Combining Ability in Grain Yield and Other Related Traits of Sweet Corn (*Zea mays sacharata* L.) in Syria

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ABSTRACT

This study aims to estimate the combining ability and heritability of traits such number-of-days-to-50% silking, plant height, ear height and yield per plot through half diallel cross among five sweet corn inbred lines in two locations (Damascus and Tartous) in the Syrian Arab Republic. Highly significant mean square among hybrids at Damascus and Tartous location and over locations in all studied traits has been indicated via analysis of variance. This analysis of variance of the diallel crosses indicated highly significant estimates (p<0.01) of General Combining Ability (GCA) and Specific Combining Ability (SCA) for all traits. The dominance degree showed that non-additive gene action has played the major role in the inheritance of studied traits in each location and over locations; however, additive gene action effects has also played an important role in the inheritance of yield per plot. Then, results revealed that a low narrow-sense heritability value for number-of-days-to-50% silking, plant height and ear height suggested that the effective selection of these traits must be through the late generations (S_5, S_6), on the other hand the value has been moderate in yield per plot.

INTRODUCTION

Corn is one of main important cereal crops; globally it ranks third after wheat and rice. There are many uses of corn but the majority goes to animal feeding (Kuşaksız 2010). Sweet corn (*Zea mays sacharata* L.) is utilized mainly for human feeding (Zare *et al*. 2011), for it accumulates two times more sugar in endosperm and eight to ten times more water soluble polysaccharides, compared to normal corn. This difference between the two types of corn is due to mutation happened in sugary locus (SU) on chromosome 4 (Srdic *et al*. 2011).

Successful crop enhancement strategy depends upon availability of genetic variability among genotypes in the interesting traits. Therefore, it is important to use contrasting parental lines in breeding programs. Estimating genetic variation and combing ability are useful to determine the breeding value of populations and the appropriate procedures to use in breeding programs. The general combining ability effects are crucial indicators of the value of genotypes in hybrid combinations. And, estimate of combining ability by diallel-mating design has been broadly used to discover information on the act of parental inbred lines and recognize heterotic groups and predict performance of new hybrids, consequents of such crosses (Miranda Filho 1985; Yan and Hunt 2002).

Combing ability analysis (general and specific) is used to identify gene action (Zare *et al*. 2011). In addition, it is used to determine the variation, heritability and stability over locations (Novoselovic *et al*. 2004). Differences in GCA effects have been contributed to additive, additive × additive and higher order additive interactions, whereas differences in SCA have been attributed to non-additive genetic variance (Falconer 1996).

The ratios σ^2 GCA/σ^2 SCA showed that non-additive gene action was more important than additive gene action in controlling all studied traits, except days-to-50-%sillking which showed predominance of additive gene action (Al

Abd Alhadi *et al*. 2011). On another diallel study, environment and hybrids× environmental effects were significant for grain yield in the analysis of combining ability (Mickelson *et al*. 2001). Tabassum *et al*. (2005) evaluated an 8 × 8 diallel study for combining ability under normal and stress conditions and reported that all studied traits were under non-additive control type genes, except plant height which was under both additive and non-additive type of genes. Parmar (2007) evaluated inbred lines and their hybrids using diallel fashion and reported that significant GCA and SCA variances, which revealing the importance of both additive and non-additive gene action for yield components.

The objective of this research was to evaluate the combing ability effects of some sweet corn inbred lines and their crosses for grain yield and other related traits within two environments.

MATERIALS AND METHODS

The experimental material comprised of 10 hybrids of sweet corn output by a diallel fashion (without reciprocal combinations) among 5 sweet corn inbred lines 'P$_1$: IL-1073-08; P$_2$: IL-1062-08; P$_3$: IL-1049-08; P$_4$: IL-209-08; P$_5$: IL-1065-08'. These lines were collected from the genetic bank of maize department, crops administration, General Commission of Scientific Agricultural Research (GCSAR), Damascus, Syria.

