1.65	-6.56**	50.15**	-1.10	65.56**	10.92	30.66**	-6.92
P_4 x P_8	-7.60**	-12.82**	-1.58	-5.56*	38.01**	-5.98	102.36**	-2.23	30.24**	-7.44
P_4 x P_9	-3.13	-4.62*	-1.03	-2.53	61.67**	1.71	57.97**	0.74	37.26**	-1.04
P_4 x P_{10}	-3.64	-5.12**	-2.05	-3.53	50.66**	2.20	119.48**	8.93	27.56*	-9.36
P_5 x P_6	-6.06**	-4.62*	-3.89	-0.50	67.05**	5.74	99.99**	17.87	32.95**	1.40
P_5 x P_7	2.88	-8.20**	2.19	-6.06*	41.90**	-4.27	54.08**	3.23	17.76	-16.12*
P_5 x P_8	0.55	-5.12**	0.54	-3.53	23.46*	-21.86**	56.66*	-24.31*	5.67	-25.64**
P_5 x P_9	-0.52	-2.05	1.03	-0.50	22.90*	-17.95**	34.62	-14.14	1.20	-27.04**
P_5 x P_{10}	-6.15**	-6.15**	-5.01*	-4.05	52.97**	-3.18	118.99**	8.69	36.70**	-3.80
P_6 x P_7	2.29	-8.72**	0.54	-7.58**	54.39**	4.15	60.00**	-5.70	8.41	-17.32*
P_6 x P_8	-5.97**	-11.28**	-5.26*	-9.09**	41.62**	-13.80*	86.95**	-9.68	19.77*	-8.63
P_6 x P_9	-6.25**	-7.69**	-4.62	-6.06*	49.23**	-0.37	72.63**	1.74	35.23**	3.12
P_6 x P_{10}	-4.11*	-4.11*	-5.01*	-4.05	51.65**	-7.69	118.49**	8.44	17.05	-10.71
P_7 x P_8	-4.02	-14.35**	-3.86	-11.62**	40.27**	-5.4	85.62**	-10.32	31.63**	-6.24
P_7 x P_9	-2.29	-12.82**	-3.30	-11.11**	27.06**	-14.3*	44.74*	-7.69	26.68*	-8.63
P_7 x P_{10}	0.57	-10.26**	-0.56	-8.59**	37.38**	-7.3	91.50**	-4.96	17.03	-16.64*
P_8 x P_9	-4.89*	-10.26**	-4.74	-8.59**	18.14*	-21.1**	51.00*	-27.05*	-3.31	-30.16**
P_8 x P_{10}	-5.43**	-10.77**	-6.84**	-10.61**	58.58**	-11.8*	94.65**	-5.96	25.65*	-16.80*
P_9 x P_{10}	-6.25**	-7.69**	-8.20**	-9.59**	32.04**	-11.8*	59.86**	-7.19	16.35	-16.12*

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

Therefore, these previous three crosses were the highest in grain yield and most yield attributed and could be used as a source of improving grain yield and yield attributes in maize breeding program. It is also clear from Table (3) that the best hybrids were P_1 x P_6, P_2 x P_8 and P_3 x P_6 for days to 50% tasseling and silking, P_4 x P_6 for ear height, P_1 x P_8 and P_5 x P_{10} for ear diameter, P_2 x P_6, P_3 x P_{10}, P_5 x P_6, P_6 x P_7, P_6 x P_9, P_6 x P_{10}, P_7 x P_8, P_7 x P_{10} and P_9 x P_{10} for no. of rows per ear and P_1 x P_5 for 100-kernel weight.

Table (3): cont.

