COMBINING ABILITY AND HETEROTIC GROUPING OF TWO SETS OF NEW MAIZE INBRED LINES

A.A. Motawei, H.E. Mosa, M.A.G. Khalil, M.M.B. Darwish and H.A.A. Mohamed

Maize Research Department, Field crop Research institute, ARC., Egypt

ABSTRACT

Two sets of white and yellow maize crosses were developed by crossing 17 new inbred lines with two testers for each set using line × tester method at Sakha Agricultural Research Station in 2015 growing season. The resulting 34 F₁ crosses plus four standard checks for each set were evaluated in 2016 summer season at two locations (Sakha and Mallawi) for set-1 and at (Sakha and Sids) for set-2. Days to 50% silking (SD) and grain yield t ha⁻¹ (GY) were recorded. Significant mean squares due to line (L) and L × Loc were found for the two traits in the two sets. Also, mean squares due to tester (T) were significant for SD in set-1 and GY in set-2. Meanwhile, mean squares due to L × T and L × T × Loc interaction were significant for all traits in the two sets, except for L × T × Loc for SD and GY in set-1. Four white inbred lines (L2, L3, L15 and L17) in set-1 and five yellow inbred lines (L18, L22, L25, L26, and L27) in set-2 exhibited positive and significant GCA effects for yield trait. The single cross L12 × Sk5 in set-1 and L32×Sk4 in set-2 manifested desirable SCA effects for SD and GY toward early maturity and high yielding ability. Days to 50% silking trait in the two sets was controlled mainly by non-additive gene action. Meanwhile, GY trait was controlled by non-additive in set-1 and additive gene action in set-2. The inbred lines in each set for grain yield based on heterotic group specific and general combining ability (HSGCA) method were classified into two heterotic groups as follows: set-1 group-1(Sk5) included L4, L5, L6, L8, L13 and L16. While, group2 (SC131) included L1, L7, L9, L10, L12 and L14. In set-2, group1 (Sk4) included L19, L20, L28 and L29. Meanwhile, in set-2, group-2 (SC177) included L24, L30, L31, L32, L33 and L34. These groups could be used in breeding programs for selecting the best parents in making crosses.

Key words: *Maize, Line×tester, Additive, Non-Additive, Gene action, Heterotic group.*

INTRODUCTION

Combining ability is a useful biometric tool to the plant breeder for formulating efficient breeding programs (Hallauer and Miranda 1981). Line×tester analysis has widely been used for evaluation new inbred lines by crossing them with testers. The value of any inbred line in hybrid breeding ultimately depends on its ability to combine very well with other lines to produce superior hybrids (Kempthorne 1957). There is no agreement among authors on the mode of gene action controlling maize yield or its related characters. Nigussie and Zelleke (2001), Vacaro *et al* (2002), El-Shouny *et al* (2003), Ojo *et al* (2007), Musila *et al* (2010), Wegary *et al* (2013), Badua-Aprakua *et al* (2015) and Hosana *et al* (2015) reported that additive gene action was more important for maize grain yield and days to 50% silking traits. Meanwhile, Chaudhary *et al* (2000), Dar *et al* (2007), Abdel-Moneam *et al* (2009), Amiruzzaman *et al* (2013), Verma *et al* (2014), Sharma *et al* (2015), Akula *et al* (2016), Ejigu *et al* (2017) and Singh *et al* (2017) showed that non-additive gene effect was important in the inheritance of maize grain yield and days to 50% silking traits.

Classifying maize inbred lines into heterotic groups is the initial step in maize breeding programs which would provide maximum exploitation of heterosis *via* determination the relationship existing among the different inbred lines. Numerous studies on classifying inbred lines into heterotic groups have been reported by Vasal *et al* (1992), Melchinger (1999), Menkir *et al* (2004), Fan *et al* (2009), Legesse *et al* (2009), Mosa *et al* (2017) and Abd El-Aty *et al* (2018). This study was conducted to estimate the general (GCA) and Specific (SCA) combining ability effects of the new white and yellow maize inbred lines for grain yield and days to 50% silking traits and to classify the new inbred lines into different heterotic groups for future use in the breeding program.