The ten hybrids and five parental lines were grown during the 2011 season at maize department, crops administration, GCSAR, Damascus, Syria. Each entry was sown in three replications by using randomized block design in two locations Damascus (DM as first location) and Tartous (TA as the second). Each replication consisted of three rows of 6 m in length with a spacing of 70 cm and among plants 25 cm. Observations were recorded on ten uniform plants from each replication leaving two border plants on either end to avoid the border effects. The data on days from farming to 50% silking, plant height, ear height and yield per plot (at the milky stage of the endosperm development, after 25 of silking) were recorded. The analysis of variance for each location

was performed according to Plabstat program, general combining ability (GCA) and specific combining ability (SCA) were analyzed according to the Griffing (1956) mathematical method 4, model 1, however, combined analysis of GCA and SCA over locations was recorded using SAS program. The σ^2GCA/σ^2SCA ratio revealed the genetic effects of different traits, the value greater than one indicating additive genetic effect, whereas value lower than one indicating dominant genetic effect.

Broad-sense heritability (h^2_b) and narrow-sense heritability (h^2_n) for mean values over locations were calculated based on the components of variance (Teklewold and Becker 2005):

$$h^2_b = [2\ \sigma^2GCA + \sigma^2SCA] / [2\ \sigma^2GCA + \sigma^2SCA + (2\sigma^2GCA/ENV) + (\sigma^2SCA/ENV) + (\sigma^2e/R\ ENV).$$

$$h^2_n = 2\ \sigma^2GCA / [2\sigma^2GCA + \sigma^2SCA + (2\sigma^2GCA/ENV) + (\sigma^2SCA/ENV) + (\sigma^2e/R\ ENV).$$

where: σ^2GCA: variance due to GCA, σ^2SCA: variance due to SCA, σ^2e: variance due to error, R: replications, Env: environments.
Genetic ratio calculated according to Baker (1978):

Genetic ratio = $2\ \sigma^2GCA/(2\sigma^2GCA + \sigma^2SCA)$.

Dominance degree for combined analysis was computed as (Mather 1949):

Dominance degree = $(VD/VA)^{1/2}$

where: VD: variance due to dominance gene action, VA: variance due to additive gene action. Had the degree of dominance ratio been more than unity, the trait would be controlled by additive gene action; on the other hand, non-additive gene action limited the inheritance of trait, if the ratio was less than unity but if the ratio equaled the unity therefore, there was a balance of additive and non-additive gene action.

RESULTS AND DISCUSSION

Analysis of variance

Highly significant differences among hybrids at the Damascus and Tartous locations indicated via analysis of variances (**Tables 1, 2**), show large variability and genetic distant among studied parents.

The analysis of variance of the diallel crosses showed highly significant values (p<0.01) of GCA and SCA for all studied traits, indicating the importance of additive and non-additive gene action of the traits,σ^2GCA/σ^2SCA ratio was 0.33, 0.07, 0.12, 0.44 for days-to-50-% silking, plant height, ear height and yield per plot, respectively at Damascus (**Table 1**), while the ratio was 0.03, 0.01, 0.28, 0.19 for the same studied traits, respectively at Tartous (**Table 2**). Therefore, the non-additive gene action played the major role in the inheritance of these traits. This result was similar to the results of earlier reports (Abdel-Moneam *et al*. 2009; Haq *et al*. 2010; Al AbdAlhadi 2011); however, Paterniani *et al*. (2001) and Al Ahmad (2004) showed that additive gene action was the more important ole in the inheritance of yield per plot.

The results of combined analysis across environments revealed that there were no significant differences (**Table 3**). However, significant variance amongst hybrids over locations for all studied traits except plant height was seen (**Table 3**), while the interaction variance (hybrids × location) was not significant for all studied traits, suggesting that genotypes maintain their rank for these traits, over coastal and in land region. Thus, selection for studied traits at one environment might be effective for a broad range of environments.

The location interaction was highly significant for all traits in both the GCA_X and the SCA_X except for ear height (**Table 3**), of the latter, i.e., the SCA_X. The ratio of σ^2GCA/σ^2SCA was 0.22, 0.44, 0.08 and 1.33, suggesting the domi-

Table 1 Analysis of variance (MS) for all studied traits at Damascus location.

