BREEDING FOR GRAIN YIELD, YIELD COMPONENTS AND QUALITY TRAITS IN YELLOW MAIZE (*Zea mays*, L.)

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ABSTARCT

A diallel cross system involving ten new inbred lines was used in this study to estimate heterosis and combining ability for growth, yield and yield components as well as quality traits in maize. The resulting 45 crosses along with two checks namely, S.C. 162 and S.C. 3084 were evaluated at Moshtohor and Munifiya locations. Significant genotypes mean squares were detected for all traits at both locations. The cross P_2 x P_5 expressed the highest significant mean values for ear length, ear diameter, number of grains/ row, 100 kernel weight and ear grain weight in the combined analysis. The three single crosses P_5 x P_9 , P_4 x P_5 and P_1 x P_3 gave the highest mean values for carbohydrate, protein and oil %, respectively in the combined analysis. The single cross P_2 x P_5 expressed highest standard heterotic values for grain weight per plant relative to both checks in the combined data. Significant mean squares due to both general and specific combining abilities were detected for all studied traits in the combined analysis. Also, high GCA/ SCA ratios which largely exceeded the unity were detected for all studied traits except shelling % and carbohydrates % in the combined analysis. The mean squares of interaction between locations and both types of combining ability were significant for all studied traits, except 100 kernel weight, carbohydrate %, protein % and SCA/ L for oil %. The parental inbred line P_1 expressed the highest significant positive ($\hat{g}_i$) effects for number of rows/ ear and oil %. The parental line P_2 was the best general combiner for grain weight/ plant in the combined data. The single cross P_2 x P_5 expressed the best specific combining effects for number of grains/ row and ear grain weight in the combined analysis. The most desirable specific combining effects were detected by the crosses P_3 x P_{10}, for carbohydrate % ; P_4 x P_5 for protein %; and P_1 x P_3 for oil %.

Key words: Combining ability, heterosis, quality traits, maize.

INTRODUCTION

Maize is a major crop for both livestock feed and human nutrition. It contributes substantially to the total cereal grain production of the world and also occupies a relevant place in the world economy and trade as a food, feed, and an industrial grain crop. Maize products are used in the manufacture of diverse commodities including glue, soap, paint, insecticides, toothpaste, shaving cream, rubber tires, rayon, molded plastics, fuels, and others (**White** and Johnson, 2003). In Egypt, the cultivated area in 2009 was 0.74 million hectares (1.76 million feddans) and produced 6.3 million tons of grains, with an average yield of 8.57 tons ha^{-1} (25.24 ardabs/ feddan)), (Statistical Year Book, 2009, ARC, Giza). (One feddan; fed =4200 m^2 and one ardab; ard = 140 Kg.

Much efforts are devoted nowadays to increase maize productivity through genetical improvement. To carry out a successful breeding programme, the breeder should have enough knowledge about heterosis, the type and relative amount of genetic variance components and their interaction by environments for the traits in question. One of the most informative methodology in this concern is a diallel analysis system which is widely and extensively used for estimating the types of gene action. The two main genetic parameters of diallel analysis are GCA and SCA which are essential in developing breeding strategies. Furthermore, the magnitude of genetic components for a certain trait would depend mainly upon the environmental fluctuations under which the breeding populations will be tested. Therefore, much effort has been devoted by corn breeders to estimate the interactions between genetic components and environments.

In this concern, several investigators reported that additive gene action was responsible for the inheritance of grain yield and most of its contributing characters, among those are, Sedhom, 1994a; Ahmed *et al*. 2000; Al- Naggar, *et al*., 2002; Mosa and Motawei, 2005; El- Badawy 2006; Sedhom *et al*. 2007; Yonan, 2009 and Al- Hadi 2010. However, Dadheech and Joshi (2007), Barakat and Osman (2008) and Irshad_El-Haq (2010) reported that non additive gene action was more important in the inheritance of grain yield and most other agronomic traits in maize.

Therefore, the main objectives of this investigation were: 1) To estimate the amount of heterosis, and 2) To establish the magnitude of both general combining ability (GCA) and specific combining ability (SCA) effects and their interaction with different locations.

MATERIALS AND METHODS

The present investigation included one set of a half diallel F_1 crosses to study the type of gene action controlling the inheritance of different traits in maize. This work was carried out at the Experiment Research Station of Moshtohor, Benha University, Kalubia and Munifiya Governorates, Egypt during the two successive seasons 2008 and 2009. Ten maize (*Zea mays* L.) yellow inbred lines were developed by quality techno-seed company and were used to establish the experiment materials for several characters in this study. These lines were selected on basis of wide range of genetic variability for yield, yield components and quality traits.

In the first summer season 2008, seeds of the ten yellow inbred lines were sown on 20th May in the Experiment Research Center of Moshtohor, Benha University, Kalubia Governorate. All possible cross combinations without reciprocals were made between the ten inbred lines by hand method giving a total of 45 crosses. In the second summer season 2009, two experiments were conducted on two locations. i.e. Moshtohor and Munifiya locations. In each experiment, the 45 hybrids along with the two yellow check hybrids S.C.162 (from A.R.C.) and S.C. 3084 (produced by Misr Pioneer Company) were evaluated for the studied traits. Planting date was on 28th May in Kalubia location while planting date in Munifiya location was on 1st June. The used experimental design was randomized complete block design with four replications. Each plot consisted of one ridge of 3 m length and 70 cm width. Each hill was spaced 25 cm apart with two kernels planted per hill and later thinned to one plant per hill. The plots were irrigated after sowing and the second irrigation was given after 21 days from sowing. The plants were then irrigated at intervals of 10-15 days. The plots were informally fertilized at the rate of 120 kg of nitrogen per feddan given before the first and second irrigations. The other cultural practices of maize growing were properly practiced.

Data for the following traits were recorded on ten individual guarded plants chosen at random from each plot, except for tasseling and silking where the plot mean basis were used. Data included tasseling date, silking date, plant height (cm), ear height (cm), ear length (cm), ear diameter (cm), No. of rows/ ear, No. of grains/ row, 100 grain weight (g), shelling %, grain yield/ plant (g), carbohydrates %, protein % and oil %. The chemical analysis was done according to **A.O.A.C. (**1980**).**

General combining ability (GCA) as well as specific combining ability (SCA) were estimated according to Griffing's diallel cross analysis **(**1956**)** designated as method 4 model 1. The combined analysis of both locations was carried out whenever homogeneity of variance was detected. Heterosis expressed as the percentage deviations of F1 mean performance from check hybrids S.C.162 and S.C. 3084.