MATERIALS AND METHODS

The materials used in this study were 34 new maize inbred lines derived from the S_5 generation developed at Sakha Agricultural Research Station (SARS). These inbred lines were placed in two sets, the first set (Set-1) consisted of 17 new white inbred lines viz., Sk5001/43, Sk5001/44, Sk5001/45, LSk5001/46, Sk5001/47, Sk5002/48, Sk5002/49, Sk5002/52, Sk5002/53, Sk5002/54, Sk5003/55, Sk5003/56, Sk5003/57, Sk5004/58, Sk5003/59, Sk5003/60 and Sk5003/61 coded numbered as L_1, L_2, L_3, L_4, L_5, L_6, L_7, L_8, L_9, L_{10}, L_{11}, L_{12}, L_{13}, L_{14}, L_{15}, L_{16} and $L_{17,}$ respectively. These inbred lines were crossed with two genetically diverse testers (inbred line Sk5 and single cross131) in the 2015 season at SARS. The resulting 34 crosses along with the two single crosses SC128, SC10 and the two three-way crosses TWC 321 and TWC324 as commercial check hybrids conducted at two locations (Sakha and Mallawi ARS) during 2016 summer season.

The second set (Set-2) included 17 new yellow maize inbred lines viz., Sk5005/64, Sk5005/65, Sk5005/66, Sk5005/69, Sk5005/70, Sk5005/71, Sk5005/72, Sk5005/73, Sk5005/74, Sk5005/75, Sk5008/76, Sk5011/77, Sk5011/78, HP704/80, CLQRCYQ/81 and CLYQ/85 coded numbered as L_{18}, L_{19}, L_{20}, L_{21}, L_{22}, L_{23}, L_{24}, L_{25}, L_{26}, L_{27}, L_{28}, L_{29}, L_{30}, L_{31}, L_{32}, L_{33} and $L_{34,}$ respectively. These inbred lines were crossed with two genetically diverse testers (inbred line Sk4 and SC177) in the 2015 season. The resulting 34 crosses along with SC162, SC168, TWC360 and TWC368 as commercial check hybrids were evaluated in the 2016 season at two locations (Sakha and Sids ARS).

All experiments were installed under a randomized complete block design with four replications. The plot consisted of one row 6m long,

spaced apart 0.80m between rows and 0.24m between hills. Trials were hand planted with two seeds per hill, and then thinned to one plant per hill after three weeks of planting, giving 25 plants per row, to get a total plant density of 50000 plant/ha (21000 plant/fed). The experiment was managed using recommended agronomic practices (planting, irrigation, thinning, fertilization, weeding and insect controls) from sowing to maturity. Data were recorded on two different traits, i.e. days to 50% silking (DS) and grain yield (GY). In each plot, days to silking were recorded as the number of days from planting to when 50% of the plants had silks emerged. Each plot was harvested and weight of the harvested ears (kg/plot), shelling percentage and grain moisture were recorded; these data were used to calculate the grain yield in ton/hectare (t/ha) adjusted at 15.5% grain moisture content. Combined analysis of variance across two locations in each set was performed when homogeneity of error variances were detected according to Snedecor and Cochran (1967). Combining ability effects were computed according to line × tester analysis for two traits when the mean squares due to crosses were significant based on the method described by Kempthorne (1957). Groupings of inbred lines were conducting based on heterotic group specific and general combining ability (HSGCA) method according to Fan *et al* (2009).

RESULTS AND DISCUSSION

Combined analysis of variance for days to 50% silking and grain yield t ha^{-1} of set-1 and set-2 across two locations is presented in Table (l). Highly significant differences were detected between two locations (Loc) for the two traits of the two sets, indicating that these traits are highly influenced by environmental factors under the two locations. Also, mean squares due to genotypes (G) and G×Loc interaction were significant or highly significant for SD and GY of the two sets, except for G×Loc of SD in set-1.

Table 1. Combined analysis of variance for days to 50% silking and grain yield (t ha^{-1}) for Set-1 and Set-2 across two locations.