S.O.V	DF	MS			
		Silk	Plant height	Ear height	Grain yield
Rep	2	0.63	54.70	8.63	1.43
Genotypes	9	2.00**	138.96**	111.34**	41.85**
Error	38	0.34	20.11	3.00	1.73
GCA	4	2.60**	152.30**	129.36**	61.41**
SCA	5	1.50**	128.30**	96.92**	27.35**
Error	18	0.34	20.10	3.00	1.60
σ^2_{GCA}		0.13	2.66	3.60	3.78
σ^2_{SCA}		0.39	36.07	31.31	8.58
Dominance		0.25	5.33	7.21	7.57
Additive		0.39	36.07	31.31	8.58
$\sigma^2_{GCA}/\sigma^2_{SCA}$		0.33	0.07	0.12	0.44
Dominance degree		1.24	2.60	2.08	1.07

* and ** significant at P= 0.05 and P= 0.01, respectively.

Table 2 Analysis of variance (MS) for all studied traits at Tartous location.

S.O.V	DF	MS			
		Silk	Plant height	Ear height	Grain yield
Rep	2	0.13	88.30	8.63	3.54
Genotypes	9	4.68**	212.11**	111.78**	2115.11**
Error	4	0.28	27.15	12.11	2.21
GCA	5	4.92**	178.42**	145.47**	9.88**
SCA	18	4.49**	175.96**	84.83**	7.06**
Error	36	0.28	24.76	12.11	2.19
σ^2_{GCA}		0.048	0.27	6.74	0.31
σ^2_{SCA}		1.40	50.39	24.24	1.63
Dominance		0.09	0.55	13.47	0.63
Additive		1.40	50.39	24.24	1.63
$\sigma^2_{GCA}/\sigma^2_{SCA}$		0.03	0.01	0.28	0.19
Dominance degree		3.82	9.59	1.34	1.61

* and ** significant at P= 0.05 and P= 0.01, respectively

Table 3 Analysis of variance for all studied traits; data are combined over two locations.

S.O.V	DF	MS			
		Silk	Plant height	Ear height	Grain yield
R	2	2.22	197.07	60.65	7.37
L	1	0.15ns	17.07ns	38.4ns	7.25ns
G	9	4.71**	156.01	176.91**	36.53**
Gl	9	0.11 ns	20.88 ns	2.33 ns	3.58 ns
Error	38	0.85	105.75	26.65	5.75
GCA	4	5.72**	269.74**	222.85**	62.81**
SCA	5	3.57**	129.31**	179.55**	14.12*
GCA×L	4	2.10**	152.41**	44.03**	11.87*
SCA×L	5	1.88**	164.91**	9.59	28.49**
Error	36	0.28	23.63	7.26	1.96
σ^2GCA		0.72	46.81	14.43	16.23
σ^2SCA		3.29	105.68	172.29	12.16
$\sigma^2_{GCA}/\sigma^2_{SCA}$		0.22	0.44	0.08	1.33
Additive		1.43	93.62	28.87	32.46
Dominance		3.29	105.68	172.29	12.16
h^2_b		0.66	0.65	0.66	0.66
h^2_n		0.20	0.31	0.10	0.48
Genetic ratio		0.30	0.47	0.14	0.73
Dominance degree		1.56	1.06	2.44	0.61

* and ** significant at P= 0.05 and P= 0.01, respectively.

nance is the major role of the inheritance of days-to-50% silking, ear height and plant height, while the additive gene action controlled the behavior of yield per plot, our result was similar to earlier reports about predominance of non-additive genetic effects for days-to-silking, plant height (Akbar *et al*. 2008; Alam *et al*. 2008), in contrast, other researchers indicated the predominance of additive genetic effects for plant height (Vacaro *et al*. 2002) and grain yield (Ojo *et al*. 2007).

Baker (1978) suggested genetic ratio, progeny perfor-

Table 4 Means performance for all studied traits at Damascus, Tartous and over locations.