Crosses	Ear Diameter		Number of rows/ ear		Number of kernels / row		100 kernel Weight		Grain yield Per plant	
	B.P	C.hv.	B.P	C.hv.	B.P	C.hv.	B.P	C.hv.	B.P	C.hv.
$P_1 \times P_2$	7.96	4.36	11.20**	0.99	59.23**	18.39	2.70	-0.34	89.73**	17.08
$P_1 \times P_3$	-17.70**	-20.51**	1.26	-13.77**	28.33	-4.58	-5.36	-8.16	17.89	-27.25*
$P_1 \times P_4$	-23.01**	-25.64**	0.63	-14.31**	8.46	-19.36	-9.22*	-11.90*	-0.67	-38.70**
$P_1 \times P_5$	-1.77	-5.13	14.74*	-0.54	30.51	-2.20	12.62**	9.29*	67.75**	3.52
$P_1 \times P_6$	3.54	2.6	13.84*	-3.06	50.51**	11.90	7.71	4.52	77.20**	9.35
P1 x P7	3.54	2.56	2.05	-1.07	63.08**	21.25	-0.91	-3.84	82.28**	9.89
$P_1 \times P_8$	13.27*	9.49*	25.16**	6.58	48.59**	10.47	-4.91	-8.16	72.44**	6.41
$P_1 \times P_9$	-5.17	-5.90	14.42*	5.05	51.15**	12.38	-7.36	-10.10*	64.91**	1.77
$P_1 \times P_{10}$	7.60	-3.33	21.02**	3.06	33.08*	-1.06	-12.72**	-15.31**	37.07	-15.41
$P_2 \times P_3$	5.41	0.77	13.48*	3.06	65.19**	17.16	-4.71	-10.54*	76.74**	2.38
$P_2 \times P_4$	8.11	2.56	12.30*	1.99	47.62**	6.38	2.79	-3.50	66.66**	-3.45
$P_2 \times P_5$	7.14	2.56	12.89*	2.52	32.23*	-0.69	3.88	-2.48	63.59**	-5.23
$P_2 \times P_6$	7.96	4.36	21.31**	10.18*	28.67	-8.01	-9.89*	-15.41**	52.76*	-11.50
P2 x P7	7.21	1.79	2.05	-1.07	26.72	-8.69	1.92	-4.32	32.80	-19.94
$P_2 \times P_8$	7.21	1.79	16.85**	6.12	51.75**	7.61	036	-6.12	76.89**	2.48
$P_2 \times P_9$	4.31	3.33	18.33**	8.65	48.25**	5.15	-0.25	-6.36	74.60**	1.15
$P_2 \times P_{10}$	-0.90	-5.90	11.79*	1.53	31.05	-7.06	-4.71	-10.54*	96.56**	13.87
$P_3 \times P_4$	0.34	-4.36	25.61**	-1.30	60.85**	15.90	3.28	-11.12*	57.80**	-44.56**
$P_3 \times P_5$	8.93	4.36	20.65**	4.59	68.53**	26.59*	23.71**	-2.48	134.39**	26.39*
$P_3 \times P_6$	2.65	-0.77	27.64**	8.11	54.13**	10.18	5.98	-6.02	102.13**	6.97
$P_3 \times P_7$	4.50	2.56	11.52*	8.11	38.76*	0.09	4.02	-5.88	55.12*	-6.49
$P_3 \times p_8$	3.60	-0.77	25.93**	4.06	51.37**	5.32	3.20	-12.35**	121.20**	-6.51
$P_3 \times P_9$	-7.76	-8.46	15.00*	5.59	43.97*	0.17	-11.24**	-17.79**	56.81*	-16.63
$P_3 \times P_{10}$	2.70	-1.79	46.70**	12.24*	35.07*	-6.01	9.21	-7.24	124.19**	-6.29
$P_4 \times P_5$	7.14	2.56	13.59*	-1.53	51.65**	13.90	14.34**	-0.44	101.74**	8.78
$P_4 \times P_6$	4.42	0.77	25.29**	6.12	55.16**	11.81	0.77	-10.65*	88.14**	-0.43
$P_4 \times P_7$	9.91*	2.56	5.21	1.99	66.40**	19.90	-0.64	-10.10*	77.68**	7.11
$P_4 \times P_8$	9.01	0.77	17.31**	-3.06	67.72**	20.88	9.09	-6.12	131.13**	7.02
$P_4 \times P_9$	-5.17	-5.90	17.25**	7.65	62.96**	17.44	-3.16	-10.31*	96.58**	4.51
$P_4 \times P_{10}$	1.80	-5.90	39.53**	9.64	37.83*	-0.69	3.04	-11.33*	103.07**	-5.97
$P_5 \times P_6$	9.73*	5.90	29.48**	12.24*	50.00**	12.67	16.23**	3.06	125.55**	21.62
$P_5 \times P_7$	1.79	-2.56	-0.55	-3.60	22.72	-7.84	10.90*	0.34	34.12	-19.15
$P_5 \times P_8$	-9.82*	-13.59**	8.56	-5.89	1.65	-23.65*	-1.29	-14.05**	4.65	-43.57**
$P_5 \times P_9$	-21.55**	-22.31**	-8.08	-15.61**	-2.66	-26.88*	-4.15	-11.22*	-23.94	-58.82**
$P_5 \times P_{10}$	14.29**	9.49*	24.18**	7.65	50.51**	13.04	13.01*	-1.60	102.30**	9.08
$P_6 \times P_7$	10.62*	6.92	22.10**	18.36**	55.73**	11.90	1.99	-8.16	90.82**	15.03
$P_6 \times P_8$	5.31	1.79	28.91**	9.18	53.57**	10.09	5.37	-6.56	96.76**	4.13
$P_6 \times P_9$	0.86	2.56	34.75**	23.72**	72.40**	23.25*	12.27*	-13.03**	131.75**	22.65*
$P_6 \times P_{10}$	1.77	-1.79	54.74**	31.06**	34.00*	-4.20	0.23	-11.12*	99.10**	5.37
$P_7 \times P_8$	11.01*	3.33	15.79**	12.24*	57.54**	13.53	9.51	-11.12*	78.20**	7.42
$P_7 \times P_9$	2.59	1.79	9.47	6.12	59.52**	14.96	-4.99	-12.01*	75.20**	5.61
$P_7 \times P_{10}$	5.50	-1.79	27.31**	23.41**	51.32**	9.04	1.50	-8.16	79.66**	8.31
$P_8 \times P_9$	-4.31	-5.13	12.50*	3.29	16.72	-23.45*	-8.30	-15.07**	5.32	-44.00**
$P_8 \times P_{10}$	16.84**	-5.13	32.69**	9.64	39.03**	-6.98	2.13	-13.50**	98.81**	-15.97
$P_9 \times P_{10}$	-2.59	-3.33	39.75**	28.31**	37.75*	-7.84	-5.36	-12.35**	73.42**	-7.80

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

General combining ability effects:

Estimates of general combining ability (GCA) effects for each parental line in each trait are illustrated in Table (4). High positive GCA values would be of interest in all studied traits except days to 50 % silking and days to 50 % tasseling where high negative values would be useful from the breeder's point of view. The parental line P_1 seemed to be the best combiner for ear length and 100 - kernel weight while, the inbred line P_2 is proposed to be the best combiner for days to 50% tasseling and silking and ear diameter. While the parental line P_3 proved to be good combiner for days to 50% tassling and silking and ear length. The parental line P_4 proved to be good combiner for plant and ear heights, ear length and number of kernels / row. The inbred line P_5 seemed to be the best combiner for 100 - kernel weight while, the parental line P_6 seemed to be the best combiner for plant and ear heights, ear diameter, number of rows per ear, number of kernels per row, 100 - kernel weight and grain yield per plant. The parental line P_7 is considered as the best combiner for days to 50% silking and tasseling and ear diameter. The parental line P_8 proved to be good combiner for days to 50% silking and tasseling while, the inbred lines P_9 and P_{10} are considered as the best combiners for number of rows per ear.

Table (4): Estimates of general combining ability effects of Maize parental lines evaluated for the studied traits.

