Diallel Analysis for Physiological Traits and Grain Yield of Seven White Maize Inbred Lines

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ABSTRACT

Diallel cross among seven diverse inbred lines of maize were evaluated for general (GCA) and specific (SCA) combining ability effects during 2011. Twenty one F_1 's and two standard white check (SC10 and SC128) were evaluated at Ismailia and Mallawy Research Stations using a randomized complete block design with four replications during the summer season of 2012. The combined analysis of variance was performed for data on days to 50% silking (DS), plant height (PH), ear height (EH), ear position% (EP), o. of rows/ear (RE), no. of grains/row (GR) and grain yield ard/fad. (GY). Estimation of combining ability effects were determined according to Griffing (1956) Method-4 Model-1 (For simplest, the all data were calculated over means of two locations).

Significant differences were found for genotypes and genotypes x location for all traits, except for RE and GR. Genotypes x location interaction was significant for all studied traits, except for RE and GR. Both additive and non-additive gene action were found to be important in controlling all studied traits. However, the non-additive gene action was more important than the additive gene action, suggesting that non-additive genetic effects played an effective role in the inheritance of all studied traits, except GY. Moreover, the magnitude of SCA x location interaction was larger than GCA x locations for all traits. Inbred line had favorable alleles for GCA effects were; P₃ for SD, EH, ELA, Chl-a, GR and GY and, inbred lines P₅ for ELA, RE, GY. Lines P₁ and P₂ had positive and significant GCA values for Chl and GY. The most superior inbred lines were P₃ and P₅ which were recommended for developing new white maize hybrids. The most superior SCA effects, were recorded for crosses (P₁ x P₂) for, ELA and GY; cross (P₂ x P₄) for ELA, GR and GY and crosses (P₃ x P₇ and P₄ x P₅) for DS, ELA, Chl-a, GR and GY. Crosses of superiority over checks in grain yield and most traits under study were; P₁ x P₂, P₁ x P₄, P₁ x P₅, P₃ x P₅ and P₄ x P₅.

Key words: maize, G. C. A., S. C. A., genetic variability, physiological, yield traits.

INTRODUCTION

Diallel mating design has utility as a method to analyze crosses or parents with crosses for general combining ability (GCA) due to additive type of gene action and specific combining ability (SCA) (Griffing, 1956). The method of diallel crosses has been widely used in genetic research to investigate the inheritance of important traits among a set of genotypes (Yan and Hunt, 2002). This design provides information about the components of genetic control, helps the breeder in the selection of desirable parents for crossing programs, and in deciding a suitable breeding procedure for genetic improvement of various quantitative traits [Jinks and Hayman (1963), Walters and Morton (1978) and Rezael *et al.* (2004)].

Studies of a genetic nature and modes of inheritance of physiological characters; ear leaf area and chlorophyll a and b, grain yield and yield contributing characters, are very important in maize breeding. Grain yield is an important, but very complex trait, whose expression is determined by several major or minor genes that are influenced by environmental conditions, which a diurnally mask their action and makes its study more difficult. Selection for general combining ability for physiological characters can be done on the basis of inbred performance per se. selection for increased physiological traits among inbred lines might result in an increased grain yield in the F1 hybrids (Johnson, 1974). Simplest explanation is the presence of more loci having a dominant or partially dominant gene in the hybrid than in lines for chlorophyll-a, chlorophyll-b contents (Fleming and Palmer, 1975). Furthermore, the performance of a hybrid is related to specific combining ability of the inbred lines involved in the cross; therefore, the production of single cross hybrid necessitates selecting suitable parental lines and the best cross combinations for further use. Both additive and nonadditive genetic effects were significant in the genetic expression of maize ear leaf area, chlorophyll-a, chlorophyll-b, grain yield and yield contributing characters [Johnson, 1974, Mousa, 1997, Iqbal et al. 2007, Akbar et al. 2008, Hefny, 2010 and Mousa et al. 2012].

The present study was carried-out to study the combining abilities and their interactions with location of some promising inbred lines. Identifying promising hybrids for yielding ability with suitable physiological and agronomic traits was another goal.