SOV	df	Set-1		Set-2	
		Days to 50% silking	Grain yield (t ha^{-1})	Days to 50% silking	Grain yield (t ha^{-1})
Locations (Loc.)	1	1950.33**	465.87**	10586.96**	492.25**
Rep/Loc.	6	7.408	1.99	21.23	4.76
Genotypes (G)	37	17.29**	4.33**	23.99**	11.67**
G x Loc.	37	3.33	3.20**	3.10*	5.13**
Error	222	2.66	0.802	2.18	1.17

*, ** Significant at the 0.05 and 0.01 levels of probability, respectively.

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Line × tester analysis for SD and GY of the two sets across two locations is presented in Table (2). Mean squares due to line (L) and L × Loc were significant or highly significant for the two traits of the two sets. Meanwhile, mean squares due to testers (T) were significant or highly significant for both SD in set-1 and GY in set-2. Also, the mean squares due to L × T and L × T × Loc interaction were significant or highly significant for the two traits in the two sets, except for L × T × Loc of both SD and GY in set-1. Significant differences among lines and among testers indicate greater diversity between parental lines and between testers. While, significance of L×T interaction variance mean that the inbred lines performed differently in their respective crosses depending on the type of tester used for these traits. The same results were obtained by numerous investigators among of them Hosana *et al* (2015), Akula *et al* (2016), Ejigu *et al* (2017), Singh *et al* (2017) and Abd El-Aty *et al* (2018).

Table 2. Line × tester analysis for days to 50% silking and grain yield (t ha-1) for Set-1 and Set-2 across two locations.

S.O.V	df	Set-1		Set-2	
		Day Days to 50% silking	Grain yield (t ha^{-1})	Days to 50% silking	Grain yield (t ha^{-1})
Lines (L)	16	19.238**	6.994**	37.24**	8.52**
Testers (T)	1	11.121*	0.791	4.504	127.03**
L x T	16	4.20*	2.292**	7.761**	3.43**
L x Loc.	16	5.407*	4.634**	4.232*	6.34**
T x Loc.	1	1.622	0.444	0.032	1.98
L x T x Loc.	16	1.512	1.012	4.26*	3.42**
Error	198	2.56	0.76	2.12	1.06

*, ** Significant at the 0.05 and 0.01 levels of probability, respectively.

Mean performances of inbred lines in their F_1 crosses and four checks for days to 50% silking and grain yield (t ha^{-1}) for set-1 and set-2 across two locations are presented in Table (3). In set-1 for days to 50% silking, the single crosses of tester inbred line Sk5 with 17 white inbred lines ranged from 64.12 days for L5×Sk5 to 68.5 days for L13×Sk5. Two single crosses (L5×Sk5 and L6 ×Sk5) were significantly early compared to two checks SC10 and SC128. Meanwhile, the three way-crosses of tester SC131 with 17 white inbred lines ranged from 63.75 days for L6×SC131to 69 days for L13×SC131.Sixteen three-way crosses were significantly early compared to the two checks TWC321and TWC324; the best crosses from them were L6×SC131, L7×SC131and L11×SC131.

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For grain yield in set-1, single crosses ranged from 9.3 t ha^{-1} for L6×Sk5 to 11.87 t ha^{-1} for L17×Sk5. Five single crosses (L17×Sk5, L3×Sk5, L12×Sk5, L2×Sk5 and L14×Sk5) significantly outyielded the check SC10. The three-way crosses ranged from 9.18 t ha^{-1} for L7×SC131 to 11.64 t ha^{-1} for L2×SC131. The five three-way crosses (L2×SC131, L3×SC131, L17×SC131, L4×SC131and L15×SC131) increased significantly over the check TWC321.These promising single and three-way crosses are suitable and will be tested in yield trails for further evaluation to use them in future maize programs to improve grain yield and earliness.

Table 3. Mean performance of inbred lines in their crosses and four checks for days to 50% silking (SD) and grain yield t ha^{-1} (GY) for each of Set-1 and Set-2 across two locations.