RESULTS AND DISCUSSION

Analyses of variance for tasseling date, silking date, plant height, ear height, ear length, ear diameter, number of rows/ ear, number of grains/ row, 100 kernel weight, shelling percentage, grain yield per plant, carbohydrate %, protein % and oil % in the combined data are presented in Table (1).

Mean squares due to locations were highly significant for all studied traits, except oil %. Such results revealed an overall differences between the two studied locations. Highly significant crosses mean squares were detected for all studied traits in the combined analysis indicating the wide genetic diversity between single crosses used in this study. Also, highly significant crosses x location interactions were detected for all studied traits, except 100 kernel weight, carbohydrate % and protein %. Such results indicated that the studied crosses behaved somewhat differently from one location to another. On the other hand, the exceptional case which expressed non significant crosses x location interaction indicated that this trait was stable in its performance from one location to another. Such variability among maize crosses and their interaction with environment were previousl

Table (١): Observed mean squares from ordinary analysis and combining ability for agronomical traits from F١ generation combined over two locations.

S.O.V	d.f	Days to tasseling	Days to silking	Plant height (cm)	Ear height(cm)	Ear length(cm)	Ear diameter(cm)	Number of rows per ear
Loc.(L.)	١	١٤١.٨٨**	١٦٥.٣٨**	٧٨٢٨٧.١٠**	١٨٦٨٨.٣٣**	٢٦٧.٢٩**	٩٣.٧٤**	٢٠.٢٤**
Rep x L.	٦	٢.٧٩	٣.٦٨**	٧٠٦.٤٠**	٢٣٣.٢٤	١٠.٢٥**	٠.٠٣	٠.٢٩
Crosses (F١)	٤٤	٥٩.٨٦**	٦١.٠٣**	٣٨١١.١٨**	٢٤٦٥.٩٨**	١٧.٦٦**	٠.٦٣**	٥.٩٤**
F١ x L.	٤٤	٢.٠٨**	١.٤٤**	٤٥٣.٧٨**	٣٢٣.٩١**	٣.٤٤**	٠.١٤**	١.١٤**
Error/ L.	٢٦٤	١.١٧	٠.٦٢	١٩٦.٦٢	١٢٢.٩٩	١.٤٧	٠.٠٤	٠.٥٤
GCA	٩	٥٧.٤٢**	٦١.١٢**	٣١١٤.٠١**	٢٣١٣.٨٦**	١٢.٧١**	٠.٦١**	٤.٢٤**
SCA	٣٥	٤.٠٦**	٣.٤٦**	٣٩٧.٠٥**	١٨٠.٠٣**	٢.٢٨**	٠.٠٤**	٠.٧٨**
GCA x L.	٩	٠.٥٧*	٠.٤١**	٢٠٩.٣٦**	١٣٤.٩٤**	٠.٧٨*	٠.٠٦**	٠.٣٠*
SCA x L.	٣٥	٠.٥١*	٠.٣٥**	٨٨.٧٨**	٦٧.١٠**	٠.٨٨**	٠.٠٣**	٠.٢٨**
Error	٢٦٤	٠.٢٩	٠.١٥	٤٩.١٦	٣٠.٧٥	٠.٣٧	٠.٠١	٠.١٤
GCA/SCA		١٤.١٦	١٧.٦٤	٧.٨٤	١٢.٨٥	٥.٥٧	١٥.٧٦	٥.٤٦
SCAxL./SCA		٠.١٣	٠.١٠	٠.٢٢		٠.٣٩	٠.٧٦	٠.٣٦

*and** indicates significant at ٠.٠٥ and ٠.٠١ levels of probability, respectively.

Table (١): Cont.

S.O.V	d.f	Number of grains per row	١٠٠ kernel weight (g)	Shelling %	Ear grain weight (g)	Carbohydrate %	Protein %	Oil %
Loc.(L.)	١	٩٦٠.٤٠**	٥٥.٢٢**	٥٠٥.١٠**	١٠٥٥٢٠.٨٣**	١٦٩.٤٨**	١١٠.٩٤**	٠.٠٠
Rep x L.	٦	٢٠.٣٠**	٦٠.٣٢**	٥.٨٩	٧٦٣٥.٤٤**	٤.٠٧	٥.١٨	٢.٠٩
Crosses (F١)	٤٤	٨٣.١٩**	٧٦.٠١**	١٧.٦٦**	٧٥١٦.٩٩**	٢٢.٨٨**	٢٥.١٧**	٧.٨٠**
F١ x L.	٤٤	١٤.٩٢**	١.٥٠	١٢.٦٧**	١٥٩٠.٠٢**	١.٠٣	٠.١٧	٠.١٩**
Error/ L.	٢٦٤	٤.٧٩	٢.٥٤	٥.٤٨	٤٢١.٢٤	١.٥٣	٠.٣٧	٠.١١
GCA	٩	٥٧.٤٥**	٤٦.٧٤**	٣.٢٢*	٤٨٤٢.٧٨**	٣.٣١**	٩.٧٣**	٤.٠٨**
SCA	٣٥	١١.٣٧**	١١.٨٧**	٤.٧٢**	١١١٧. ٢٠**	٦.٣٤**	٥.٤١**	١.٤٠**
GCA x L.	٩	٤.٩٥**	٠.٥٢	٤.٨٦**	٤١١.٥٣**	٠.١٩	٠.٠٤	٠.٠٦*
SCA x L.	٣٥	٣.٤٢**	٠.٣٤	٢.٧٣**	٣٩٣.٩٠**	٠.٢٧	٠.٠٤	٠.٠٤
Error	٢٦٤	١.٢٠	٠.٦٣	١.٣٧	١٠٥.٣١	٠.٣٨	٠.٠٩	٠.٠٣
GCA/SCA		٥.٠٥	٣.٩٤	٠.٦٨	٤.٣٣	٠.٥٢	١.٨٠	٢.٩٠
SCAxL./SCA		٠.٣٠	٠.٠٣	٠.٥٨	٠.٣٥	٠.٠٤	٠.٠١	٠.٠٣

*and** indicates significant at ٠.٠٥ and ٠.٠١ levels of probability, respectively.

reported by several investigators, among those are, El-Hosary and Sedhom (1990), Sedhom (1994 a,b), Yonan (2009), and El- Badawy *et al.* (2010).