MATERIALS AND METHODS

Plant materials: Seven white inbred lines of corn (Zea mays L.) were used in this study. Five inbred lines of them were newly developed at Ismailia Agricultural Research Station and were isolated from different populations. The other lines were the commercial inbred lines Sids-34 and Giza-628. The pedigree and origin of the seven inbred lines were illustrated in Table (1).

Field experiments: All possible cross combinations excluding the reciprocals were made among the seven inbred lines by hand method giving a total of 21 crosses at Ismailia Agricultural Research Station in 2011 summer season. The resultant 21 single crosses in addition to two white commercial hybrids SC10 and SC128 were evaluated in a randomized complete block design experiment with four replications under two different locations i.e., Ismailia and Mallawy Agric. Res. Stns. in 2012 summer season. Each experimental plot consisted of one row six meters long and 80 cm apart. Hills were spaced 25 cm with three kernels per hill. The seedling was thinned to one plant per hill. All other agricultural practices were carried out according to the standard commercial recommendation for maize at each location.

Collected data:

(A): Field data: Data were recorded for days to 50% silking (DS), plant height (PH), ear height (EH), ear position% (EP), number of rows/ear (RE), number of grains/row (GR) and grain yield per plot which was converted to ardab/feddan (GY), adjusted to 15.5% moisture.

(B)- Laboratory determinations:

- 1- Ear leaf area (ELA) according Montgomery (1911): leaf length x maximum leaf width x 0.75 cm².
- 2- Chlorophyll-a (Chl-a) and Chlorophyll-b (Chl-b).

The content of Chlorophyll-a (Chl-a) and Chlorophyll-b (Chl-b) were assessed at flowering stage. Sample was taken from ear leaf including ten disks of 0.5 cm². Using the method outlined by (Moran and Porath, 1980; Moran, 1982 and Rabie *et al*, 1997).

Statistical analysis:

Data were analyzed across two locations after testing the homogeneity of error mean squares according to Snedecore and Cochran, 1967. Combining ability variances; general combining ability (GCA), specific combining ability (SCA) and effects and their interaction with locations were calculated according to the method-4 model-1 (Fixed model) of Griffing, 1956. Hybrids effect considered fixed. While, location effect considered random.

RESULTS AND DISCUSSION

A- Combined analysis of variance:

Combined analysis of variance for ten studied traits (Table-2) revealed highly significant

differences among locations for most traits i.e.; DS, PH, EH, EP, Chl-a, RE, GR and GY. Mean squares due to crosses (C) and crosses x locations (C x L) were found significant or highly significant for all studied traits, except for RE and GR. This result indicated wide genetic diversity between the studied materials which obviously were effected by change in environmental conditions. These results are supported by Abdel-Sattar *et al.* (1999), Amer (2002), Aly and Mousa (2011) and Mousa *et al.* (2012).

B- Mean performances.

Mean performance of 21 crosses and two checks SC10 and SC128 for ten studied traits over locations are presented in Table-3. Great variation were found among the F₁ crosses for all traits, where mean ranged from 57.6 to 64.3 days for days to 50% silking, from 253.0 to 294.5 cm for plant height, from 134.7 to 168.6 cm for ear height, from 51.8 to 66.7% for ear position, from 829.3 to 1227.1 cm² for ear leaf area, from 24.1 to 40.1 mg/cm² for chlorophyll-a, from 12.0 to 19.0 for chlorophyll-b, from 12.0 to 14.0 for no. of rows/ear, from 33.6 to 49.1 for no. of grains/row and from 31.6 to 43.6 for grain yield (ard/fad). The best single crosses for earliness were P1 x P2, P1 x P3, P3 x P7 and P4 x P5 gave magnitude and significant values toward compared with check hybrid SC10. On the other hand, 9 new single crosses; P1 x P7, P2 x P5, P2 x P6, P₂ x P₇, P₃ x P₅, P₃ x P₆, P₅ x P₆, P₅ x P₇ and P₆ x P₇ showed significant late flowering and shorter stem compared to the check SC10. For physiological traits, four new single crosses P1 x P4, P1 x P5, P3 x P_5 and $P_4 \ge P_5$ had highest significant values for ear leaf area, chlorophyll-a and chlorophyll-b compared to check hybrids SC10 and SC128. Also, the crosses P₁ x P₃ and P₅ x P₇ for ear leaf area, P₁ x P₂, P3 x P6 and P6 x P7 Chl-a and eleven crosses for chlorophyll-b showed positive significant values compared to the check SC10 and SC128. In this connection, significant and greet amount of genetic variability between single crosses were detected for physiological traits (ear leaf area, chlorophyll-a and chlorophyll-b by (Johnson 1974, Fleming and Palmer 1975 and Mousa 1997).