	Set-1				Set-2			
Inbred line	SD		GY		Inbred line	SD		GY	
	Sk-5	SC131	Sk-5	SC131		Sk-4	SC177	Sk-4	SC177
L1	66.12	67.50	10.38	10.02	L18	65.87	64.37	12.29	10.46
L2	67.00	66.75	11.14	11.64	L19	68.12	66.50	11.06	9.90
L3	65.75	67.75	11.82	11.34	L20	66.00	65.00	10.88	10.59
L4	66.00	65.37	9.96	11.25	L21	64.87	65.25	11.54	10.56
L5	64.12	65.87	9.76	10.45	L22	64.25	65.25	11.69	10.05
L6	64.25	63.75	9.30	10.06	L23	65.12	64.87	11.49	10.03
L7	64.62	64.75	9.94	9.18	L24	65.62	64.12	11.12	9.26
L8	66.12	66.25	9.84	10.16	L25	64.12	63.62	11.48	11.42
L9	65.37	67.12	10.27	9.59	L26	65.37	63.37	11.59	10.76
L10	66.25	67.12	10.09	9.68	L27	67.87	67.37	11.72	10.57
L11	66.62	64.87	10.76	10.82	L28	67.37	65.62	9.71	9.44
L12	66.37	67.00	11.63	9.78	L29	64.62	62.50	9.89	9.38
L13	68.50	69.00	9.94	9.55	L30	64.25	65.00	12.13	9.36
L14	64.87	66.00	11.04	10.32	L31	64.12	65.25	10.97	9.40
L15	65.75	65.87	10.91	11.25	L32	64.50	66.37	12.46	9.15
L16	65.87	65.12	10.49	10.92	L33	67.87	69.25	10.10	7.78
L17	67.00	67.37	11.87	11.29	L34	67.50	69.37	10.94	8.71
SC10	69.00	-	10.14	-	SC 162	69.50	-	7.76	-
SC128	66.00	-	11.43	-	SC 168	67.25	-	10.82	-
TWC321	-	69.87	-	10.15	TWC 360	-	67.62	-	10.07
TWC324	-	69.62	-	10.98	TWC 353	-	68.12	-	7.83
LSD 0.05	1.56		0. 87		LSD 0.05	1.44		1.06	

In set-2 for days to 50% silking, all yellow single crosses decreased significantly toward earliness when compared to the check SC162. Furthermore, 10 out of 17 single crosses, i.e. L21×Sk4, L22×Sk4, L23×Sk4, L24×Sk4, L25×Sk4, L26×Sk4, L29 ×Sk4, L30×Sk4, L31×Sk4, and L32×Sk4 decreased significantly toward earliness from the earlier check SC168. Meanwhile, 12 three-way crosses were earlier than the two checks TWC353 and TWC360. The best crosses from them were L29×SC177, L26×SC177 and L25×SC177. For GY in set-2, the single crosses ranged from 9.71 t ha^{-1} for L28×Sk5 to 12.46 t ha^{-1} for L32×Sk4. Three single crosses, (L18×Sk4, L30×Sk4 and L32×Sk4) significantly outyielded the two checks SC162 and SC168. Meanwhile, the three-way crosses ranged from 7.78 t ha^{-1} for L33×SC177 to 110.42 t ha^{-1} for L25×SC177. All three-way crosses significantly outyielded the check TWC353 and one from them (L25×SC177) significantly outyielded the check TWC360.These promising single and three-way crosses which had high yielding ability would be fruitful and suitable to use in future maize breeding programs.

General combining ability effects of 17 inbred lines for each of Set-1 and Set-2 for days to 50% silking and grain yield across two locations are presented in Table (4). The results revealed that, three white inbred lines (L5, L6 and L7) in set-1 and 7 yellow inbred lines (L22, L24, L25, L26, L29, L30 and L31) in set-2 exhibited negative and significant estimates of GCA effects for SD, indicating that these inbred lines had favorable allele frequency for early maturity. While, four white inbred lines (L2, L3, L15 and L17) in set-1and   five yellow inbred lines (L18, L22, L25, L26, and L27) in set-2 exhibited positive and significant estimates of GCA effects for GY which could be utilized in maize grain yield improvement program. From the previous results, it could be concluded that the yellow inbred lines L22, L25 and L26 had good alleles and were the best combiners for earliness and yielding ability simultaneously. These inbred lines are very important and could be used in future maize breeding programs for the introgression of genes of early maturity with high yielding ability. The tester Sk5 in set-1 showed desirable GCA effects for SD while, inbred line Sk4 as tester in set-2 exhibited positive and significant estimates of GCA effects for GY trait. The current results are in general agreement with the findings of many researchers (Meseka and Ishaaq 2012, Dar *et al* 2017, Hundera 2017 and Abd El-Aty *et al* 2018), who reported significant positive and negative GCA effects for GY and SD, respectively.