The mean performance of studied single crosses for all traits in the combined data is presented in Table (2). For tasseling and silking dates, the single cross P_6 x P_8 expressed the lowest mean values in the combined data. It is also clear that this cross P_6 x P_8 was significantly superior in earliness rather than both checks (S.C. 162 and S.C. 3084) used in this study. Therefore, it is considered the best cross among all the studied genotypes for earliness. For plant height, the single cross P_3 x P_{10} was the best among all studied hybrids while the cross P_6 x P_7 exhibited the most desirable values for ear height. The cross P_2 x P_5 expressed the highest significant mean values for ear length, ear diameter, number of grains/ row, 100 kernel weight and grain yield/ plant being 21.43, 4.46, 42.88, 50.00 g, and 333.50 g respectively based on the combined analysis. Therefore, such cross seemed to be the best among all studied hybrids. For number of rows/ ear, the single cross P_1 x P_7 recorded the highest desirable mean values. The best crosses for quality traits were P_5 x P_9, P_4 x P_5 and P_1 x P_3 for carbohydrate %, protein % and oil % , respectively in the combined analysis.

Standard heterosis values expressed as the percentage deviation of F_1 mean performance from each of S.C.162 and S.C. 3084 were estimated for grain yield/ plant in the combined analysis (Table 3). Results indicated that there were two single crosses namely, P_1 x P_7 and P_2 x P_5 expressed the most desirable heterotic effects relative to both checks in the combined data. Moreover, the heterotic values relative to S.C. 162 were 12.31% for the cross P_1 x P_7 and 22.43% for the cross P_2 x P_5 in the combined data. Heterotic values relative to S.C. 3084 were 11.12% for the cross P_1 x P_7 and 21.13% for the cross P_2 x P_5 based on the combined analysis. The foregoing results indicated an accumulation of dominant alleles which are responsible for increasing maize grain yield.

These two single crosses (P_1 x P_7 and P_2 x P_5) offer possibility for improving grain yield in maize. Several investigators reported high heterosis

Table (2): Genotypes mean performance for the agronomical traits from the F_1 generation combined over both locations.

Genotype	Days to tasseling	Days silking	Plant height (cm)	Ear height (cm	Ear length (cm)	Ear diameter (cm)	Number of rows per ear
P_1 x P_2	57.50	57.75	277.13	143.53	19.58	4.28	15.47
P_1 x P_3	56.75	57.88	270.50	128.88	19.10	4.10	15.73
P_1 x P_4	60.00	60.63	264.25	127.45	19.90	4.00	14.36
P_1 x P_5	67.00	67.38	248.70	120.43	18.10	4.05	14.73
P_1 x P_6	54.13	54.88	269.33	120.55	19.73	4.15	15.37
P_1 x P_7	57.38	57.75	283.78	126.60	21.40	4.45	16.55
P_1 x P_8	55.75	56.25	270.80	119.60	19.78	4.16	14.62
P_1 x P_9	55.25	56.25	248.65	119.43	18.50	4.38	16.01
P_1 x P_{10}	56.75	58.13	263.53	123.05	21.00	3.88	15.27
P_2 x P_3	56.63	57.88	255.73	127.53	18.00	3.73	14.63
P_2 x P_4	56.63	58.13	271.83	128.93	20.78	4.14	14.75
P_2 x P_5	59.50	60.50	297.38	141.40	21.55	4.49	16.19
P_2 x P_6	55.13	55.75	254.66	115.43	20.10	4.24	13.66
P_2 x P_7	56.75	57.50	260.30	108.18	19.23	4.38	15.03
P_2 x P_8	55.50	56.25	252.40	114.18	20.75	4.20	13.78
P_2 x P_9	55.75	56.75	260.30	131.60	19.18	4.48	14.50
P_2 x P_{10}	55.88	57.38	240.48	110.43	19.48	3.79	13.86
P_3 x P_4	55.38	58.13	252.80	118.03	19.40	3.84	13.63
P_3 x P_5	59.63	60.75	293.58	158.28	19.35	3.75	14.06
P_3 x P_6	54.00	54.63	250.60	107.08	18.90	3.84	13.62
P_3 x P_7	55.25	55.50	236.73	98.98	18.20	3.75	13.71
P_3 x P_8	55.38	55.75	244.95	100.38	17.20	3.54	13.18
P_3 x P_9	53.88	55.38	232.48	106.10	17.75	4.09	13.50
P_3 x P_{10}	59.63	60.75	202.25	99.70	15.05	3.14	13.13
P_4 x P_5	62.88	64.25	274.08	129.48	20.83	4.35	14.29
P_4 x P_6	55.75	56.38	269.13	113.68	20.93	4.20	13.75
P_4 x P_7	57.88	58.13	257.43	105.35	20.63	4.33	14.86
P_4 x P_8	56.38	57.00	266.58	104.05	21.28	4.00	13.96
P_4 x P_9	58.13	59.13	229.63	105.58	16.35	4.04	14.73
P_4 x P_{10}	55.75	57.38	252.10	122.28	20.20	3.91	14.67
P_5 x P_6	56.38	56.63	285.90	130.60	20.43	4.11	14.24
P_5 x P_7	59.88	60.50	298.63	138.53	20.65	4.40	15.92
P_5 x P_8	59.00	59.25	305.65	138.28	18.38	4.40	14.10
P_5 x P_9	59.63	60.63	269.78	133.95	17.55	4.41	14.53
P_5 x P_{10}	61.63	62.38	282.43	141.15	21.15	3.85	14.15
P_6 x P_7	54.63	55.13	245.40	81.73	20.73	4.14	16.08
P_6 x P_8	52.88	53.50	256.48	90.35	20.00	4.18	13.82
P_6 x P_9	53.25	53.63	240.55	95.35	17.85	4.31	15.18
P_6 x P_{10}	53.63	54.00	254.85	107.18	20.45	3.90	14.09
P_7 x P_8	55.63	55.75	274.13	103.55	21.48	4.24	14.94
P_7 x P_9	55.75	56.25	236.41	88.08	18.15	4.34	15.53
P_7 xP_{10}	56.25	56.63	236.15	93.03	20.40	3.83	14.88
P_8 x P_9	54.50	55.38	220.60	88.93	17.45	4.40	16.02
P_8 x P_{10}	55.13	56.25	238.23	90.58	20.13	3.91	14.45
P_9x P_{10}	53.75	55.25	223.28	98.70	17.93	4.00	15.28
S.C. 162	61.75	62.50	296.13	143.88	19.50	4.11	13.73
S.C. 3084	59.50	62.63	296.88	142.88	20.25	4.18	13.80
L.S.D 5%	1.59	1.11	20.82	15.37	1.70	0.30	1.02
L.S.D 1%	2.11	1.48	27.58	20.36	2.25	0.40	1.35

Table (2): Cont.