Parental lines	Days to 50% tasseling	Days to 50% silking	Plant height	Ear height	Ear length	Ear diameter	Number of rows/ ear	Number of kernels / row	100 kernel weight	Grain yield Per plant
P_1	1.16**	1.06**	3.15	6.85	0.69*	-0.15**	-1.06**	0.30	0.69*	-0.48
P_2	-1.26**	-1.32**	-12.77**	-0.62	-0.59*	0.15**	-0.22	-0.45	0.10	4.78
P_3	-1.22**	-1.98**	-1.43	-10.23**	0.70*	-0.08	-0.28	1.06	-0.34	-4.06
P_4	1.74**	2.52**	13.61**	9.76*	0.86*	-0.08	-0.66**	2.00*	-0.49	-3.18
P_5	1.66**	2.10**	2.94	5.63	-0.11	-0.01	-0.78**	-1.55	1.94**	-4.81
P_6	0.49	0.60	13.15**	10.47**	0.17	0.16**	1.12**	1.71*	0.60*	18.15**
P_7	-1.47**	-1.65**	1.90	-1.43	-0.39	0.14**	0.28	1.47	0.36	6.73
P_8	-1.97**	-1.69**	-14.10**	-17.73**	-0.64*	0.04	-0.09	-1.16	-0.74*	-9.19*
P_9	0.28	0.18	-5.72	-7.70*	-0.14	-0.15**	0.41**	-1.10	-1.06**	-10.77*
P_{10}	0.58	0.18	-0.72	4.99	-0.55	-0.02	1.29**	-2.28**	-1.06**	2.82
LSD 0.05%	1.21	1.45	14.80	15.52	1.20	0.18	0.58	3.44	1.17	18.41
LSD 0.01%	0.92	1.11	11.24	11.79	0.91	0.13	0.44	2.61	0.89	13.64

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

Specific combining ability effects:

Specific combining ability effects for all studied traits are presented in Table (5). For days to 50 % tasseling, five hybrids (P_1 x P_6, P_2 x P_8, P_3 x P_6, P_4 x P_8, and P_7 x P_9) exhibited significant and negative specific combining ability (SCA) effects toward earliness. Thus, these five hybrids are considered good F_1- cross combinations for this trait as they showed high SCA effects and involved at least one parent as good general combiner. Regarding silking date, negative

Table (5). Estimates of specific combining ability effects for forty five maize crosses.

Crosses	Days to 50% tasseling	Days to 50% silking	Plant height	Ear height	Ear length
P_1 x P_2	-0.17	0.54	2.79	3.22	1.18
P_1 x P_3	1.46	2.86**	-21.88*	-15.49	-0.70
P_1 x P_4	2.83**	2.03*	-33.92**	-20.83*	-1.60
P_1 x P_5	-0.75	-1.55	5.74	7.57	-0.50
P_1 x P_6	-2.92**	-3.38**	7.54	4.46	-0.44
P_1 x P_7	0.04	-0.47	2.46	9.36	0.12
P_1 x P_8	0.88	0.24	17.46	1.33	0.63
P_1 x P_9	-0.71	-0.30	28.41**	12.63	1.90*
P_1 x P_{10}	-0.66	0.04	-8.59	-2.26	-0.59
P_2 x P_3	-0.79	-0.09	4.70	9.98	-0.25
P_2 x P_4	-0.75	-1.92*	0.99	-1.36	-1.04
P_2 x P_5	-0.67	-0.85	5.00	6.12	-0.64
P_2 x P_6	2.84**	3.32**	-19.55*	-1.73	-1.92*
P_2 x P_7	3.13**	2.90**	-26.63**	-21.50*	0.46
P_2 x P_8	-2.05*	-2.71**	10.37	4.07	0.86
P_2 x P_9	-0.95	-0.93	9.66	4.77	0.78
P_2 x P_{10}	-0.59	-0.26	12.66	-3.58	0.57
P_3 x P_4	-0.13	0.07	-5.00	-8.40	0.60
P_3 x P_5	-1.37	-1.51	17.00	3.06	1.97*
P_3 x P_6	-3.88**	-4.68**	-9.88	-11.78	-1.48
P_3 x P_7	-0.59	-2.09*	4.71	11.79	-0.79
P_3 x p_8	2.25**	0.95	14.04	0.09	1.47
P_3 x P_9	1.33	2.08*	1.66	3.39	-0.10
P_3 x P_{10}	1.71*	2.41*	-5.34	7.37	-0.72
P_4 x P_5	-1.00	-1.34	-2.72	-2.27	1.34
P_4 x P_6	2.17**	1.82	7.08	14.22	-0.37
P_4 x P_7	-0.54	-0.59	1.00	9.12	0.08
P_4 x P_8	-2.71**	0.11	3.67	7.75	0.24
P_4 x P_9	0.38	0.24	16.29	1.72	0.96
P_4 x P_{10}	-0.25	-0.42	12.62	0.04	-0.22
P_5 x P_6	0.25	1.58	19.08	10.68	2.10*
P_5 x P_7	-0.12	0.16	2.99	2.92	-0.72
P_5 x P_8	2.38**	1.87	-29.01**	-17.78	-2.30*
P_5 x P_9	2.13**	1.99*	-26.71**	-14.15	-3.07**
P_5 x P_{10}	-0.84	-0.35	8.62	3.84	1.82*
P_6 x P_7	0.71	0.66	15.79	-13.92	-1.23
P_6 x P_8	-0.46	-0.30	-17.21	-2.96	0.69
P_6 x P_9	-0.38	-0.18	11.08	2.35	2.45**
P_6 x P_{10}	1.66*	1.15	-13.92	-1.33	0.21
P_7 x P_8	-0.50	0.28	17.03	8.08	1.71
P_7 x P_9	-1.75*	-1.26	-15.67	1.58	0.75
P_7 x P_{10}	-0.38	0.40	-1.67	-7.44	-0.38
P_8 x P_9	0.41	0.45	-18.34	-8.12	-3.14**
P_8 x P_{10}	-0.21	-0.88	2.00	7.53	-0.16
P_9 x P_{10}	-0.46	-2.09*	-6.38	-4.17	-0.53
LSD (sij-sik)0.05%	2.44	2.93	29.74	31.21	2.42
LSD (sij-sik)0.01%	3.21	3.86	39.16	41.08	3.18
LSD (sij-skl)0.05%	2.26	2.71	27.54	28.89	2.24
LSD (sij-skl)0.01%	2.97	3.57	36.25	38.03	2.95

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

Table (5):Cont.