Hybrid	Silk			Plant height			Ear height			Yield per plot		
	DM	TA	Comb	DM	TA	Comb	DM	TA	Comb	DM	TA	Comb
$P_1 \times P_2$	51.7	50.7	51.2	188.3	176.7	182.5	92.7	83.3	93.0	14.0	13.197	12.8
$P_1 \times P_3$	53.0	52.0	52.5	186.7	165.0	175.8	88.3	83.0	86.5	16.5	12.694	14.4
$P_1 \times P_4$	51.3	49.7	50.5	184.3	174.0	179.2	84.3	71.7	86.8	8.2	9.500	8.9
$P_1 \times P_5$	50.3	50.3	50.3	185.0	181.7	178.3	87.0	81.7	81.7	13.4	15.578	14.5
$P_2 \times P_3$	51.7	52.3	52.0	167.7	176.7	172.2	77.0	75.0	76.0	8.1	12.101	9.2
$P_2 \times P_4$	51.0	48.7	49.8	186.7	178.3	182.5	75.0	74.0	75.8	7.6	10.683	8.7
$P_2 \times P_5$	51.7	50.7	51.2	186.7	176.7	185.0	87.7	86.3	88.0	14.7	12.531	13.3
$P_3 \times P_4$	50.7	48.7	49.7	187.3	171.7	179.5	85.0	85.0	80.7	7.9	11.200	9.6
$P_3 \times P_5$	50.7	51.0	50.8	183.0	195.0	189.0	94.67	91.3	86.5	17.2	10.863	14.0
$P_4 \times P_5$	50.3	51.3	50.8	194.3	179.0	186.7	86.0	83.0	83.0	14.9	12.251	13.6
GM	51.2	50.5	50.9	185.0	177.5	181.1	85.8	81.4	83.8	12.3	12.06	11.9
L.S.D (0.05)	1.4	1.3	1.1	10.5	12.3	12.0	4.1	8.2	6.0	3.5	3.5	2.8
L.S.D (0.01)	1.0	0.9	1.4	7.7	8.9	16.1	2.9	5.9	8.1	2.5	2.5	3.8

DM: Damascus, TA: Tartous, Com: combined over locations. p_1, p_2, p_3, p_4, p_5 indicated to parental lines: (IL-1073-08, IL-1062-08, IL-1049-08, IL-209-08, IL-1065-08) respectively.

Table 5 General combining ability of 5 parents for silk and plant height traits at Damascus and Tartous locations and over locations.

Parent	Silk			Plant height		
	DM	TA	Comb	DM	TA	Comb
P_1	0.467[*]	0.178[**]	0.389[*]	1.444	-4.178[*]	-1.256
P_2	0.356	0.067	0.167	-3.556	-0.511	-1.644
P_3	0.356	0.622[*]	0.444[*]	-5.111	-0.511	-4.089[**]
P_4	-0.533	-1.267[**]	-0.944[**]	4.222[*]	-2.289	0.800
P_5	-0.644	0.400[*]	-0.056	3.000	7.489[**]	6.189[**]
SE[g(i)]	0.173	0.158	0.113	1.337	1.483	1.025

DM: Damascus, TA: Tartous, Comb: combined over locations, [*] and [**] significant at P= 0.05 and P= 0.01, respectively.. p_1, p_2, p_3, p_4, p_5 indicated to parental lines: (IL-1073-08, IL-1062-08, IL-1049-08, IL-209-08, IL-1065-08) respectively.

Table 6 General combining ability of 5 parents for ear height and yield per plot at Damascus and Tartous locations and over location.

Parent	Ear height			Yield per plot		
	DM	TA	Comb	DM	TA	Comb
P_1	3.09[**]	-2.022	0.367	1.032	0.909	1.024[*]
P_2	-3.58	-2.356	-2.856[**]	-1.510	0.090	-0.745
P_3	0.64	2.867[*]	1.867[*]	0.256	-0.460	-0.137
P_4	-4.24	-4.022[*]	-4.022[**]	-3.500	-1.535[*]	-2.553[**]
P_5	4.09[**]	5.533[**]	4.644[**]	3.723[**]	0.900	2.412[**]
SE[g(i)]	o.516	1.037	0.568	0.439	0.440	0.295

DM: Damascus, TA: Tartous, Comb: combined over locations, [*] and [**] significant at P= 0.05 and P= 0.01, respectively.. p_1, p_2, p_3, p_4, p_5 indicated to parental lines: (IL-1073-08, IL-1062-08, IL-1049-08, IL-209-08, IL-1065-08) respectively.

mances could be predicted by using the ratio of combining ability variance components. In this study, we found that genetic ratio was closely to unity (0.73) in yield per plot (**Table 3**) thus, it controlled by additive gene action, however, the values of genetic ratio of other studied traits was low indicating that non-additive gene action control.