Genotype	Number of grains per row	100 kernel weight (g)	Shelling %	Ear grain weight (g)	Carbohy-drate %	Protein %	Oil %
P_1 x P_2	37.13	42.00	79.33	233.25	82.76	14.57	7.85
P_1 x P_3	35.75	40.25	80.06	230.75	81.40	13.21	8.21
P_1 x P_4	37.13	42.88	78.70	242.13	82.15	13.97	5.41
P_1 x P_5	34.38	43.25	74.93	210.50	76.82	11.15	4.90
P_1 x P_6	38.25	43.88	78.88	251.88	79.80	15.58	4.37
P_1 x P_7	40.63	46.13	77.46	305.00	81.94	12.29	3.97
P_1 x P_8	36.38	44.13	78.84	231.50	81.33	12.69	4.65
P_1 x P_9	36.13	42.38	80.77	238.50	81.70	11.21	5.37
P_1 x P_{10}	36.13	42.75	78.78	226.63	82.08	15.43	4.85
P_2 x P_3	32.75	42.25	81.11	263.88	82.49	14.95	4.13
P_2 x P_4	38.88	43.25	78.04	247.25	77.65	14.17	4.50
P_2 x P_5	42.88	49.88	77.64	337.25	81.84	15.68	4.12
P_2 x P_6	38.63	41.50	83.99	236.25	80.79	13.22	4.94
P_2 x P_7	39.75	45.00	78.53	251.38	80.72	11.13	4.47
P_2 x P_8	42.38	47.25	78.33	239.13	81.87	14.35	4.69
P_2 x P_9	38.25	46.25	80.32	248.63	82.49	15.16	4.83
P_2 x P_{10}	36.13	43.75	84.12	236.28	80.34	14.30	3.97
P_3 x P_4	36.13	46.25	76.70	199.50	77.03	13.52	4.57
P_3 x P_5	33.63	43.75	79.40	196.38	81.70	13.24	6.05
P_3 x P_6	38.00	44.00	80.16	209.13	81.06	11.94	3.48
P_3 x P_7	34.75	40.25	79.67	186.63	77.95	10.33	3.50
P_3 x P_8	32.13	44.75	80.21	173.88	77.45	9.14	4.94
P_3 x P_9	33.13	44.75	74.71	209.75	78.29	12.34	4.50
P_3 x P_{10}	24.38	32.75	81.22	219.88	82.86	13.14	3.70
P_4 x P_5	35.38	45.38	79.36	256.25	81.43	15.72	3.07
P_4 x P_6	38.38	44.50	82.04	253.38	79.02	13.83	3.67
P_4 x P_7	37.50	41.63	78.05	236.75	82.32	15.41	3.93
P_4 x P_8	37.38	44.00	78.13	222.50	81.06	9.14	4.31
P_4 x P_9	29.50	44.50	81.38	232.63	82.62	13.77	3.49
P_4 x P_{10}	37.38	45.75	84.16	199.30	80.31	11.17	4.15
P_5 x P_6	37.25	46.38	78.74	235.50	82.38	11.15	5.33
P_5 x P_7	37.38	46.50	78.16	251.50	80.72	11.10	4.42
P_5 x P_8	33.38	49.38	78.07	220.13	80.58	11.15	4.53
P_5 x P_9	34.38	44.88	78.32	238.88	83.23	11.08	3.92
P_5 x P_{10}	34.13	45.63	78.91	202.88	79.87	11.96	3.83
P_6 x P_7	39.38	41.75	80.75	215.25	82.86	15.58	4.23
P_6 x P_8	39.50	46.25	80.55	214.13	82.49	14.04	3.87
P_6 x P_9	37.25	46.38	77.88	221.75	79.56	13.57	4.32
P_6 x P_{10}	39.50	41.25	79.07	221.00	81.09	13.74	3.91
P_7 x P_8	39.50	43.25	78.63	243.00	81.43	13.11	3.88
P_7 x P_9	36.38	41.75	82.25	210.25	82.93	11.15	5.21
P_7 xP_{10}	37.50	37.75	78.91	198.88	80.25	11.93	4.00
P_8 x P_9	33.63	45.75	80.44	204.00	79.43	11.96	3.77
P_8 x P_{10}	36.38	37.75	77.34	167.63	82.11	11.15	4.46
P_9x P_{10}	34.38	39.25	76.92	180.25	81.19	14.22	3.35
S.C. 162	41.63	44.63	78.28	269.38	80.50	13.81	3.96
S.C. 3084	41.00	45.88	78.13	272.25	80.75	13.44	4.10
L.S.D 5%	3.13	2.24	3.59	28.54	1.72	0.84	0.48
L.S.D 1%	4.15	2.97	4.75	37.80	2.27	1.11	0.64

Table (3): Percentage of standard heterosis in the F_1 generation for ear Grain weight (g) relative to S.C. 162 and S.C. 3084 in combined data.

genotypes	S.C. 162	S.C. 3084
P_1 x P_2	-13.34*	-14.26**
P_1 x P_3	-14.14**	-15.07**
P_1 x P_4	-9.84	-10.81*
P_1 x P_5	-21.84**	-22.67**
P_1 x P_6	-6.31	-7.31
P_1 x P_7	13.26*	12.05*
P_1 x P_8	-13.88*	-14.81**
P_1 x P_9	-11.14*	-12.11*
P_1 x P_{10}	-15.77**	-16.67**
P_2 x P_3	-1.85	-2.90
P_2 x P_4	-7.96	-8.96
P_2 x P_5	25.23**	23.90**
P_2 x P_6	-12.13*	-13.08*
P_2 x P_7	-6.37	-7.39
P_2 x P_8	-11.01	-11.97*
P_2 x P_9	-7.37	-8.38
P_2 x P_{10}	-12.22*	-13.15
P_3 x P_4	-25.75**	-26.55**
P_3 x P_5	-26.92**	-27.70**
P_3 x P_6	-22.24**	-23.07**
P_3 x P_7	-30.59**	-31.33**
P_3 x P_8	-35.59**	-36.27**
P_3 x P_9	-21.91**	-22.76**
P_3 x P_{10}	-18.35*	-19.21**
P_4 x P_5	-4.64	-5.67
P_4 x P_6	-5.67	-6.69
P_4 x P_7	-11.93*	-12.88*
P_4 x P_8	-17.35*	-18.23**
P_4 x P_9	-13.59*	-14.51**
P_4 x P_{10}	-26.04**	-26.82**
P_5 x P_6	-12.25*	-13.20*
P_5 x P_7	-6.30	-7.31
P_5 x P_8	-17.91**	-18.81**
P_5 x P_9	-11.09**	-12.05*
P_5 x P_{10}	-24.44**	-25.26**
P_6 x P_7	-19.85**	-20.71**
P_6 x P_8	-20.42**	-21.27**
P_6 x P_9	-17.53**	-18.41**
P_6 x P_{10}	-17.70**	-18.59**
P_7 x P_8	-9.64	-10.61*
P_7 x P_9	-21.70**	-22.55**
P_7 xP_{10}	-25.99**	-26.79**
P_8 x P_9	-24.23**	-25.03**
P_8 x P_{10}	-37.65**	-38.32**
P_9x P_{10}	-32.92**	-33.64**
L.S.D 5%	28.71	28.65
L.S.D 1%	38.04	37.95

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

for maize yield , i.e. El-Badawy (2006), Sedhom *et al*. (2007), Amer and El-Shenawy (2007), Yonan (2009), and El- Badawy *et al*. (2010).