Crosses	Ear diameter	Number of rows/ ear	Number of kernels / row	100 kernel weight	Grain yield per plant
P_1 x P_2	0.24*	0.72	5.01*	1.15	24.61**
P_1 x P_3	-0.50**	-1.16**	-4.53	-0.72	-28.89**
P_1 x P_4	-0.70**	-0.84*	-10.64**	-1.67*	-45.77**
P_1 x P_5	0.03	1.08*	-1.09	2.13*	14.86
P_1 x P_6	0.06	-1.15**	0.58	2.08*	0.24
P_1 x P_7	0.08	-0.05	4.09	-0.14	12.66
P_1 x P_8	0.55**	1.32**	2.96	-0.18	23.23*
P_1 x P_9	0.14	0.62	3.57	-0.56	18.49
P_1 x P_{10}	0.11	-0.52	0.04	-2.09*	-19.43
P_2 x P_3	0.02	0.21	3.81	-0.83	7.20
P_2 x P_4	0.10	0.45	-0.89	1.39	-1.68
P_2 x P_5	0.03	0.64	0.19	-0.74	-2.72
P_2 x P_6	-0.08	-0.25	-5.64*	-3.19**	-34.35**
P_2 x P_7	-0.15	-0.88*	-5.63*	0.31	-34.59**
P_2 x P_8	-0.06	0.42	2.70	0.88	12.65
P_2 x P_9	0.19	0.25	1.78	1.13	12.23
P_2 x P_{10}	-0.30*	-1.56**	-1.31	-0.10	16.65
P_3 x P_4	0.06	0.08	0.93	-0.42	-25.85**
P_3 x P_5	0.33**	0.97*	8.22**	2.70**	50.78**
P_3 x P_6	-0.05	-0.47	-0.79	0.00	0.82
P_3 x P_7	0.01	0.37	-4.10	0.28	-6.76
P_3 x p_8	0.07	0.21	0.39	-0.52	8.82
P_3 x P_9	-0.04	-0.10	-1.47	-1.80*	-3.60
P_3 x P_{10}	0.09	-0.10	-2.45	1.30	-2.51
P_4 x P_5	0.26*	0.55	2.84	0.45	24.91*
P_4 x P_6	0.02	-0.35	-1.15	-1.21	-11.05
P_4 x P_7	0.11	-0.05	1.92	-0.81	11.02
P_4 x P_8	0.14	-0.34	4.89	1.46	26.61**
P_4 x P_9	0.07	0.56	3.63	0.55	25.19*
P_4 x P_{10}	-0.06	-0.06	-1.53	0.25	-3.39
P_5 x P_6	0.15	0.57	2.70	0.39	21.90
P_5 x P_7	-0.15	-0.66	-4.23	-0.16	-24.35**
P_5 x P_8	-0.49**	-0.59	-7.13**	-3.30**	-42.43**
P_5 x P_9	-0.64**	-2.36**	-8.32**	-2.15*	-62.51**
P_5 x P_{10}	0.47**	-0.20	6.82**	0.68	19.57
P_6 x P_7	0.04	0.32	-0.59	-1.19	0.69
P_6 x P_8	-0.06	-0.52	1.41	0.24	1.61
P_6 x P_9	0.05	0.88*	5.95*	3.67**	28.86**
P_6 x P_{10}	-0.14	0.96*	-2.47	-0.78	-8.72
P_7 x P_8	0.02	0.72	2.85	2.15*	17.70
P_7 x P_9	0.15	-0.58	3.29	-0.79	16.61
P_7 x P_{10}	-0.12	0.80*	2.40	0.34	7.03
P_8 x P_9	-0.03	-0.58	-7.50**	-0.59	-37.13**
P_8 x P_{10}	-0.15	-0.63	-0.57	-0.13	-11.06
P_9 x P_{10}	0.10	1.31**	-0.93	0.53	1.68
LSD (sij-sik)0.05%	0.36	1.17	6.92	2.36	36.08
LSD (sij-sik)0.01%	0.48	1.55	9.11	3.11	48.71
LSD (sij-skl)0.05%	0.33	1.09	6.40	2.18	33.40
LSD (sij-skl)0.01%	0.44	1.43	8.43	2.87	45.10

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

and significant SCA values were observed in the six crosses, P_1 x P_6, P_2 x P_4, P_2 x P_8, P_3 x P_6, P_3 x P_7 and P_9 x P_{10},. Therefore, these hybrids are considered as the good F_1 cross combinations for this trait. These results are supported by those of El-Zeir *et al*, 2000 and Abdel - Sattar and Ahmed, 2004.

Concerning plant height, one cross (P_1 x P_9) out of the forty five crosses showed positive and significant SCA effects. These hybrids are considered as the good F_1 cross combinations for this trait. On the other hand, the six hybrids, P_1 x P_3, P_1 x P_4, P_2 x P_6, P_2 x P7, P_5 x P_8 and P_5 x $P_{\mathbf{9}}$**,** exhibited significant and negative SCA effects. The data for ear height show that, two hybrids (P_1 x P_4 and P_2 x P_7) exhibited significant and negative SCA values. These results are agreement with those reported by El- Shouny *et al*, 2003 and Abdel - Sattar and Ahmed, 2004.

Regarding ear length, five out of the forty five hybrids, P_1 x P_9, P_3 x P_5, P_5 x P_6, P_5 x P_{10} and P_6 x P_9, exhibited positive and significant SCA effect.

Data regarding ear diameter indicate that, the five hybrids (P_1 x P_2, P_1 x P_8, P_3 x P_5, P_4 x P_5 and P_5 x P_{10}) had significant positive SCA effects. Thus, these hybrids are considered good F_1- cross combinations for this trait. Similar results were obtained by many investigators among whom El-Shenawy, 2005 and Ibrahim, 2005.Concerning number of rows per ear, seven out of the forty five hybrids, P_1 x P_5, P_1 x P_8, P_3 x P_5, P_6 x P_9, P_6 x P_{10}, P_7 x P_{10} and P_9 x P_{10}, showed positive and significant SCA effects. One hybrid (P_7 x P_{10}) out of the previous seven crosses included low x high general combiner parents and three hybrids (P_6 x P_9, P_6 x P_{10} and P_9 x P_{10}) out of these previous seven hybrids included high x high general combiner parent for this trait. Thus, these hybrids are considered good F_1 cross combination for this trait.