Mean performance

The mean number of days to silking of the hybrids at each location and combined over locations (**Table 4**) indicated that the average number-of-days-to-50% silking ranged from 50.33 days for hybrids $P_1 \times P_5$, $P_4 \times P_5$ to 53 days for hybrid $P_1 \times P_3$ at Damascus location, and from 48.7 days for the hybrids $P_2 \times P_4$, $P_3 \times P_4$ to 52.3 days for hybrid $P_2 \times P_3$ at Tartous location, while the data ranged from 49.7 days to 52.5 days over locations.

Plant height does not only depend on the genetic background of the varieties, but are also influenced by many environmental effects and the cultivated method. Data showed that plant height ranged from 167.7 cm in hybrid $P_2 \times P_3$ to 194.3 cm in hybrid $P_4 \times P_5$ at Damascus and from 165 cm in hybrid $P_1 \times P_3$ to 195 cm in hybrid $P_3 \times P_5$ at Tartous, and from 172.2 cm for hybrid $P_2 \times P_3$ to 189 cm for hybrid $P_3 \times P_5$ over locations.

Ear height is one of the most important selection criteria in maize breeding programs, the plant breeders prefer to select lower ear position thus adopt to stalk lodging (Hee Chung *et al.* 2006). High ear position is likely to become more susceptible to root and stalk lodging. Results showed that the lowest ear height was 75.0 cm and 74 cm in hybrid

$P_2 \times P_4$ at Damascus and Tartous, respectively with 75.8 cm over locations (**Table 4**).

Grain yield per plot was highest in hybrids $P_3 \times P_5$, $P_1 \times P_3$ and $P_4 \times P_5$ at Damascus (**Table 4**), however, in Tartous it was 13.19 and 15.57 ton/ha for hybrids $P_1 \times P_2$ and $P_1 \times P_5$, respectively (**Table 4**). In the combined data the highest mean was 14.5 ton/ha in hybrid $P_1 \times P_5$ while the lowest mean was 8.7 ton/ha for hybrid $P_2 \times P_4$.

GCA and SCA effects

A parent with a significant negative value of GCA or SCA would contribute a low value in breeding, whereas a parent with a positive value would contribute towards a high value in it. Therefore, parental lines with the highest GCA for a specific trait should be used. The potential of a parent in hybridization may be assessed by its performance, F_1 performance and GCA effects. Thus, positive GCA effects were desirable for yield per plot and plant height while the negative GCA effects were the best for days-to-50% silking and ear height.

Results of the GCA effects of studied traits (**Tables 5, 6**) indicate that the inbred line P_4 had negative and significant GCA effects in days-to-50% silking and ear height at Tartous and over locations. However, the inbred line P_5 had positive and significant GCA for plant height at Tartous and over locations and it was the best combiner for grain yield at Damascus and over locations.

Estimation of specific combining ability effects of 10 hybrids for the studied traits at two locations and their combined analysis are presented in **Tables 7** and **8**. And, hybrids

Table 7 Specific combining ability of 10 hybrids for silk and plant height traits at Damascus and Tartous locations and over locations.

Hybrid	Silk			Plant height		
	DM	TA	Comb	DM	TA	Comb
$P_1 \times P_2$	-0.389	-0.111	-0.306	5.444[*]	3.889	4.250[*]
$P_1 \times P_3$	0.944[*]	0.667[*]	0.750[**]	5.333[*]	-7.778[*]	0.028
$P_1 \times P_4$	0.167	0.222	0.139	-6.333[*]	3.000	-1.528
$P_1 \times P_5$	-0.722	-0.778[*]	-0.583[*]	-4.444	0.889	-2.75
$P_2 \times P_3$	-0.278	1.111[**]	0.472[*]	-8.667[*]	0.222	-5.750[**]
$P_2 \times P_4$	-0.056	-0.667[*]	-0.306	1.000	3.667	3.028
$P_2 \times P_5$	0.722[*]	-0.333	0.139	2.222	-7.778[*]	-1.528
$P_3 \times P_4$	-0.389	-1.222[**]	-0.750[**]	3.222	-3.000	-0.028
$P_3 \times P_5$	-0.278	-0.556[*]	-0.472	0.111	10.556[**]	5.750[**]
$P_4 \times P_5$	0.278	1.667[**]	0.917[**]	2.111	-3.667	-1.472
SE[$s_{(i,j)}$]	0.237	0.216	0.155	1.831	2.032	1.403