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Table 4. General combining ability effects of 17 inbred lines for days to 50% silking (SD) and grain yield t ha^{-1} (GY) for Set-1 and Set-2 across two locations.

Set-1			Set-2		
Inbred line	**SD**	**GY**	**Inbred line**	**SD**	**GY**
L1	0.691	-0.284	L18	-0.481	0.816*
L2	0.753*	0.906*	L19	1.765*	-0.075
L3	0.629	1.099*	L20	-0.106	0.182
L4	-0.434	0.121	L21	-0.544	0.494
L5	-1.121*	-0.379	L22	-0.856*	0.814*
L6	-2.121*	-0.800*	L23	-0.606	0.205
L7	-1.434*	-0.923*	L24	-0.731*	-0.366
L8	0.066	-0.486*	L25	-1.731*	0.897*
L9	0.129	-0.552*	L26	-1.231*	0.621*
L10	0.566	-0.597*	L27	2.018*	0.588*
L11	-0.371	0.308	L28	0.893*	-0.983*
L12	0.566	0.218	L29	-2.044*	-0.920*
L13	2.629*	-0.739*	L30	-0.951*	0.194
L14	-0.684	0.194	L31	-0.919*	-0.369
L15	-0.309	0.599*	L32	-0.169	0.249
L16	-0.621	0.220	L33	2.955*	-1.619*
L17	1.066*	1.096*	L34	2.83*	-0.729*
Tester SK 5	-0.26*	0.053	Tester SK 4	0.128	0.683*
Tester SC 131	0.26*	-0.053	Tester SC177	-0.128	-0.683*
LSD g_i (L) 0.05	0.784	0.430	LSD g_i (L) 0.05	0.710	0.504
LSD g_i-g_j (L) 0.05	1.109	0.604	LSD g_i-g_j (L) 0.05	1.009	0.713
LSD g_i (T) 0.05	0.260	0.141	LSD g_i (T) 0.05	0.24	0.173
LSD g_i-g_j (T) 0.05	0.380	0.207	LSD g_i-g_j (T) 0.05	0.346	0.245

* Significant at the 0.05 level of probability.

Specific combining ability effects of 34 top crosses for each of set-1 and set-2 across two locations are presented in Table (5). In set-1 the best crosses of SCA effects were L11×SC131 for earliness and L4×SC131 and L12×Sk5 for grain yield. According to set-2, the two yellow single crosses L32×Sk4 and L34×Sk4 possessed negative and significant SCA effects toward earliness while, only one single cross L32×Sk4 expressed positive and significant SCA effects for grain yield. Hence, such cross combinations could effectively be exploited in hybrid breeding program in maize research for early maturity and for the improvement maize grain yield. This finding

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agrees with Meseka and Ishaaq (2012), Hundera (2017), Larièpe *et al* (2017), Dar *et al* (2017) and Abd El-Aty *et al* (2018) who found positive and negative SCA effects for GY and SD, respectively.

Table 5. Specific combining ability effects of 34 top crosses for days to 50% silking (SD) and grain yield t ha^{-1} (GY) for each of set-1 and set-2 across two locations.