For number of kernels per row, four crosses (P_1x P_2, P_3 x P_5, P_5 x P_{10} and P_6 x P_9) out of the forty five crosses manifested positive and significant SCA effects. The results for 100 – kernels weight indicate that, five crosses (P_1 x P_5, P_1 x P_6, P_3 x P_5, P_6 x P_9 and P_7 x P_8) out of the forty five cross showed positive and significant SCA effect. Two out of the five previous crosses (P_1 x P_5 and P_1 x P_6) included high×high general combiner parents and two (P_3 x P_5 and P_6 x P_9) out of the five previous hybrids included low x high general combiner parents. Therefore, these crosses are considered as the good F_1- cross combinations for this trait.

With respect to grain yield per plant, seven out of the forty five crosses (P_1 x P_2, P_1 x P_8, P_3 x P_5, P_4 x P_5, P_4 x P_8, P_4 x P_9 and P_6 x P_9) manifested positive and significant SCA effect. Out of the seven crosses, one crosses (P_6 x P_9) included only one high general combiner parent, and the rest crosses included two low general combiner parents for this trait. Therefore, this cross is considered as the good F_1- cross combinations for this trait. These results are in coincidence with those mentioned by El-Shenawy, 2005;Mosa and Motawei, 2005 and Barakat and Abd El-Aal, 2006.

Biochemical genetic studies:

1- Protein electrophoresis.

The electrophoretic patterns for water soluble proteins (albumin and globulin) of the five maize inbred lines (P_1‘ P_3‘ P_5‘ P_9 and P_{10}) and their ten F_1 hybrids are illustrated in Figure (1) and Table (6). From the SDS-PAGE (sodium dodycyl sulphate polyacrylamide gel electrophoresis) analysis, 25 bands were observed with different molecular weights (MW) and relative mobilities (Rm).

One band is commonly present in all five parental lines of MW 92.90 KDa, and two bands are commonly present in their ten hybrids of MW 43.20 and 30.56 KDa. These bands were considered as marker bands for these genotypes. Substantial differences among the studied parental lines in their molecular weights and relative mobilities were recorded. These parental lines were discriminated from each other by some unique bands, where the parental line (P_1) exhibited two unique bands of MW 79.39 and 22.78 KDa. The parental line (P_2) characterized by one unique band of MW 52.72 KDa. One band of MW 16.28 KDa characterized the parental line (P3). The parental line (P_4) distinguished with one unique band of MW 72.99 KDa. Two unique bands of MW 102.1 and 14.06 KDa characterized the parental line (P_5). From these results it is concluded that the analysis of water soluble protein electrophoretic bands could be a useful tool for the identification and characterization of the five parental lines of maize. Consistent results were obtained by Esmail *et al*,1999and Abdel - Sattar and Ahmed, 2004.

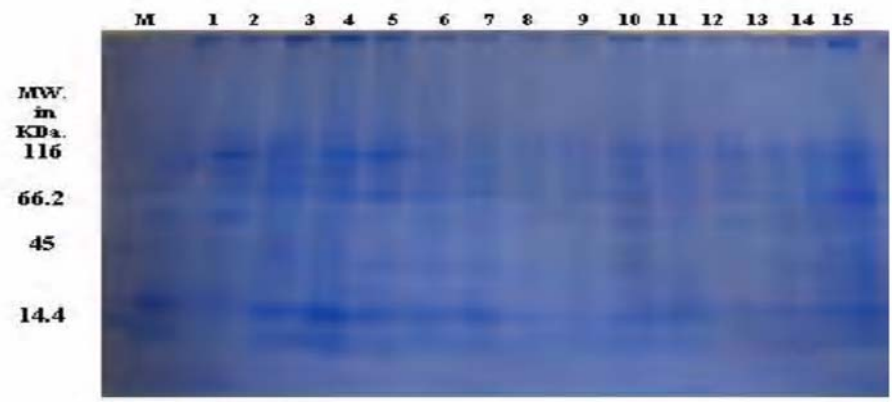
Table (6). Densitometer analysis of water soluble proteins (SDS-PAGE) showing number of bands (B.no.), Relative mobility (Rm) and molecular weight (Mw) for 5 x 5 Maize diallel crosses.

B. no.	R.m	M.W. K.Da	Parental lines					Hybrids									
			P_1	P_3	P_5	P_9	P_{10}	P_1 x P_3	P_1 x P_5	P_1 x P_9	P_1 x P_{10}	P_3 x P_5	P_3 x P_9	P_3 x P_{10}	P_5 x P_9	P_5 x P10	P_9 x P10
1	0.291	107.6	0	0	0	0	0	0	1	0	1	0	0	0	0	0	1
2	0.308	102.1	0	0	0	0	1	0	1	0	0	0	0	1	0	0	0
3	0.329	95.9	0	0	0	0	0	0	0	1	0	1	1	0	0	1	1
4	0.339	92.9	1	1	1	1	1	0	1	0	0	0	1	0	0	0	0
5	0.377	82.78	0	0	0	0	0	1	0	1	1	1	0	1	1	1	0
6	0.391	79.39	1	0	0	0	0	0	1	0	0	0	0	0	0	0	1
7	0.405	76.14	0	1	1	0	1	1	1	0	0	1	1	1	0	0	1
8	0.412	72.99	0	0	0	1	0	0	0	1	0	0	0	0	1	0	0
9	0.460	64.36	1	0	1	0	0	1	1	0	1	1	1	1	0	1	0
10	0.478	61.07	0	0	0	1	1	0	1	1	0	1	1	1	1	0	1
11	0..526	52.72	0	1	0	0	0	0	1	1	1	0	0	0	0	1	1
12	0..547	49.52	0	1	0	0	1	0	0	1	1	1	1	1	0	0	0
13	0..592	43.20	1	0	1	1	0	1	1	1	1	1	1	1	1	1	1
14	0.647	36.52	1	1	1	1	0	0	0	0	0	1	1	0	1	1	1
15	0.678	33.23	1	1	1	0	0	0	1	1	1	1	0	0	0	0	0
16	0.706	30.56	0	0	0	1	1	1	1	1	1	1	1	1	1	1	1
17	0.751	26.66	0	1	1	0	0	0	0	1	0	0	0	0	0	1	0
18	0.803	22.78	1	0	0	0	0	1	1	0	0	1	1	0	0	0	1
19	0.834	20.73	0	1	1	0	0	1	0	1	0	1	0	1	1	1	1
20	0.837	20.51	0	0	0	1	1	0	0	0	1	0	0	0	0	0	0
21	0.862	19.06	0	0	0	0	0	1	1	1	1	0	1	1	0	0	0
22	0.896	17.16	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0
23	0.914	16.28	0	0	1	0	0	1	1	1	1	0	1	0	0	1	1
24	0..938	15.13	1	0	0	1	0	0	0	0	0	1	0	1	1	1	0
25	0.962	14.06	0	0	0	0	1	0	1	1	1	1	1	1	0	0	1