For grain yield and yield component traits, the results showed that, six single crosses, in no. of rows/ear, five crosses for no. of grains/row and grain yield ard/fad) showed high positive and significant values compared to the best check SC10. Moreover, the results showed that six crosses, seven crosses and three crosses exhibited similar values in RE, GR and GY, respectively. Significant differences among maize genotype have been recorded for grain yield and yield components by Amer 2002, Hefny 2010, Mousa *et al.* 2012 and Aly and Mousa 2012.

inbreds	Р	edigree		0	rigin							
P_1	Sd-34 Gz-628 Ism-6144-2 Ism-6165-2 Ism-6167-2 Ism-6177-2 Ism-6177-2 Ism-6179-2 ombined analysis of d.f. d.f. L) 1 25 6 20 21		Derived from	American-early	dent population							
P ₂	Gz-62	28	(B73 x Sd-62)S ₁ BC ₆ ,S ₄									
P ₃	Ism-6	144-2011										
P ₄	Ism-6	165-2011	Derived from	Giza-2 populatio	on							
P ₅	Ism-6	167-2011	-									
P ₆	Ism-6	177-2011	- Derived from American early dent nonulation									
P ₇	Ism-6	179-2011	 Derived from American-early dent population 									
Fable 2: Combin	ed analys	sis of variance	e for ten traits of	maize across lo	ocations.							
	d f	SD	PH	EH	EP	ELA						
S.O.V.	u. 1.	50	(cm)	(cm)	%	(cm ²)						
Locations (L)	1	252.5**	123934.3**	17344.3**	15309.7**	513936.0 ^{n.s}						
Reps / L	6	1.1	109.5	1569.3	230.7	173392.3						
Crosses C)	20	23.3**	1262.0**	502.7**	102.4**	55960.4**						
C. X L.	20	14.2**	1241.6**	17.5**	60.4**	166.0**						
Pooled error	120	0.77	145.2	7.02	7.01	376.6						
		Chla				CV						

Table 1. Padigrap and origin of the seven nerantal inbred lines

S.O.V.	d.f.	Chl-a (mg/cm ²)	Chl-b (mg/cm ²)	RE	GR	GY (Ard/fad)
Locations (L)	1	3078.0**	2.38 ^{n.s}	9300.5**	11383.4**	3924.6**
Reps / L	6	62.4	2.07	994.3	914.4	338.3
Crosses C)	20	172.3**	38.6**	4.03 ^{n.s}	156.9**	121.2**
C. X L.	20	87.1**	9.01**	0.60 ^{n.s}	13.6 ^{n.s}	4.6*
Pooled error	120	12.9	0.76	0.44	12.37	2.12

*,** significant at 0.05 and 0.01 levels of probability, respectively. n.s; not significantly different

DS = days to 50% silking

Chl-a=chlorophyll-a

EH = ear height

PH = plant height Chl-b=chlorophyll-b RE= no. of rows/ear

C- Gene action:

Data in (Table-4) showed the mean squares of general (GCA) and specific (SCA) combining abilities and their interactions with locations for the studied traits. General (GCA) and specific (SCA) combining abilities were highly significant for all traits, indicating that, additive and non-additive gene actions were important in controlling the studied traits. These results are in agreement with those obtained by (EL-Rouby and Galal 1972; Katta, et al. (1975); Morshed et al. (1989) and Sadek et al. (1992) for grain yield, El-Hosary (1989), Abdel-Aziz (1991), Al-Naggar (1991), Amer et al. (1998), Aly and Mousa (2011) and Mousa et al. (2012) for all studied traits except for physiological traits and Mousa (1997) and Rabie et al. (1997) for Chl-a and Chl-b.