	Set-1				Set-2				
Inbred line	**SD**		**GY**		**Inbred line**	**SD**		**GY**	
	Sk5	**SC131**	**Sk5**	**SC131**		**Sk4**	**SC177**	**Sk4**	**SC177**
L1	-0.485	0.485	0.130	-0.130	**L18**	0.621	-0.621	0.231	-0.231
L2	0.327	-0.327	-0.307	0.307	**L19**	0.683	-0.683	-0.104	0.104
L3	-0.798	0.798	0.187	-0.187	**L20**	0.371	-0.371	-0.537	0.537
L4	0.515	-0.515	-0.696*	0.696*	**L21**	-0.316	0.316	-0.196	0.196
L5	-0.673	0.673	-0.400	0.400	**L22**	-0.628	0.628	-0.365	0.365
L6	0.452	-0.452	-0.433	0.433	**L23**	-0.003	0.003	0.044	-0.044
L7	0.139	-0.139	0.329	-0.329	**L24**	0.621	-0.621	0.247	-0.247
L8	0.139	-0.139	-0.215	0.215	**L25**	0.121	-0.121	-0.650	0.650
L9	-0.673	0.673	0.281	-0.281	**L26**	0.871	-0.871	-0.270	0.270
L10	-0.235	0.235	0.154	-0.154	**L27**	0.121	-0.121	-0.106	0.106
L11	1.100*	-1.100*	-0.084	0.084	**L28**	0.746	-0.746	-0.547	0.547
L12	-0.110	0.110	0.869*	-0.869*	**L29**	0.933	-0.933	-0.424	0.424
L13	-0.047	0.047	0.144	-0.144	**L30**	-0.503	0.503	0.700	-0.700
L14	-0.360	0.360	0.305	-0.305	**L31**	-0.691	0.691	0.100	-0.100
L15	0.139	-0.139	-0.223	0.223	**L32**	-1.066*	1.066*	0.968*	-0.968*
L16	0.577	-0.577	-0.270	0.270	**L33**	-0.816	0.816	0.476	-0.476
L17	0.14	-0.14	0.231	-0.231	**L34**	-1.066*	1.066*	0.434	-0.434
LSD S$_{ij}$ 0.05	1.100		0.604		**LSD S$_{ij}$**	1.00		0.713	
LSD S$_{ij}$-S$_{kl}$ 0.05	1.568		0.854		**LSD S$_{ij}$-S$_{kl}$**	1.427		1.009	

* Significant at the 0.05 level of probability.

Estimates of general and specific combining ability variances (additive and non additive gene action) for SD and GY in the two sets are presented Table (6). Silking date in the two sets was controlled mainly by non- additive gene action. Meanwhile GY trait was controlled mainly by non-additive gene action in set-1 and additive gene action in set-2. These results are in agreement with those obtained by many investigators among of them Amiruzzaman *et al* (2013), Verma *et al* (2014), Akula *et al* (2016), Ejigu *et al* (2017) and Singh *et al* (2017) who reported that non-additive gene action played an important role in the inheritance of grain yield and days to 50% silking. Meanwhile, Ojo *et al* (2007), Musila *et al* (2010), Wegory *et al* (2013) and Hosana *et al* (2015) suggested that additive gene action represented main role in the behavior of grain yield trait.

Table 6. Estimates of general (K^2GCA) and specific (K^2SCA) combining ability effects for days to 50% silking (SD) and grain yield t ha^{-1} (GY) in Set-1 and Set-2 across two locations.

Genetic component	Set-1		Set-2	
	SD	GY	SD	GY
K^2GCA	0.113	0.017	0.246	0.837
K^2SCA	0.324	0.16	0.437	0.001

Estimates of heterotic groups based on specific and general combining ability (HSGCA) effects for days to 50% silking and grain yield in two sets are presented in Table (7). Fan *et al* (2009) proposed that method of heterotic grouping based on specific and general combining ability effects (HSGCA). The inbred lines were divided into groups as follows: Step-1, placed all tested inbred lines in the same heterotic group as their tester. Step-2, kept the inbred lines with heterotic group where its HGCA effects had the smallest value (or largest negative value) and removed it from other heterotic group. Step-3, if the inbred line had positive HSGCA effects with all representative testers, it will be cautious to assign that line to any heterotic group because the line might belong to a heterotic group different from the testers used in the investigation.