1=Present of band and 0= Absent of band

Regarding the hybrids, eight out of the ten crosses (P_1 x P_5, P_1 x P_9, P_1 x P_{10}, P_3 x P_5, P_3 x P_9, P_3 x P_{10}, P_5 x P_{10} and P_9 x P_{10}) showed number of bands which exceeded their respective parents (Table 6) and were characterized by having more hybrid bands. In the same time, all of these hybrids showed substantial hybrid vigor with regard to grain yield per plant for better parent (Table 3) and some of them showed positive significant or insignificant specific combining ability effects with regard to grain yield per plant (Table 5). Two hybrids (P_1 x P_3 and P_5 x P_9) exhibited a number of bands which did not exceed the number of bands of their parental lines. These crosses showed insignificant heterosis and negative and insignificant specific combining ability with regard to grain yield per plant (Tables 3 and 5).

These results indicate to some extent the effectiveness of using soluble grain protein electrophoresis in the identification of the highly heterotic hybrids and high specific combining ability as biochemical genetic markers associated with hybrid vigor and specific combining ability in hybrid maize.



SDS-SP 1→15
Figure(1) SDS Electrophoretic patterns of water soluble protein in 15 Maize genotypes

2- RAPD-PCR techniques.

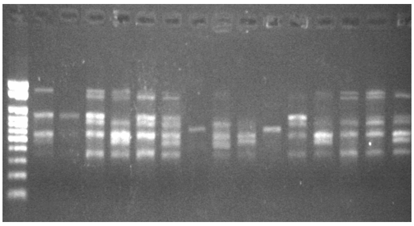
The DNA of the five maize inbred lines (P_1، P_3، P_5، P_9 and P_{10}) and their ten F_1 crosses, were tested against six 10-mer random primers to study the possibility of predicting heterosis and combining ability. Banding pattern for the six primers (A02, A08, A13, C02, C03 and B15) were illustrated in figure (2) and scored as present (1) or absent (0) as shown in Table (7). Three out of the six primers (A02, A08 and A13) were relative distinguished the five maize inbred lines by one or more unique bands from each primer as follows:

For PCR reaction with the primer A02, three universal bands at molecular weights 946bp, 676bp and 370bp were shown to be present for the five inbred lines, while it were absent for most of the ten hybrids. The inbred lines P_5 and P_9 were distinguished with Mw 1737bp band. One unique band at Mw 1057bp characterized the inbred lines P_1. The inbred line P_3 was characterized with Mw 490bp band. The inbred line P_{10} was distinguished with 582bp band.

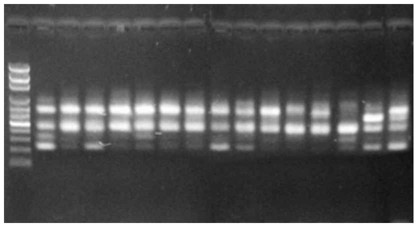
With respect to PCR reaction with the primer A08, two universal bands at molecular weights 678bp and 397bp were shown to be present for the five maize inbred lines. The inbred line P_1 was characterized with absent band at molecular weight 210 bp, while the inbred line P_5 was distinguished with one unique band at molecular weight 287 bp. One band at molecular weight 527 bp was characterized the two inbred lines P_9 and P_{10}.

Regarding PCR reaction with the primer A13, two universal bands at molecular weight 651 bp and 359 bp were showed to be present for the five maize inbred lines. The inbred lines P_1 and P_9 were characterize with one unique band at molecular weight 959 bp. The inbred lines P_3 and P_{10} were distinguished with one absence band at molecular weight 610 bp. One unique band at molecular weight 880bp was characterized the inbred lines P_5. The inbred line P_{10} was distinguished with one absence band at molecular weight 1460 bp. From this result, we conclude that, PCR – RAPD technique could be a useful tool for the identification and characterization of the five maize inbred lines. These results are in agreement with those obtained by Abdel-Sattar and Ahmed, 2005 and El-Hosary *et al*, 2006. They indicated that PCR – RAPD technique can be used as a tool for determining the extent of genetic diversity among maize inbred lines. In a trial to predict heterosis and specific combining ability via PCR-RAPD technique, two primers could be considered as reliable molecular markers positively linked with heterosis and SCA as follows:

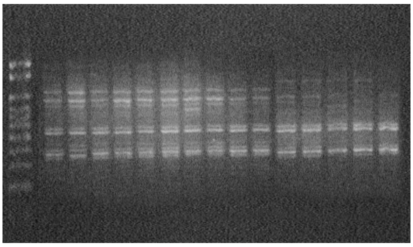
Fig (2): RAPD–PCR profiles of the 15 maize genotypes with different primers.