The analysis of variance for combining ability for the combined for all the studied traits is presented in Table (1).

Results indicated significant mean squares due to both general and specific combining abilities for all studied traits in the combined data. High GCA/ SCA ratios which largely exceeded the unity were detected for all studied traits, except shelling % and carbohydrates % in the combined analysis. Such results indicated that the large part of the total genetic variability associated with these traits was mainly due to additive and additive by additive gene action. Moreover, low GCA/ SCA ratio was detected for shelling percentage and carbohydrate % in the combined analysis, indicating the predominance of non additive type of gene action in controlling these traits.

The additive genetic variance was previously reported to be the most prevalent for grain yield and most attributing characters by Sedhom, 1994b; Ahmed et al. 2000; Al- Naggar, *et al*. 2002; Mosa and Motawei, 2005; El-Badawy 2006; Amer and El- Shenawy , 2007; Sedhom *et al*. 2007; Yonan, 2009 and Al- Hadi, *et al*.2010. However, Dadheech and Joshi (2007), Barakat and Osman (2008), Irshad_El-Haq (2010) and Sarla Yadova *et al*. (2010) revealed that non additive gene action was more important in the inheritance grain yield and most other agronomic traits in maize.

The mean squares of interaction between locations and both types of combining ability were significant for all studied traits except 100 kernel weight, carbohydrate %, protein % and SCA/ L for oil %. Such results showed that the magnitude of all types of gene action varied from one location to another. It is fairly evident that the ratio for SCA x L/SCA was higher than the ratio of GCA x L/GCA for all studied traits except oil %. These results indicated that non-additive genetic effects were more influenced by the environmental conditions than additive genetic effects of these traits. These conclusions are in well agreement with those reported by Gelbert (1958), Amer and El- Shenawy (2007), and Barakat and Osman (2008).

Estimations of G.C.A effects ($\hat{g}_i$) for individual parental inbred lines for each trait in the combined analysis are presented in Table (4).

Table (4): Estimates of general combining ability effects for all parents in the agronomical traits in the F1 generation combined over two locations.

Parent	Days to tasseling	Days to silking	Plant height (cm)	Ear height (cm)	Ear length(cm)	Ear diameter(cm)	Number of rows per ear
P1	1.21**	1.08**	9.07**	11.29**	0.26	0.08*	0.79**
P2	-0.19	-0.05	5.76*	10.25**	0.46*	0.11**	-0.01
P3	-0.54**	-0.20	-10.56**	0.71	-1.50**	-0.38**	-0.82**
P4	0.99**	1.36**	1.71	1.95	0.66**	0.00	-0.34**
P5	4.34**	4.25**	29.00**	24.11**	0.37	0.12**	-0.06
P6	-2.63**	-2.9**	0.35	-9.66**	0.52*	0.03	-0.24
P7	-0.18	-0.64**	0.61	-11.90**	0.73**	0.13**	0.72**
P8	-1.33**	-1.61**	0.71	-11.17**	0.18	0.03	-0.36**
P9	-1.37**	-1.20**	-20.30**	-8.94**	-1.78**	0.20**	0.44**
P10	-0.30	-0.02	-16.35**	-6.64**	0.10	-0.33**	-0.25
LSD 5% (gi)	0.36	0.26	4.67	3.69	0.40	0.07	0.24
LSD 1% (gi)	0.48	0.35	6.19	4.89	0.53	0.09	0.32
LSD 5% (gi-gj)	0.54	0.39	6.96	5.51	0.60	0.10	0.37
LSD 1% (gi-gj)	0.71	0.52	9.22	7.29	0.80	0.13	0.48

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

Table (4): Estimates of general combining ability effects for all parents in the agronomical traits in the F1 generation combined over two locations.

Parent	Days to tasseling	Days to silking	Plant height (cm)	Ear height (cm)	Ear length(cm)	Ear diameter(cm)	Number of rows per ear
P1	1.21**	1.08**	9.07**	11.29**	0.26	0.08*	0.79**
P2	-0.19	-0.05	5.76*	10.25**	0.46*	0.11**	-0.01
P3	-0.54**	-0.20	-10.56**	0.71	-1.50**	-0.38**	-0.82**
P4	0.99**	1.36**	1.71	1.95	0.66**	0.00	-0.34**
P5	4.34**	4.25**	29.00**	24.11**	0.37	0.12**	-0.06
P6	-2.63**	-2.9**	0.35	-9.66**	0.52*	0.03	-0.24
P7	-0.18	-0.64**	0.61	-11.90**	0.73**	0.13**	0.72**
P8	-1.33**	-1.61**	0.71	-11.17**	0.18	0.03	-0.36**
P9	-1.37**	-1.20**	-20.30**	-8.94**	-1.78**	0.20**	0.44**
P10	-0.30	-0.02	-16.35**	-6.64**	0.10	-0.33**	-0.25
LSD 5% (gi)	0.36	0.26	4.67	3.69	0.40	0.07	0.24
LSD 1% (gi)	0.48	0.35	6.19	4.89	0.53	0.09	0.32
LSD 5% (gi-gj)	0.54	0.39	6.96	5.51	0.60	0.10	0.37
LSD 1% (gi-gj)	0.71	0.52	9.22	7.29	0.80	0.13	0.48

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

Table (4):Cont.