DM: Damascus, TA: Tartous, Comb: combined over locations, [*] and [**] significant at P= 0.05 and P= 0.01, respectively. p_1, p_2, p_3, p_4, p_5 indicated to parental lines: (IL-1073-08, IL-1062-08, IL-1049-08, IL-209-08, IL-1065-08) respectively.

Table 8 Specific combining ability of 10 hybrids for ear height and yield per plot traits at Damascus and Tartous locations and over locations.

Hybrid	Ear height			Yield per plot		
	DM	TA	Comb	DM	TA	Comb
$P_1 \times P_2$	7.389[**]	6.278[**]	6.972[**]	2.271[*]	0.136	1.160[*]
$P_1 \times P_3$	-1.167	0.722	-0.083	2.974[**]	0.185	1.536[*]
$P_1 \times P_4$	-0.278	-3.722	-1.861	-1.623	-1.935[*]	-1.821[**]
$P_1 \times P_5$	-5.944	-3.278	-5.028[**]	-3.623	1.614[*]	-0.875
$P_2 \times P_3$	-5.833	-6.944	-6.528[**]	-2.862	0.411	-1.182[*]
$P_2 \times P_4$	-2.944	-1.056	-2.139[*]	0.339	0.067	0.246
$P_2 \times P_5$	1.389	1.722	1.694	0.252	-0.614	-0.224
$P_3 \times P_4$	2.833[*]	4.722[*]	3.639[**]	-1.100	1.136	0.061
$P_3 \times P_5$	4.167[**]	1.500	2.972[*]	0.987	-1.731[*]	-0.415
$P_4 \times P_5$	0.389	0.056	6.972[**]	2.384[*]	0.731	1.514[*]
SE[$s_{(i,j)}$]	0.707	1.420	0.778	0.601	0.603	0.404

DM: Damascus, TA: Tartous, Com combined over locations, [*] and [**] significant at P= 0.05 and P= 0.01, respectively. p_1, p_2, p_3, p_4, p_5 indicated to parental lines: (IL-1073-08, IL-1062-08, IL-1049-08, IL-209-08, IL-1065-08) respectively.

$P_1 \times P_5$ and $P_3 \times P_4$ that had negative and significant SCA effects in days-to-50% silking at Tartous and over locations. However, $P_1 \times P_2$ and $P_1 \times P_3$ hybrids had positive and significant SCA effects on the plant height at Damascus, while $P_3 \times P_5$ hybrids had positive and high significant SCA effects at Tartous and over two locations. In respect to ear height, hybrids $P_2 \times P_3$, $P_1 \times P_5$ and $P_2 \times P_4$ had negative and significant SCA effects in combined analysis over locations. Regarding to yield per plot $P_1 \times P_3$, $P_1 \times P_2$, $P_4 \times P_5$ hybrids had the best positive and significant SCA effects at Damascus and over locations, while $P_1 \times P_5$ has the best SCA effects at Tartous location.

Broad and narrow-sense heritability

High broad-sense heritability values was estimated for days-to-50% silking, plant height, yield per plot and ear height, the results of narrow-sense heritability showed low and medium for different plant traits under study (**Table 3**). The narrow-sense heritability was moderate for grain yield per plot (0.48), indicating the importance of additive component in the phenotypic variability. Such result was expected due to the fact that additive gene action was predominant in yield per plot. This result is similar to an earlier report (Khalil 1999), while high value of heritability was concluded by Rafiq (2010). The narrow-sense heritability was 0.20, 0.31 and 0.10 for days-to-50% silking, plant height and the controlling of non-additive gene action, suggesting that the effective selection for these traits must be through the late generations (S_4, S_5). High heritability estimation in plant height were reported (Yasien 2000; Abd El-Sattar 2003), while low narrow-sense heritability estimation was obtained in grain yield and silking date (Abd El Sattar 2003; Wannows *et al*. 2010).