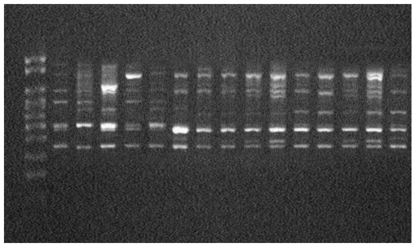
Pattern obtained primer A02



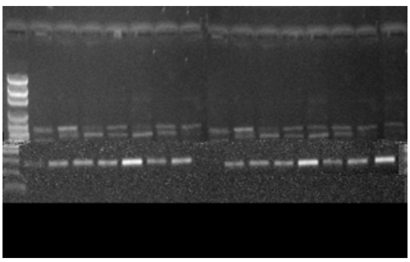
Pattern obtained primer A08



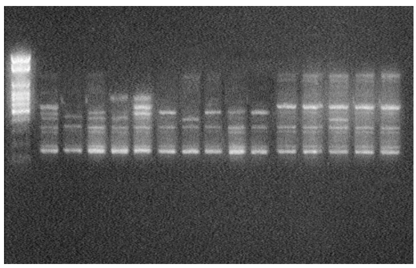
Pattern obtained primer A13



Pattern obtained primer B15



Pattern obtained primer C02



Pattern obtained primer C03

With respect to PCR reaction with the primer A13 (Fig.2), all the hybrids showed higher number of bands which exceeded the number of bands present in their respective parents (Table7) except three hybrids (P_1 x P_3, P_1 x P_9 and P_3 x P_9) which showed the same number of bands found in their parents. In the same time, all of these hybrids except two hybrids (P_1 x P_3 and P_5 x P_9) showed significant positive heterosis and most of them showed significant positive SCA effects (Tables 3 and 5). Similar results were detected for the primer B15, the two hybrids (P_1 x P_3 and P_5 x P_9) contained four bands, all of these bands were found in their respective parent except one band at molecular weight 885bp is a unique band for the hybrid P_1 x P_3. These two hybrids had number of bands which were less than those of their respective parent, and in the same time showed insignificant heterosis and negative significant SCA effects (Tables 3 and 5).

Table (7): DNA polymorphism using randomly amplified polymorphic DNA, A02, A08, A13, C02, C03 and B15 primers (P.) for the five inbred lines and their ten F_1's showing number of the band (B.No.), molecular weight (MW) and the total number of bands / each colum.

P.	B. No	M. W. bp.	The Five inbred lines					The ten hybrids									
			P_1	P_3	P_5	P_9	P_{10}	P_1 x P_3	P_1 x P_5	P_1 x P_9	P_1 x P_{10}	P_3 x P_5	P_3 x P_9	P_3 x P_{10}	P_5 x P_9	P_5 x P_{10}	P_9 x P_{10}
A02	1	2048	0	0	1	1	1	1	0	0	1	0	0	0	0	0	0
	2	1737	0	0	1	1	0	0	0	1	1	1	1	0	0	0	0
	3	1057	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
	4	946	1	1	1	1	1	1	1	1	0	1	1	0	0	0	0
	5	818	0	0	0	0	0	0	0	1	1	1	1	0	1	1	0
	6	676	1	1	1	1	1	0	0	0	0	0	0	1	0	0	1
	7	582	0	0	0	0	1	1	0	1	1	1	1	0	1	1	0
	8	490	0	1	0	0	0	0	0	0	0	0	1	0	1	1	0
	9	370	1	1	1	1	1	0	0	1	1	1	1	0	1	1	0
T.			4	4	5	5	5	3	1	5	5	5	6	1	4	4	1
A08	1	678	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
	2	527	0	0	0	1	1	0	0	0	0	0	0	0	0	0	0
	3	397	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
	4	326	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0
	5	287	0	0	1	0	0	1	0	0	0	1	0	1	0	0	1
	6	210	0	1	1	1	1	1	0	1	0	1	1	1	1	1	1
T.			2	3	4	4	4	4	2	3	2	4	4	4	3	3	4
A13	1	1460	1	1	1	1	0	0	0	0	0	0	0	1	0	0	0
	2	1267	0	0	0	0	0	1	1	1	1	1	1	1	1	1	1
	3	1069	1	1	1	0	1	1	1	1	1	1	1	1	1	1	1
	4	959	1	0	0	1	0	1	1	1	1	1	1	0	1	1	0
	5	880	0	0	1	0	0	0	0	0	0	0	0	1	0	0	0
	6	774	1	1	0	1	1	0	0	0	1	1	0	1	0	0	0
	7	610	1	0	1	1	0	1	1	1	1	1	1	0	1	1	1
	8	561	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
	9	444	0	0	0	0	0	0	1	0	0	1	0	1	1	0	1
	10	407	0	0	0	0	0	0	0	0	1	1	0	0	0	1	0
	11	380	0	0	0	0	0	1	1	1	1	1	1	1	1	1	1
	12	359	1	1	1	1	1	1	1	0	0	0	0	0	0	0	0
T.			7	5	6	6	4	7	8	6	8	9	6	8	7	7	6

Table (7):Cont.