Parent	Number of grains per row	100 kernel weight	Shelling percentage	Ear grain weight (g)	Carbohydrate %	Protein %	Oil %
P1	0.51	-0.62*	-0.40	14.99**	0.21	0.45**	1.16**
P2	2.37**	1.07**	0.26	30.38**	0.33	1.38**	0.40**
P3	-3.40**	-1.70**	-0.18	-20.06**	-1.01**	-0.59**	0.35**
P4	-0.02	0.69*	0.74	4.93	-0.59**	0.52**	-0.40**
P5	-0.63	2.80**	-0.43	12.38**	0.04	-0.54**	-0.02
P6	2.29**	0.41	0.78*	1.00	0.10	0.76**	-0.27**
P7	1.87**	-1.07**	-0.26	6.05	0.36	-0.56**	-0.34**
P8	0.35	1.24**	0.02	-16.79**	-0.07	-1.22**	-0.15**
P9	-1.85**	0.41	-0.25	-8.20**	0.41*	-0.26*	-0.20**
P10	-1.49**	-3.24**	-0.28	-24.69**	0.23	0.07	-0.51**
LSD 5%	0.73	0.53	0.76	6.84	0.40	0.20	0.11
LSD 1%	0.97	0.70	1.03	9.06	0.55	0.27	0.15
LSD 5%	1.09	0.79	1.16	10.19	0.61	0.30	0.16
LSD 1%	1.44	1.05	1.54	13.50	0.81	0.40	0.22

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

General combining ability effects estimated herein were found to differ significantly from zero. The obtained high positive and significant values for all traits in question except tasseling date, silking date as well as plant and ear heights would be useful from the breeder's point of view.

The parental inbred line P_1 expressed the highest significantly positive ($\hat{g}_i$) effects for number of rows/ ear and oil % in the combined data. The parental line P_2 was the best general combiner for ear grain weight and protein %, since it expressed the highest positive and significant ($\hat{g}_i$) effects in the combined analysis. The parental inbred line P_3 had desirable ($\hat{g}_i$) effects for tasseling date and plant height in the combined data. Meanwhile, the parental inbred line P_4 had significant desirable ($\hat{g}_i$) effects for 100 kernel weight in the combined data.

Moreover, the parental inbred line P_5 seemed to be the best general combiner for 100 kernel weight, since it expressed the most desirable ($\hat{g}_i$) effects for this trait in the combined data. The parental inbred line P_6

showed the highest negative and significant ($\hat{g}_i$) effects for tasseling date and silking date in the combined data. The parental line P_7 expressed the highest desirable ($\hat{g}_i$) effects for ear height, ear diameter, carbohydrate % and ear length in the combined data. The parental P_8 exhibited negative and significant ($\hat{g}_i$) effects for tasseling and silking dates and ear height in the combined analysis. The parental line P_9 seemed to be the best general combiner for plant height since it expressed the highest negative and significant ($\hat{g}_i$) effects for this trait in the combined data. The parental P_{10} expressed significantly negative ($\hat{g}_i$) effects for short plant height and ear height in the combined data.

From the previous results, it could be concluded that the parental inbred line P_6 was the best general combiner for earliness while, parents P_1, P_2, P_5 and P_7 were the best combiner for grain yield/ plant and most of its components.

Specific combining ability effects were estimated for all studied traits in the combined over both locations and data were presented in Table (5).

Highly negative and significant SCA effects were detected in nine, thirteen, six and six crosses for tasseling date, silking date, plant height and ear height in the combined analysis, respectively. However, the most desirable

Table (5): Specific combining ability effects for all studied traits in F_1 generation for combined over both locations.

Cross	Days to tasseling	Date to silking	Plant height (cm)	Ear height (cm)	Ear length (cm)	Ear diameter (cm)	Number of rows per ear
P_1 x P_2	-0.27	-0.86*	4.06	6.52	-0.59	-0.01	0.02
P_1 x P_3	-0.68	-0.58	13.76*	1.41	0.90	0.31**	1.12**
P_1 x P_4	1.04*	0.60	-4.77	-1.25	-0.47	-0.17	-0.73*
P_1 x P_5	4.69**	4.46**	-47.60**	-30.44**	-1.98**	-0.24**	-0.76*
P_1 x P_6	-1.21*	-0.82*	1.67	3.46	-0.49	-0.05	0.18
P_1 x P_7	-0.41	-0.27	15.87*	11.75*	0.96	0.15	0.40
P_1 x P_8	-0.88	-0.80*	2.78	4.01	-0.11	-0.03	-0.45
P_1 x P_9	-1.35**	-1.21**	1.65	1.61	0.58	0.00	0.14
P_1 x P_{10}	-0.91	-0.52	12.57*	2.94	1.20*	0.03	0.08
P_2 x P_3	0.60	0.54	2.29	1.10	-0.39	-0.10	0.80*
P_2 x P_4	-0.93	-0.77*	6.12	1.26	0.21	-0.06	0.44
P_2 x P_5	-1.40**	-1.29**	4.38	-8.42	1.28*	0.16	1.48**
P_2 x P_6	1.19*	1.18**	-9.68	-0.63	-0.31	0.00	-0.75*
P_2 x P_7	0.37	0.60	-4.30	-5.64	-1.41**	0.04	-0.34
P_2 x P_8	0.27	0.32	-12.31*	-0.37	0.67	-0.03	-0.51
P_2 x P_9	0.55	0.42	16.61**	14.82**	1.06*	0.07	-0.59
P_2 x P_{10}	-0.38	-0.15	-7.17	-8.65	-0.52	-0.09	-0.55
P_3 x P_4	-1.84**	-0.61	3.42	-0.11	0.80	0.13	0.15
P_3 x P_5	-0.93	-0.88*	16.90**	17.98**	1.04	-0.08	0.18
P_3 x P_6	0.41	0.21	2.58	0.55	0.45	0.10	0.04
P_3 x P_7	-0.79	-1.24**	-11.55	-5.31	-0.47	-0.09	-0.82*
P_3 x P_8	0.49	-0.02	-3.43	-4.64	-0.92	-0.20*	-0.28
P_3 x P_9	-0.98*	-0.80*	5.11	-1.14	1.60**	0.17	-0.76*
P_3 x P_{10}	3.71**	3.39**	-29.07**	-9.84*	-2.99**	-0.25**	-0.44
P_4 x P_5	0.79	1.06**	-14.87*	-12.05*	0.35	0.14	-0.06
P_4 x P_6	0.63	0.40	8.83	5.92	0.31	0.08	-0.30
P_4 x P_7	0.30	-0.18	-3.13	-0.17	-0.21	0.11	-0.15
P_4 x P_8	-0.04	-0.33	5.92	-2.20	0.99	-0.12	0.03
P_4 x P_9	1.74**	1.39**	-10.02	-2.90	-1.97**	-0.26**	0.00
P_4 x P_{10}	-1.70**	-1.55**	8.51	11.50*	0.00	0.15	0.62
P_5 x P_6	-2.09**	-2.24**	-1.68	0.68	0.09	-0.13	-0.21
P_5 x P_7	-1.04*	-0.69*	10.79	10.85*	0.10	0.06	0.51
P_5 x P_8	-0.76	-0.97**	17.70**	9.87**	-1.62**	0.16	-0.23
P_5 x P_9	-0.10	-0.01	2.84	3.31	-0.48	-0.01	-0.60
P_5 x P_{10}	0.84	0.56	11.54	8.22	1.23*	-0.04	-0.30
P_6 x P_7	0.68	1.15**	-13.79*	-12.18*	0.03	-0.11	0.96**
P_6 x P_8	0.09	0.49	-2.82	-4.29	-0.14	0.03	-0.22
P_6 x P_9	0.49	0.21	2.27	-1.52	-0.32	-0.01	0.35
P_6 x P_{10}	-0.20	-0.60	12.62*	8.01	0.39	0.10	-0.06
P_7 x P_8	0.38	0.42	14.57*	11.15*	1.12*	-0.01	-0.05
P_7 x P_9	0.54	0.51	-2.12	-6.55	-0.24	-0.08	-0.27
P_7 xP_{10}	-0.02	-0.30	-6.34	-3.90	0.12	-0.07	-0.23
P_8 x P_9	0.44	0.60	-18.04**	-6.44	-0.39	0.08	1.30**
P_8 x P_{10}	0.01	0.29	-4.37	-7.08	0.40	0.12	0.42
P_9x P_{10}	-1.34**	-1.11**	1.70	-1.19	0.17	0.03	0.45
LSD5%(sij)	0.95	0.69	12.28	9.71	1.06	0.18	0.64
LSD1%(sij)	1.25	0.91	16.27	12.87	1.41	0.24	0.85
LSD5%(sij-sik)	1.42	1.03	18.42	14.57	1.59	0.27	0.97
LSD1%(sij-sik)	1.88	1.37	24.40	19.30	2.11	0.36	1.28
LSD5%(sij-ski)	1.31	0.96	17.05	13.49	1.47	0.25	0.89
LSD1%(sij-ski)	1.74	1.27	22.59	17.87	1.95	0.33	1.18