The non-additive gene action (K^2SCA) appeared to play a more important role than the additive gene action (K²GCA) in the expression of all traits under study except for grain yield (Table 5). Numerous investigators reported that additive gene action represented the major role in the inheritance of DS and GY as El-Hosary (1989), Morshed et al. (1990), Abdel-Aziz (1991), Al-Naggar (1991), Vesal et al. (1993), Gado (2000) and Motawei and Mosa (2009). Meanwhile, similar results had reported by Amer et al. (1998) for PH and GR, Mousa and Abd El-Azeem (2009) for PH,

Ep% = ear position%

ELA= ear leaf area

GR= no. of grains/row GY= grain yield EH and EP, Aly and Mousa (2011) for EH and RE, Fleming and Palmer (1975) for chlorophyll-a and chlorophyll-b and Smith et al. (1982), Abdel-Aziz (1991) and Mousa (1997) for ear leaf area.

The GCA x location and SCA x location interactions were highly significant for the traits; except for GCA x L interaction for GY (Table 4). These results indicated that, more environments would be required to salute the studied materials in respect to general (GCA) and specific (SCA) combining ability assessments. In the connection similar finding was reported by Mousa (1997) for DS, PH, ELA and Chl-a and both of Morshed et al. (1990) and Amer (2002) for DS and PH.

The magnitude of the interaction for σ^2 SCA x location was higher than that of σ^2 GCA x location for all studied traits (Table 5) indicating that the non-additive gene action was much more influenced by the change in environments than the additive gene action. These results are in agreement with those previously attained by Abdel-Sattar et al. (1999) and Motawei and Mosa (2009) for grain yield. El-Shenawy et al. (2005) for days to 50% silking, plant height and grain yield, Aly and Mousa (2011) and El-Gazzar et al. (2013) for DS, PH, EH and GY. In contrary, Mousa et al. (2012), found that additive gene effect was more interacted with environment rather than non-additive type of gene action for DS, PH, EH, RE, GR and GY.

Crosses	DS	РН	EH	EP	ELA	Chl-a	Chl-b	RE	GR	GY
Crosses	05	(cm)	(cm)	%	(cm^2)	(mg/cm^2)	(mg/cm^2)	KĽ	GK	(Ard/fad)
1x2	59.00	289.20	168.60	59.10	986.60	37.60	16.80	13.60	49.10	40.50
1x3	59.30	270.50	153.70	58.50	1146.70	37.90	12.40	12.40	43.80	38.80
1x4	61.50	290.30	160.30	56.80	1153.20	38.90	17.20	14.00	48.90	41.90
1x5	62.00	271.70	160.10	59.90	1159.90	38.60	17.40	13.00	42.60	43.60
1x6	61.70	283.00	158.60	56.60	1001.30	33.60	16.60	12.50	37.50	37.00
1x7	63.70	253.00	156.20	64.20	885.00	29.00	17.60	12.30	36.10	35.60
2x3	61.50	277.20	165.30	62.40	859.50	25.50	18.00	12.90	40.60	40.10
2x4	61.70	271.70	157.80	58.50	948.20	28.90	16.60	13.60	39.80	40.30
2x5	61.10	256.00	167.80	66.70	829.30	27.10	17.50	12.80	41.30	38.80
2x6	62.00	255.60	145.00	57.30	770.20	31.10	19.00	12.20	41.90	37.40
2x7	63.30	269.00	154.00	58.80	888.60	35.40	18.10	12.80	42.40	37.90
3x4	62.80	290.30	147.10	51.80	1008.40	30.10	15.00	12.50	38.50	34.00
3x5	61.80	263.10	148.80	57.10	1085.90	34.90	16.80	13.80	45.40	40.90
3x6	60.20	265.70	150.80	58.70	980.60	37.40	12.00	12.20	39.96	34.90
3x7	57.60	288.00	150.20	52.30	997.10	24.10	15.20	13.10	37.06	35.00
4x5	58.30	279.30	158.60	57.10	1227.10	40.10	18.70	13.60	47.36	42.30
4x6	60.20	275.80	153.70	56.40	1022.10	32.50	17.10	12.70	41.56	35.70
4x7	61.70	294.50	158.10	54.80	1029.40	30.70	16.10	12.80	43.16	35.10
5x6	62.00	269.20	151.30	56.20	1046.90	28.00	18.00	12.90	43.46	38.30
5x7	61.70	269.20	160.70	60.80	1101.20	28.10	17.50	13.20	39.40	37.40
6x7	64.30	257.00	134.70	54.20	887.20	37.10	14.10	12.00	33.60	31.60
Check SC 10	61.13	285.25	140.88	49.39	1052.8	30.3	14.8	12.70	40.73	38.57
Check SC 128	58.13	242.63	132.00	54.40	1010.2	32.4	15.4	13.90	38.40	36.92
LSD 0.05	0.86	11.81	2.60	2.59	19.02	3.53	0.86	0.66	3.45	1.43
0.01	1.24	15.49	3.40	3.39	24.94	4.62	1.12	0.86	4.52	1.87