In set-1, for days to 50% silking group-1 (Tester SK5) included inbred lines L3, L5, L9 and L14 while group-2 (tester SC131) included inbred lines L4, L6, L7, L8, L11, L15 and L16. However, the method was not able to classify the inbred lines L1, L2, L10, L12, L13 and L17. For grain yield, group-1(tester SK5) included inbred lines L4, L5, L6, L8, L13 and L16 while group-2 (tester SC131) included L1, L7, L9, L10, L12 and L14. However, the method was not able to classify the inbred lines L2, L3, L11, L15 and L17.In set-2, for days to 50% silking group-1 (tester SK4) contained the inbred lines L21, L22, L23, L30, L31 and L32, meanwhile group-2 (tester SC177) contained the inbred lines L18, L20, L24, L25, L26 and L29. while, inbred lines L19, L27, L28, L33 and L34 were not classified. For grain yield, group-1(tester SK4) included inbred lines L19, L20, L28 and L29 while group-2 (tester SC177) included L24, L30, L31, L32, L33 and L34. Meanwhile, the method was unable to categorize the inbred lines L18, L21, L22, L23, L25, L26 and L27.

Table 7. Estimates of heterotic groups using specific and general combining ability (HSGCA) method for days to 50% silking and grain yield t ha^{-1} in Set-1 and Set-2 across locations.

Inbred line	SD		GY		Inbred line	SD		GY	
	Sk5	SC131	Sk5	SC131		Sk4	SC177	Sk4	SC177
L1	0.206	1.176	-0.154	-0.414≠	L18	0.14	-1.102≠	1.047	0.585
L2	1.08	0.426	0.599	1.213	L19	2.448	1.082	-0.179≠	0.029
L3	-0.169≠	1.427	1.286	0.912	L20	0.265	-0.477≠	-0.355≠	0.719
L4	0.081	-0.949≠	-0.575≠	0.817	L21	-0.86≠	-0.228	0.298	0.69
L5	-1.794≠	-0.448	-0.779≠	0.021	L22	-1.484≠	-0.228	0.449	1.179
L6	-1.669	-2.573≠	-1.233≠	-0.367	L23	-0.609≠	-0.603	0.249	0.161
L7	-1.295	-1.573≠	-0.594	-1.252≠	L24	-0.11	-1.352≠	-0.119	-0.613≠
L8	0.205	-0.073≠	-0.701≠	-0.271	L25	-1.61	-1.852≠	0.247	1.547
L9	-0.544≠	0.802	-0.271	-0.833≠	L26	-0.36	-2.102≠	0.351	0.891
L10	0.331	0.801	-0.443	-0.751≠	L27	2.139	1.897	0.482	0.694
L11	0.729	-1.471≠	0.224	0.392	L28	1.639	0.147	-1.53≠	-0.436
L12	0.456	0.676	1.087	-0.651≠	L29	-1.111	-2.977≠	-1.344≠	-0.496
L13	2.582	2.676	-0.883≠	-0.595	L30	-1.454≠	-0.448	0.894	-0.506≠
L14	-1.044≠	-0.324	0.499	-0.111≠	L31	-1.61≠	-0.228	-0.269	-0.469≠
L15	-0.17	-0.448≠	0.376	0.822	L32	-1.235≠	0.897	1.217	-0.719≠
L16	-0.044	-1.198≠	-0.050≠	0.490	L33	2.139	3.771	-1.143	-2.095≠
L17	1.206	0.926	1.327	0.865	L34	1.764	3.896	-0.295	-1.163≠

≠ means that this inbred line belongs to tester group.

Such heterotic grouping method could be recommended for breeding programs in selecting the best parents for making crosses. Lee (1995) and Mosa *et al* (2017) stated that the heterotic group is a collection of closely related inbred lines which tend to result in vigorous hybrids when crossed with lines from a different heterotic group, but not when crossed to other lines of the same heterotic group. Also, Vasal *et al* (1992), Melchinger, (1999), Menkir *et al* (2004), Legesse *et al* (2009) and Abd El-Aty *et al* (2018) classified inbred lines into heterotic groups for grain yield and reported that the classification of inbred lines into heterotic groups facilitates the exploitation of heterosis in maize, which can contribute to hybrid performance.