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

Table (5): Cont.

	Number of grains per row	100 kernel weight	Shelling %	Ear grain weight (g)	Carbohy-drate %	Protein %	Oil %
P_1 x P_2	-2.18*	-2.07**	-2.03	-39.92**	1.29*	-0.20	1.82**
P_1 x P_3	2.22*	-1.05	1.06	8.02	1.27*	0.41	2.23**
P_1 x P_4	0.22	-0.82	0.18	-5.60	1.60**	0.06	0.17
P_1 x P_5	-1.93*	-2.55**	-2.11*	-44.67**	-4.35**	-1.70**	-0.72**
P_1 x P_6	-0.97	0.46	0.63	8.08	-1.43*	1.42**	-0.99**
P_1 x P_7	1.82	4.20**	-0.42	56.16**	0.46	-0.54*	-1.33**
P_1 x P_8	-0.91	-0.12	0.58	5.50	0.26	0.52	-0.84**
P_1 x P_9	1.04	-1.04	2.41*	3.91	0.18	-1.93**	-0.07
P_1 x P_{10}	0.68	2.99**	-0.31	8.52	0.72	1.97**	-0.27
P_2 x P_3	-2.64**	-0.74	0.63	25.75**	2.24**	1.22**	-1.09**
P_2 x P_4	0.11	-2.13**	-0.35	-15.87	-3.01**	-0.67*	0.03
P_2 x P_5	4.72**	2.38**	1.06	66.69**	0.55	1.90**	-0.74**
P_2 x P_6	-2.46*	-3.60**	0.52	-22.94*	-0.56	-1.87**	0.34*
P_2 x P_7	-0.91	1.38	-0.27	-12.86	-0.89	-2.63**	-0.07
P_2 x P_8	3.23**	1.32	-1.96	-2.27	0.69	1.25**	-0.03
P_2 x P_9	1.31	1.15	-0.36	-1.36	0.84	1.09**	0.15
P_2 x P_{10}	-1.18	2.31**	2.76**	2.78	-1.14*	-0.09	-0.40**
P_3 x P_4	3.12**	3.63**	-3.33**	-13.18	-2.30**	0.64*	0.14
P_3 x P_5	1.23	-0.98	1.32	-23.75*	1.75**	1.43**	1.24**
P_3 x P_6	2.68**	1.66*	1.15	0.38	1.05	-1.19**	-1.07**
P_3 x P_7	-0.14	-0.60	0.52	-27.17**	-2.31**	-1.47**	-0.99**
P_3 x P_8	-1.25	1.59*	1.06	-17.08	-2.40**	-1.99**	0.27
P_3 x P_9	1.95*	2.41**	-3.53**	10.21	-2.02**	0.24	-0.13
P_3 x P_{10}	-7.16**	-5.93**	1.11	36.82**	2.72**	0.72**	-0.61**
P_4 x P_5	-0.39	-1.74*	0.63	11.14	1.06	2.79**	-0.98**
P_4 x P_6	-0.32	-0.23	0.45	19.64	-1.41*	-0.40	-0.14
P_4 x P_7	-0.77	-1.62*	-0.46	-2.04	1.63**	2.51**	0.19
P_4 x P_8	0.62	-1.55*	0.45	6.56	0.79	-3.10**	0.38*
P_4 x P_9	-5.05**	-0.23	1.23	8.09	1.89**	0.56*	-0.39**
P_4 x P_{10}	2.47*	4.68**	1.21	-8.74	-0.25	-2.36**	0.59**
P_5 x P_6	-0.83	-0.46	-0.96	-5.69	1.33*	-2.02**	1.14**
P_5 x P_7	-0.28	1.15	-0.11	5.27	-0.59	-0.75**	0.30*
P_5 x P_8	-2.77**	1.71*	-0.26	-3.26	-0.31	-0.03	0.22
P_5 x P_9	0.43	-1.96**	-0.30	6.89	1.88**	-1.07**	-0.34*
P_5 x P_{10}	-0.18	2.45**	0.73	-12.62	-1.32*	-0.52	-0.12
P_6 x P_7	-1.21	-1.21	0.48	-19.61*	1.49**	2.43**	0.36*
P_6 x P_8	0.43	0.98	0.96	2.11	1.54**	1.55**	-0.18
P_6 x P_9	0.39	1.93**	-1.27	1.14	-1.85**	0.11	0.31*
P_6 x P_{10}	2.28*	0.46	-1.95	16.88	-0.15	-0.04	0.22
P_7 x P_8	0.86	-0.54	-0.80	25.94**	0.22	1.95**	-0.11
P_7 x P_9	-0.07	-1.21	1.44	-15.40	1.26*	-0.97**	1.27**
P_7 xP_{10}	0.70	-1.55*	-0.38	-10.29	-1.25*	-0.52	0.37*
P_8 x P_9	-1.30	0.48	1.76	1.19	-1.82**	0.49	-0.36*
P_8 x P_{10}	1.09	-3.87**	-1.79	-18.69*	1.03	-0.64*	0.65**
P_9x P_{10}	1.29	-1.54*	-1.39	-14.66	-0.35	1.47**	-0.44**
LSD5%(sij)	1.92	1.39	2.05	17.97	1.08	0.53	0.29
LSD1%(sij)	2.54	1.85	2.72	23.81	1.44	0.70	0.38
LSD5%(sij-sik)	2.88	2.09	3.08	26.96	1.63	0.79	0.43
LSD1%(sij-sik)	3.81	2.77	4.07	35.72	2.15	1.05	0.58
LSD5%(sij-skl)	2.66	1.94	2.85	24.96	1.51	0.74	0.40
LSD1%(sij-skl)	3.53	2.57	3.77	33.07	1.99	0.97	0.53