Table 3: Mean performances for 21	hybrids a	and the two	check hybrids	for all the	e studied traits
combined across two locations.					

*,** significant at 0.05 and 0.01 levels of probability, respectively. DS = days to 50% silking PH = plant height EH = ear height Chl-a=chlorophyll-a Chl-b=chlorophyll-b RE= no. of rows/ear

Ep% = ear position% GR= no. of grains/row ELA= ear leaf area GY= grain yield

Table 4:Mean so	uares from dialle	el analysis for ter	n traits combined	across locations.

S.O.V.	d.f.	SD	PH (cm)	EH (cm)	EP %	ELA (cm²)
GCA	6	13.99**	1881.80**	965.57**	175.74**	27619.57**
SCA	14	27.25**	996.40**	304.46**	71.03**	68106.57**
GCA x L.	6	14.66**	1323.21**	15.19 ^{n.s}	49.30**	1412.06*
SCA x L.	14	14.13**	1206.66**	4.22 ^{n.s}	65.36**	1660.61**

S.O.V.	d.f.	Chl-a (mg/cm ²)	Chl-b (mg/cm ²)	RE	GR	GY (Ard/fad)
GCA	6	260.09**	48.19**	8.38**	131.61**	361.10**
SCA	14	134.79**	34.54**	2.17**	167.87**	18.46**
GCA x L.	6	133.05**	8.98**	0.93 ^{n.s}	11.71 ^{n.s}	4.66 ^{n.s}
SCA x L.	14	67.46**	9.03**	0.24 ^{n.s}	14.45 ^{n.s}	5.00*

*,** significant at 0.05 and 0.01 levels of probability, respectively. n.s; not significantly different

DS = days to 50% silking	PH = plant height	EH = ear height	Ep% = ear position%	ELA= ear leaf area
Chl-a=chlorophyll-a	Chl-b=chlorophyll-b	RE= no. of rows/ear	GR= no. of grains/row	GY= grain yield