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القدرة على التالف والتجميع الهجينى لمجموعتين من سلالات الذرة الشامية الجديدة

عاصم عبده مطاوع، حاتم الحمادى موسى، محمد عطوة جمال الدين خليل، محمد موسى درويش و هانى عبدالله عبدالمجيد محمد

مركز البحوث الزراعية – معهد بحوث المحاصيل الحقلية – قسم الذرة الشامية

تم تكوين مجموعتين من الذرة الشامية البيضاء والصفراء بتهجين ١٧ سلالة جديدة مرباة داخليا مع اثنين من الكشافات لكل مجموعة بنظام السلالة×الكشاف وذلك بمحطة البحوث الزراعية بسخا موسم ٢٠١٥. تم تقييم الـ٣٤ هجين الناتجة مع أربعة هجن مقارنة لكل مجموعة موسم ٢٠١٦ تحت موقعى سخا وملوى للمجموعة الأولى وسخا وسدس للمجموعة الثانية. تم قياس صفة عدد الأيام اللازمة حتى خروج ٥٠% من حرائر النورات المؤنثة ومحصول الحبوب بالطن/هكتار. – وجدت تباينات معنوية راجعة للسلالات وتفاعلها مع المواقع لكلا الصفتين فى المجموعتين. كما كانت التباينات الراجعة للكشافات معنوية لصفة عدد الأيام اللازمة حتى خروج ٥٠% من حرائر النورات المؤنثة فى المجموعة الأولى وصفة محصول الحبوب للمجموعة الثانية. بينما كانت التباينات الراجعة لتفاعل السلالة×الكشاف وكذلك تفاعل السلالة×الكشاف×المواقع معنوية لكل الصفات فى كلا المجموعتين فيما عدا تفاعل السلالة×الكشاف× المواقع لكلا الصفتين فى المجموعة الأولى. أظهرت أربعة سلالات بيضاء وهى السلالة ٢، ٣، ١٥، ١٧ فى المجموعة الأولى وسبعة سلالات صفراء وهى ١٨، ٢٢، ٢٥، ٢٦، ٢٧ قيم موجبه ومعنوية لتأثيرات القدرة العامة على التالف لصفة المحصول. كما أظهرت الهجن الفردية (السلالة ١٢×السلالة سخا٥) فى المجموعة الأولى و (السلالة ٣٢×السلالة سخا٤) فى المجموعة الثانية قيم مرغوبة لتأثيرات القدرة الخاصة على التآلف لصفتى عدد الأيام اللازمة حتى خروج ٥٠% من حرائر النورات المؤنثة والمحصول فى اتجاه التبكير والقدرة المحصولية العالية. لعب الفعل الجينى غير المضيف الدور الأهم والرئيسى فى وراثة صفة عدد الأيام اللازمة حتى خروج ٥٠% من حرائر النورات المؤنثة فى كلتا المجموعتين . بينما كان للفعل المضيف الدور الأهم فى وراثة صفة المحصول فى المجموعة الثانية وغير المضيف فى المجموعة الأولى. تم تقسيم السلالات فى كل مجموعة لصفة المحصول على أساس طريقة HSGCA إلى مجموعتين هجينيتين كما يلي :– فى Set-1 تضم المجموعة الهجينية الأولى (سخا٥) السلالات ٤، ٥، ٦، ٨، ١٣، ١٦. بينما تضم المجموعة الهجينية الثانية (هـ.ف١٣١) السلالات ١، ٧، ٩، ١٠، ١٢٣، ١٤. بينما فى Set-2 تضم المجموعة الهجينية الأولى (سخا٤) السلالات ١٩، ٢٠، ٢٨، ٢٩. بينما تضم المجموعة الهجينية الثانية (هـ.ف١٧٧) السلالات ٢٤، ٣٠، ٣١، ٣٢، ٣٣، ٣٤. وهذه المجاميع الهجينية من المؤمل أن تستخدم فى برنامج التربية لانتخاب أفضل الإباء لتكوين هجن جديدة ذات قوة هجين عالية.