CONCLUSION

Estimation of GCA and SCA was significant, indicating the importance of (additive and non-additive) gene action in the inheritance of traits. Non-additive gene effects estimated based on $\sigma^2 GCA/\sigma^2 SCA$ ratio were found to play a more significant role in the expression of days-to-50% silking, ear height, plant height and yield per plot at Damascus, Tartous and over locations. On the other hand, yield per plot in combined analysis showed that additive gene action was more important than non-additive gene action. These results were validated by the average degree of dominance and genetic ratio which was also assured by heritability in narrow-sense. Heritability in broad-sense was high in all the cases, showing the high proportion of genetic variability in the whole phenotypic variability.

Significant GCA effects for the inbreds P_5, P_1, concerning ear yield and plant height, referred to possible value in sweet corn breeding programs. Regarding to SCA effects the $P_1 \times P_3$, $P_1 \times P_2$, $P_4 \times P_5$ hybrids had the best positive and significant SCA effects for yield per plot at Damascus and over locations, while $P_1 \times P_5$ had the best SCA at Tartous location.

REFERENCES

Abd El-Sattar AA (2003) Genetic parameters estimation from design-1 and S1 lines in maize. *Minufiya Journal of Agriculture Research* **28 (5)**, 1387-1402

Abdel Moneam MA, Attia AN, EL-Emery MI, Fayed EA (2009) Combining ability and heterosis for some agronomic traits in crosses of maize. *Pakistan Journal of Biotechnology Science* **12 (5)**, 433-438

Akbar M, Saleem M, Azhar FM, Ashraf MY, Ahmad R (2008) Combining ability analysis in maize under normal and high temperature conditions. *Journal of Agriculture Research* **46 (1)**, 261-277

Al AbdAlhadi RA (2010) Inheritance of Some yield and quality traits of maize (*Zea mays* L.) using half diallel cross. MSc thesis, Faculty of Agriculture, Damascus University, Syria, 131 pp

Al Ahmad SA (2004) Genetic parameters for yield and its components in some new yellow maize crosses. PhD thesis, Faculty of Agriculture, Ain Shams University, Egypt, 180 pp

Alam A, Ahmed S, Begum M, Sultan MK (2008) Heterosis and combining ability for grain yield and its contributing characters in maize. *Bangladesh*

Journal of Agriculture Research **33 (3)**, 375-379

Baker RJ (1978) Issues in diallel analysis. *Crop Science* **18**, 535- 536

Dudley JW, Moll RH (1969) Interpretation and use of estimates of heritability and genetic variances in plant breeding. *Crop Science* **9**, 257-262

Falconer DS (1981) *Introduction to Quantitative Genetics*, The Ronald Press Co., New York, pp 281-286

Fehr WR (1991) *Principles of Cultivar Development. Theory and Technique*, MacMillan Publishing Co., New York, 1536 pp

Gamble EE (1962) Gene effects in corn (*Zea mays* L.). II. Relative importance of gene effects for plant height and certain attributes of yield. *Canadian Journal of Plant Science* **42**, 349-358

Haq MIUL, Ajmal SU, Munir M, Gulfaraz M (2010) Gene action studies of different quantitative traits in maize. *Pakistan Journal of Botany* **42 (2)**, 1021-1030

Heechung JI, Cho JW, Yamakawa T (2006) Diallel analysis of plant and ear heights in tropical maize (*Zea mays* L.). *Journal of the Faculty of Agriculture, Kyushu University* **51 (2)**, 233-238

Jones KR, Frey KJ (1960) Heritability percentages and degrees of dominance for quantitative characters in oats. *State Journal of Science* **35**, 49-58

Khalil ANM (1999) Genetic effects estimated from generation means in two maize crosses. *Minufiya Journal of Agriculture Research* **24 (6)**, 1911-1924

Kusaksiz T (2010) Adaptability of some new maize (*Zea mays* L.) cultivars for silage production as main crop in Mediterranean environment. *Turkish Journal of Field Crops* **15 (2)**, 193-197