ELA= ear leaf area GY= grain yield		Ep% = ear position% GR= no. of grains/row	Ep% = GR = nc		EH = ear height	EH =	ht	PH = plant height	05 and 0.01 level	** significant at 0.05 and 0.01 levels of probability, respectively DS = days to 50% silking PH = plant height
	4.44.0	0.420	0.022	2.277	12.274	1.674	1.733	7.62	0.553	S.E.(gi.gj)
0.000	1.400	0.277	0.550	1.490	8.035	1.095	1.134	4.98	0.362	S.E. gi
100.0-	1767-		0.557	1.188	19.230*	-0.587	-3.596**	-1.796	0.910*	7
-0.411	*100 0		0.182	1.021	-37.110**	-1.741	-7.546**	-6.721	0.510	6
2 177**	1.102		0.457	-2.761*	18.620*	1.950	3.103**	-6.271	-0.189	5
> 000 **	1 100		0.57	-1.348	0.900	-2.524*	0.753	12.428*	-0.314	4
1.00.	2.702		-2.242***	2.186*	29.400**	-1.450	-3.171**	2.978	-0.914*	S
*200 6	*	0.500	1.132**	-5.481*	3,220	2.959**	5.328**	-4.246	0.136	2
2 942**	-1217	202.0	/ 100.40	5.190"	-34.260**	1.394	5.128**	3.628	-0.139	_
** 200 2	2155	2000		(mg/cm)	(cm)	0/0	(cm)	(cm)	CU	Indreus
(Ard/fad)	GR	RE	(ma/am ²)	Cni-a	ELA	EP	EH	PH	ne	
in yield	GY= grain yield	ins/row	GR= no. of grains/row	nt ws/ear ions.	EH = ear height RE= no. of rows/ear across two locations.	its combined	PH = plant height Chl-b=chlorophyll-b s for all studied tra	PH = ChI-l	silking .a	DS = days to 50% silking PH = plant height EH = car height Chl-a=chlorophyll-a Chl-b=chlorophyll-b RE= no. of rows/ca Chl-a=chlorophyll-a Chl-b=chlorophyll-b RE= no. of rows/ca
ET A = oor loof grog	EI A= an	.170	2.000	13.024	20.990	14.591	1.802	265.353	3.343	σ^2 SCA x L.
0 720	0.518		114.0	0.000	1.//1	2.115	0.409	58.898	0.695	σ^2 GCA x L.
0.127	0.067		0.411	077°CI	8400.240	8.004	37.181	106.394	3.311	K ² SCA
2.042	10 437		1.100	0.1/0	681.075	4.218	23.964	43.414	0.331	K ² GCA
8.974	7 981	0 108	1 1 2 4	1.170	(111)	0/	(CIII)	(cm)		components
(Ard/fad)	GR	RE	(mg/cm ²)	(mg/cm ²)	LLA (cm ²)	er	EH	H	DS	Genetic

DS = days to 50% silking $PH = p$,** significant at 0.05 and 0.01 levels of probability, respectively	S.E.(Sij-Skl) 0.958 13.202	S.E.Sij 0.714 9.840	6x7 1.608* -7.83		5x6 0.333 8.89				-3.716**	3x6 -0.691 -3.85	3x5 1.633* -6.93	3x4 2.758** 1.61	0.983	2x6 0.008 -6.75		2x4 0.583 -9.78	2x3 0.933 5.16	1x7 1.633* -21.80*	1x6 0.033 12.74	0.983	1 _X 4 0.608 0.96	-0.916	1x2 -2.341** 16.51	Crosses DS (cm)	Hd
PH = plant height	bability, respectively.	202 3.002	40 2.238	83 -9.45**	96 5.89*	89 0.46	.51 5.61*	18 5.19*	13 -0.58	13.46 1.66	85 6.24*	93 -6.40*	61 -5.80*	.691 -3.08	75 -8.13**		78 -3.55		80* -0.63	.74 5.69*	1.04 -3.45	96 -0.85	45 -3.55	.51 2.81		H EH
EH = ear height RE= no of rows		2.899	2.161	-1.489	1.41	-2.038	-0.049	2.62	-0.31	-3.676	3.891	-1.403	-2.257	-1.612	-1.882	3.825	0.054	2.918	5.418*	-1.101	-1.483	-0.057	0.526	-3.303	0/0	EP
EH = ear height RF= no_of rows/ear		21.259	15.846	-15.92	-82.15**	146.89**	24.17	-35.09*	36.68*	164.52**	-74.94**	-17.92	-111.80**	0.65	-32.21*	0.96	**80.12	-74.92**	-91.27**	11.27	-84.46**	14.96	115.06**	34.44*	(cm ²)	ELA
Ep ⁹ GR ²		3.944	2.940	1.41	-3.795	2.672	-2.607	-5.922*	6.590*	6.882*	0.675	1.957	1.095	2.025	0.042	-0.287	0.237	-6.685*	-2.415	-4.135	0.31	3.497	-3.925	2.367	(mg/cm ²)	PH EH EP ELA Chi-a
Ep% = ear position% GR= no. of grains/row		0.956	0.713	-2.806**	0.491	1.366	-0.808	0.566	-1.083	0.941	-1.691*	-2.083*	0.866	0.471	1.691*	-0.083	-0.883	3.116**	1.541*	0.916	1.391	1.341	-0.980	-4.283**	(mg/cm ²)	Chl-b
		0.733	0.546	-1.015	-0.28	0.59	0.02	0.815	-0.175	0.68	-0.175	-0.04	-0.19	0.755	-0.175	-0.340	-0.115	-0.355	-0.160	-0.040	0.245	-0.355	0.080	0.230	NE	DF
ELA= GY=g		3.854	2.872	-4.928	3.031	2.764	-2.315	-0.408	5.691*	8.67	-1.47	-2.435	-5.008	-0.945	3.051	-4.3	*100.0	-4.55	-3.648	1.124	-1.29	-1.038	1.259	0.194	UN	CD
ELA= ear leaf area GY= grain yield		1.597	1.190	0.226	-2.293	0.266	0.166	0.826	3.306**	2.446*	0.206	0.386	-3.033*	0.166	-0.//5	-0.693	2.3357	-2.986*	-2.213	-1.233	-1.6/3	0./86	1.166	2.486*	(Ard/fad)	U Y