P.	B. No	M. W. bp.	The Five inbred lines					The ten hybrids									
			P_1	P_3	P_5	P_9	P_{10}	P_1 x P_3	P_1 x P_5	P_1 x P_9	P_1 x P_{10}	P_3 x P_5	P_3 x P_9	P_3 x P_{10}	P_5 x P_9	P_5 x P_{10}	P_9 x P_{10}
C02	1	686	1	1	1	1	1	0	1	0	1	0	1	1	0	1	1
	2	564	1	1	1	0	0	1	1	1	1	1	1	0	1	1	1
	3	467	0	0	0	0	0	1	0	0	0	0	0	0	1	0	0
	4	255	1	1	1	1	1	1	1	1	1	1	1	1	0	1	1
T.			3	3	3	2	2	3	3	2	3	2	3	2	2	3	3
C03	1	1261	1	1	1	1	1	0	0	1	0	0	0	1	0	0	0
	2	664	0	0	0	0	0	0	0	0	1	1	0	0	0	0	0
	3	513	1	1	1	1	1	1	0	0	0	1	0	0	0	0	0
	4	440	0	0	0	0	0	1	0	1	0	1	1	0	1	1	1
	5	374	0	0	1	0	0	1	1	1	1	0	0	1	0	0	0
	6	287	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
	7	252	1	1	1	1	1	1	0	1	0	0	0	0	0	1	0
	8	165	1	1	1	1	1	1	0	0	0	0	1	0	0	0	0
	9	145	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
T.			6	6	7	6	6	7	3	6	4	5	4	4	3	4	3
B15	1	1829	0	0	0	0	0	0	1	1	1	0	0	1	0	0	0
	2	1521	1	1	1	1	1	0	1	0	1	1	1	1	1	1	1
	3	1425	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0
	4	1214	0	0	0	1	0	0	0	1	0	0	0	0	0	0	1
	5	1110	1	1	0	1	1	1	1	0	1	1	1	1	1	1	1
	6	1001	0	0	1	1	0	0	0	0	0	0	0	0	0	1	1
	7	885	0	0	0	0	0	1	1	0	1	1	0	0	0	0	0
	8	741	1	1	1	1	1	0	1	1	0	1	0	0	0	0	0
	9	688	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0
	10	517	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
	11	412	0	0	1	1	1	0	0	0	0	0	1	0	0	0	1
	12	359	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
T.			5	5	6	9	6	4	7	6	6	6	5	5	4	5	7

The other eight hybrids except hybrids P_3 x P_9, P_5 x P_{10} and P_9 x P_{10} showed higher number of bands which exceeded the number of bands present in their respective parents (Table7) and in the same time, these hybrids showed significant positive heterosis and most of them exhibited significant positive SCA effects (Tables 3 and 5).It is evident therefore that, these two PCR-RAPD products could generally agree with the actual field performance of the crosses. This indicates that, it is quite possible to elucidate reliable molecular genetic markers associated with heterosis and specific combining ability in maize. Some studies detected positive association between parental genetic distance based on DNA marker and hybrid field performance.

Consistent results were obtained by Nagy *et al*, 2003; Abdel-Sattar and Ahmed, 2005 and El-Hosary *et al*, 2006.

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تحليل الهجن التبادلية للمحصول فى الذرة الشامية والمعلمات الوراثية لقوة الهجين والقدرة على التآلف

[1]كمال عبد العزيز الشوني - [1]كمال إمام محمد ابراهيم - [1]مصطفى فزاع أحمدً - [2]رانيا احمد احمد يونس - [1]وليد سعيد محمد.

[1]- قسم المحاصيل - كلية الزراعة - جامعة عين شمس – القاهرة - مصر.

[2]-قسم الوراثة - كلية الزراعة - جامعة عين شمس – القاهرة - مصر.

يهدف البحث إلى دراسة قوة الهجين والقدرة على الائتلاف لبعض التراكيب الوراثية من الذرة الشامية بمحطة البحوث والتجارب الزراعية بكلية الزراغة جامعة عين شمس _ شلقان _ قليوبية. وكذلك محاولة التنبؤ بقوة الهجين والقدرة على الائتلاف من خلال نماذج التفريد الكهربى لبروتينات الذرة الذائبة و تقنية PCR-RAPD. فى موسم 2007 تم عمل كافة الهجن التبادلية دون العكسية بإستخدام عشرة تراكيب وراثية من الذرة . وفى موسم 2008 تم تقييم الاباء والجيل الاول الهجين فى تصميم تجريبى قطاعات كاملة العشوائية من ثلاثة مكررات.

ويمكن تلخيص أهم النتائج فيما يلى:-

1 - كان تباين التراكيب الوراثية في كل الصفات عالي المعنوية مما يدل علي التباعد الوراثي والاختلافات الوراثية بين السلالات المستخدمة في إنتاج هذه الهجن .

2 - كان تباين القدرة العامة والقدرة الخاصة على الأئتلاف عالي المعنوية لكل الصفات المدروسة مما يدل على أهمية كلا من التباين الوراثي المضيف والغير مضيف في وراثة معظم الصفات المدروسة.

3- كان تباين النسبة بين القدرة العامة إلي القدرة الخاصة على الأئتلاف اقل من الوحدة لكل الصفات تحت الدراسة ما عدا صفة ارتفاع الكوز مما يدل على اهمية التباين الوراثي الغيرمضيف في وراثة هذة الصفات.

4 - أظهرت قوة الهجين لافضل الاباء والصنف القياسي ان الهجينين P_3 x P_5 و P_6 x P_9 انهم افضل الهجن لصفة محصول الحبوب للنبات الفردي ومعظم الصفات المدروسة.

5- أظهرت السلالة الابوية P_6 انها احسن السلالات من حيث القدرة العامة علي التالف لصفة محصول الحبوب للنبات الفردي ومعظم الصفات المحصولية. في حين كانت السلالتين P_6و P_2 افضل السلالات من حيث القدرة العامة علي التالف بالنسبة لصفات عدد الايام حتي تفتح 50% من النورات المذكرة والمؤنثة . في حين اظهرت كلا من السلالات P_{10} وP_1، P_3، P_4، P_5، P_8، P_9 انهم ذات قدرة عامة علي الائتلاف مرتفعة لصفة أو أكثر من الصفات المحصولية.

6 - أظهرت سبعة هجن (P_6 x P_9، P_4 x P_9 ، P_4 x P_8 ، P_4 x P_5 ، P_3 x P_5 ، P_1 x P_8 و الهجين P_1 x P_2) قدرة خاصة علي الائتلاف عالية ومعنوية لصفة محصول النبات الفردي من الحبوب ومعظم الصفات المدروسة.

7- أظهر نماذج التفريد الكهربى للبروتينات وتقنية PCR-RAPD انهم يمكن الاعتماد عليهم كاداة فعالة في التعرف علي وتوصيف السلالات النقية من الذرة كما يمكن الاعتماد عليهم في التعرف علي الهجن المتفوقة ذات القدرة الخاصة علي الائتلاف وهذا كادلة وراثية جزيئية مرتبطة بقوة الهجين والقدرة الخاصة علي الائتلاف في الذرة .