single crosses were P_5 x P_6 for early tasseling and silking and P_5 x P_6 for plant and ear height in the combined analysis.

Highly negative and significant SCA effects were detected in six, one, five, eight, twelve, two, five, thirteen, sixteen and thirteen single crosses. However, the most desirable single crosses were P_3 x P_9, P_1 x P_3, P_2 x P_5, P_2 x P_5, P_4 x P_{10}, P_2 x P_{10} , P_2 x P_5, P_3 x P_{10} , P_4 x P_5 and P_1 x P_3; for ear length, ear diameter, number of rows/ ear, number of grains/ row, 100 kernel weight, shelling percentage, grain yield/ plant, carbohydrate %, protein %, and oil %, respectively, in the combined analysis. The previous crosses indicated at least one of good general combiner parent.

In conclusion, the best cross combination was P_2 x P_5 followed by the cross P_1 x P_7 for grain yield/plant in the combined analysis, and the previous crosses seemed to be the best combinations, where they had positive significant heterosis and S.C.A effects for grain yield/plant as well as most of the yield components. Therefore, the previous crosses might be of prime importance in maize breeding program for developing new hybrids.

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الملخص العربى

التربية للمحصول ومكوناته وصفات الجودة فى الذرة الشامية الصفراء

تهدف هذه الدراسة الى تقدير قوة الهجين والقدرة العامة والخاصة على التآلف لبعض صفات النمو والمحصول ومكوناته وكذلك نسبة الكربوهيدرات والبروتين والزيت فى بعض هجن الذرة الشامية الصفراء. أستخدم لهذا الغرض عشرة سلالات جديدة من الذرة الشامية الصفراء وهى: P_1, P_2, P_3, P_4, P_5, P_6, P_7, P_8, P_9 and P_{10}. وتم اختيار هذه الاباء لتمثل مدى واسع من التباينات الوراثية للصفات المدروسة. وتم إجراء جميع الهجن التبادلية الممكنة دون العكسية معطية ٤٥ هجيناً فردياً تم تقييمهم فى موقعين مختلفين هما مشتهر والمنوفية بجانب هجينين للمقارنة هما هجين فردى ١٦٢، وهجين فردى ٣٠٨٤، تم تسجيل صفات، عدد الأيام حتى ظهور ٥٠% من النورة المذكرة، عدد الأيام حتى ظهور ٥٠% من النورة المؤنثة، طول النبات (سم)، ارتفاع الكوز (سم)، طول الكوز (سم)، قطر الكوز (سم)، عدد صفوف الكوز، عدد حبوب الصف، وزن ١٠٠ حبة، معدل التصافى، وزن حبوب الكوز، نسبة الكربوهيدرات، نسبة البروتين، نسبة الزيت بالحبوب. تم تقدير القدرة العامة والخاصة على التآلف طبقا لطريقة Griffing (١٩٥٤)، الطريقة الرابعة النموذج الأول.

وأظهرت النتائج ان التباينات الراجعة الى المواقع كانت معنوية لجميع الصفات تحت الدراسة. كما كان التباين الراجع الى التراكيب الوراثية كان معنويا لجميع الصفات تحت الدراسةعلى اساس التحليل التجميعى. وأعطى الهجين P_2 x P_5 أعلى متوسط لصفة طول الكوز وقطر الكوز وعدد حبوب الصف ووزن ١٠٠ حبة ومحصول النبات من الحبوب فى التحليل التجميعى. وأعطت الهجن الثلاثة P_5 x P_9 , P_4 x P_5 and P_1 x P_3 اعلى متوسط لمحتوى الحبوب من الكربوهيدات والبروتين والزيت على الترتيب.

وأمكن الحصول على أعلى قوة هجين قياسية لصفة محصول الحبوب/ نبات فى الهجين P_2 x P_5 مقارنة بالهجين الفردى ١٦٢ ، ٣٠٨٤ فى التحليل التجميعى للموقعين معا.

وكان متوسط مربعات انحرافات كلا من القدرة العامة والخاصة على التآلف معنويا لجميع الصفات تحت الدراسة فى التحليل التجميعى ولكن كانت نسبة القدرة العامة على التآلف الى القدرة الخاصة اكبر من الوحدة لجميع الصفات ماعدا نسبة التفريط ومحتوى الحبوب من الكربوهيدات. وكان تباين التفاعل بين القدرة العامة والخاصة على التألف مع المواقع معنوياً لجميع الصفات ماعدا وزن ١٠٠ حبة ومحتوى الحبوب من الكربوهيدات والبروتين.

وأعطت السلالة الأبوية P_1 أفضل قدرة عامة على التآلف لصفة عدد صفوف الكوز ونسبة الزيت بالحبوب، وأعطت السلالة الأبوية P_2 اعلى قدره عامة لصفة محصول الحبوب/ نبات. وأعطى الهجين P_2 x P_5 افضل قدرة خاصة على التآلف لصفات عدد حبوب الصف ومحصول الحبوب/ نبات فى التحليل التجميعى. كما أمكن الحصول على أفضل قدرة خاصة على التآلف لنسبة الكربوهيدرات والبروتين والزيت فى الهجن P_3 x P_{10} ، P_4 x P_5، P_1 x P_3 ، على الترتيب.