D- General and specific combining ability effects.

Estimates of general combing ability (GCA) effects of the 7 parental inbred lines for the ten studied traits combined across the two locations Ismailia and Mallawy are given in (Table 6). The results revealed that the parental inbred line (P_3) was an ideal general combiner for earliness, EH, ELA, Chl-a, GR and GY. Also, inbred line (P₅) for ELA, GR and GY. Also inbred lines (P₃ and P₅) were assumed as the most useful source of favorable alleles for earliness, physiological traits as well as grain yield and yield components. Also, the inbred lines P_1 and P_2 were the best general combiner for Chl-a and GY. Mousa (1997), reported that GCA effects were desirable and significant for earliness, physiological traits, grain yield and yield components.

Commonly, maize hybrid involving inbreds, P_1 , P_3 and P_5 in single or triple crosses might be useful for earliness, ideal physiological system/plant and grain yield. Selection for increasing physiological traits among inbred lines might result in an increased grain yield in the F_1 hybrids (Johnson 1974).

Estimates of specific combining ability (SAC) effects for 21 F₁'s for over locations were shown in (Table 7). The most desirable and significant SCA effects were obtained for earliness in the crosses; P₁ x P_2 , P_3 x P_7 and P_4 x P_5 , for plant height, in the cross $P_1 \times P_7$ for ear height, in the crosses $P_2 \times P_6$, P_3 $x\ P_4,\ P_3\ x\ P_5$ and $P_6\ x\ P_7$ for ear leaf area, in the crosses P₁ x P₂, P₁ x P₃, P₂ x P₄, P₃ x P₇, P₄ x P₅ and $P_5 \ge P_6$ for chlorophyll-a, in the crosses $P_3 \ge P_7$ and $P_4 \times P_5$ for chlorophyll-b, in the crosses $P_1 \times P_7$, $P_2 \times P_7$ P_3 and $P_2 \times P_6$ for number of grains/row, in the crosses P₂ x P₄, P₃ x P₇ and P₄ x P₅, for grain yield. The crosses $P_1 \times P_2$, $P_3 \times P_7$ and $P_4 \times P_5$ are the best desirable combination of inbred lines for improving earliness, physiological traits and grain yield of maize.

Finally, this study was an attempt to show that there were maize inbred lines might produce single crosses with, earliness, shorter plant, lower ear, and high grain yield. It might be concluded that the most superior crosses for physiological traits, grain yield and yield components were $P_1 x P_4$, $P_1 x P_5$, $P_3 x P_5$ and $P_4 x P_5$ while, the crosses $P_1 x P_2$, $P_1 x P_3$, $P_3 x P_7$ and $P_4 x P_5$ for earliness. Inbred line P_3 showed desirable and general combining ability effect for DS, EH, ELA, Chl-a, RE and GY, while line P_5 was good combiner for LA, RE and GY. These lines with favorable alleles for grain yield and other studied traits, might be utilized in developing new white maize hybrids.

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$$(P_4 x P_5) (P_3 x P_7) /$$

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$P_4 \ x \ P_5$, $P_3 \ x \ P_5$, $P_1 \ x \ P_5, \ P_1 \ x \ P_4, \ P_1 \ x \ P_2$