Mather K (1949) *Biometrical Genetics*, Dover Publication, Inc., New York, 671 pp

Mickelson H R, Cordova H, Pixley KV, Bjarnason MS (2001) Heterotic relationships among nine temperate and subtropical maize populations. *Crop Science* **41**, 1012-1020

Miranda Filho JB (1985) Breeding methodologies for tropical maize. In: Brandolini A, Salamini F (Eds) *Breeding Strategies for Maize Production Improvement in the Tropics*, Instituto Agronomica per l'Oltremare, FAO, Firenze, pp 45-111

Novoselovic D, Baric M, Drezner G, Gunjaca J, Lalic A (2004) Quantitative inheritance of some wheat plant traits. *Genetic Molecular Biology* **27 (1)**, 92-98

Nyhus KA, Russel WA, Guthrie WD (1989) Change in agronomic traits associated with recurrent selection in two maize synthetics. *Crop Science* **29**, 269-275

Ojo GOS, Adedzwa DK, Bello LL (2007) Combining ability estimates and heterosis for grain yield and yield components in maize (*Zea mays* L.). *Journal of Sustainable Development in Agriculture and the Environment* **3**, 49-57

Pajić Z, Srdić J, Filipović M (2008) Sweet maize breeding for different consumption purposes. *Journal on Processing and Energy in Agriculture* **12**, 12-14

Parmar HP (2007) Combining ability and stability analysis in forage maize (*Zea mays* L.). PhD thesis, B.A. College of Agriculture, Gujarat Agricultural University, India

Paterniani MEAGZ (2001) Use of heterosis in maize breeding history, methods and perspectives. *Crop Breeding and Applied Biotechnology* **1 (2)**, 159-178

Rafiq Ch M, Rafique M, Hussain A, Altaf M (2010) Studies on heritability, correlation and path analysis in maize (*Zea mays* L.). *Journal of Agriculture Research* **48 (1)**, 35-38

Srdić J, Pajić Z, Drinić SM (2007) Inheritance of maize grain yield components. *Maydica* **52**, 261-264

Srdić J, Pajić Z, Filipovic M, Babić M, Sečanski M (2011) inheritance of ear yield and its components in sweet corn (*Zea mays* L. *Saccharat*). *Genetika* **43 (2)**, 341-348

Tabassum MI, Saleem M, Ali A, Malik MA (2005) Genetic mechanisms of leaf characteristics and grain yield in maize under normal and b moisture stress conditions. *Biotechnology (Pakistan)* **4**, 243-254

Teklewold A, Becker HC (2005) Heterosis and combining ability in a diallel cross of Ethiopian mustard inbred lines. *Crop Science* **45**, 2629-2635

Thompson SA (1983) Mass selection for prolificacy in corn at high and low plant densities: Cycle means and genotypic variations. *Dissertation Abstracts International* **43**, 2414

Troyer AF, Larkins JR (1985) Selection for early flowering in corn: 10 late synthetics. *Crop Science* **25**, 695-697

Vacaro E, Neto JFB, Pegoraro DG, Nuss CN, Conceição LDH (2002) Combining ability of twelve maize populations. *Pesquisa Agropecuária Brasileira* **37**, 67-72

Wannows AA, Azzam HK, Al-Ahmad SA (2010) Genetic variances, heritability, correlation and path coefficient analysis in yellow maize crosses (*Zea mays* L.). *Agriculture of Biology Journal, North America* **1 (4)**, 630-637

Yan W, Hunt LA (2002) Biplot analysis of diallel data. *Crop Science* **42**, 21-30

Yap TC, Tan ST (1974) Evaluation of recurrent selection based on rouging, S1 progeny test and S1 line breeding in a sweet corn variety. *Malaysian Agriculture Research* **3**, 222-226

Yasien M (2000) Genetic behavior and relative importance of some yield components in relation to grain yield in maize (*Zea mays* L.). *Annals of Agriculture Science Moshtohor* **38 (2)**, 689-700

Zare M, Choukan R, Heravan EM, Bihamta MR, Kourosh O (2011) Gene action of some agronomic traits in corn (*Zea mays* L.) using diallel cross analysis. *African Journal of Agricultural Research* **6 (3)**, 693-703