EVALUATION AND CLASSIFICATION OF TWO SETS OF YELLOW MAIZE INBRED LINES BY LINE × TESTER ANALYSIS

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ABSTRACT

Two sets of yellow maize crosses were constructed by crossing 18 new inbred lines with two testers for each set using line × tester method at Sakha Agricultural Research Station in 2017 growing season. The resulting 36 F_1 crosses in addition to three commercial check hybrids for each set were evaluated in 2018 at two locations (Sakha and Ismailia) for set-1 and at two locations (Sakha and Sids) for set-2. Days to 50% silking (DS) and grain yield ard/fed (GY) were recorded. The three inbred lines L-7, L-10, L-13 in Set-1 and L-32 in Set-2 were the best combiners for earliness and yielding ability simultaneously. Therefore, these lines can be utilized as promising inbred lines in hybridization programs to develop high yielding and early maturing yellow maize hybrids in the same time. The best hybrid for specific combining ability was L-7×Sk-1 for days to 50% silking and L-10×Sk-2 for grain yield in Set-1 and L-27×Gz-658 for days to 50% silking and L-29×Gz-658 for grain yield in Set-2. Also hybrid L-13×Sk-1 in Set-1 and L-23×Sk-11 in Set-2 outyielded and matured earlier than the best check. Days to 50% silking in the two sets was controlled mainly by additive gene action. Meanwhile, grain yield was controlled by additive gene effects in set-1 and non-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(Sk-1) included L-2, L-3, L-4, L-5, L-8, L-9, L-10, L-14 and L15. While, group2 (Sk-2) included L-1, L-11, L-16 and L-17. In set-2, group1 (Sk-11) included L-20, L-22, L-29, L-30 and L34. Meanwhile, in set-2, group-2 (Gz-658) included L-19, L-25, L-26, L-27, L28 and L-33. These groups could be used in breeding programs for selecting the best parents in developing new crosses.
Key word: *Line × tester, Combining ability, Additive and non-additive gene effects.*

INTRODUCTION

The procedure of top crosses suggested by Davis (1927) was used to estimate combining ability. The concept of general combining ability (GCA) and specific combining ability (SCA) is useful for characterizing the inbred lines in its crosses as defined by Sprague and Tatum (1942).

Combining ability estimates of inbred lines are very important for maize improvement not only in choosing parents and crosses but also in illustrating the relation between additive and non-additive portions of the genetic effects in the available germplasm. Line×tester analysis has widely been used for evaluation of 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). The information on the type of gene effects is very important for the breeder in making decisions for the collocation resources and expected response to selection for different traits. There is no agreement

among researchers on the mode of gene effects controlling maize yield or its related characters. Vacaro *et al* (2002), Musila *et al* (2010), Wegary *et al* (2013), Badua-Aprakua *et al* (2015) and Hosana *et al* (2015) reported that additive gene effects were more important for grain yield and days to 50% silking. Meanwhile, Dar *et al* (2007), Amiruzzaman *et al* (2013), Verma *et al* (2014), Sharma *et al* (2015), Akula *et al* (2016), Ejigu *et al* (2017), Singh *et al* (2017) and Motawei *et al* (2019) showed that non-additive gene effects were predominant in the inheritance of maize grain yield and days to 50% silking traits.

Heterotic groups and patterns are extremely important in hybrid breeding programs (Melchinger and Gumber 1998). Classifying maize inbred lines into heterotic groups is the initial step in maize breeding programs which would provide maximum exploitation of heterosis *via* determination of 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 Motawei *et al* (2019).

The objectives of this investigation were to estimate both general (GCA) and specific (SCA) combining ability effects of some yellow maize inbred lines and their interactions with locations, identify the superior hybrids in grain yield and earliness and to classify the new inbred lines into different heterotic groups for future use in breeding programs.

MATERIALS AND METHODS

The materials used in the study were 36 new yellow maize inbred lines which were developed at Sakha Agricultural Research Station. Names and coded numbers of yellow inbred lines are presented in Table 1. These inbred lines were placed in two sets; the first set (set-1) included 18 new yellow inbred lines were crossed with two genetically diverse testers (inbred lines; Sk-1 and Sk-2). Also the second set (set-2) consisted of 18 new yellow maize inbred lines were crossed with two genetically diverse testers (inbred lines; Sk-11 and Gz-658) in 2017 season at Sakha Agricultural Research Station. During 2018 summer season the resulting 36 crosses in each set along with the three single crosses SC-168, SC-178 and SC-3444 as commercial check hybrids were evaluated at two locations (Sakha and Ismailia) and (Sakha and Sids) for set-1 and set-2, respectively.

Table 1. Name and code numbers of yellow inbred lines used in the present study for Set-1 and Set-2.

Set-1		Set-2	
Inbred line name	Code number	Inbred line name	Code number
Sk5001/42	L-1	Sk5001/81	L-19
Sk5002/43	L-2	Sk5003/82	L-20
Sk5003/44	L-3	Sk5025/83	L-21
Sk5004/45	L-4	Sk5025/84	L-22
Sk5004/46	L-5	Sk5025/85	L-23
Sk5006/47	L-6	Sk5025/86	L-24
Sk5008/48	L-7	Sk5006/87	L-25
Sk5010/49	L-8	Sk5008/88	L-26
Sk5012/50	L-9	Sk5011/89	L-27
Sk5019/51	L-10	Sk5013/90	L-28
Sk5021/53	L-11	Sk5019/91	L-29
Sk5022/54	L-12	Sk5020/92	L-30
Sk5023/55	L-13	Sk5021/93	L-31
Sk5024/56	L-14	Sk5021/94	L-32
Sk5004/57	L-15	Sk5023/96	L-33
Sk5004/58	L-16	Sk5024/97	L-34
Sk5004/59	L-17	Sk5025/98	L-35
Sk5005/60	L-18	Sk5025/99	L-36

All experiments were executed using a Randomized Complete Block Design with four replications. The plot consisted of one row 6 m long, spaced apart 0.80 m between rows and 0.25 m between hills to secure 25000 plants/feddan (one feddan=4200m^2). All cultural practices were carried out as recommended. Data were recorded on two different traits, *i.e.* number of days to 50% silking and grain yield in ardab/feddan (ard/fed) adjusted to 15.5% grain moisture content. Combined analysis of variance across two locations in each set was performed when homogeneity test was calculated 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). Heterotic groups using specific and general combining ability (HSGCA) were made according to Fan *et al* (2009).

RESULTS AND DISCUSSION

Combined analysis of variance for days to 50% silking and grain yield (ard/fed) of set-1 and set-2 across the two locations is presented in Table (2). Highly significant differences were detected between two locations (Loc.) for the two traits of the two sets, indicating that these traits are highly affected by environmental conditions prevailed in testing locations. Mean squares due to crosses (C) were highly significant for the two studied traits in the two sets. Also, mean squares due to C × Loc interaction were significant or highly significant for days to 50% silking and grain yield in the two sets.

Table 2. Combined analysis of variance for days to 50% silking and grain yield for Set-1 and Set-2 across the two locations.

SOV	df	Set-1		Set-2	
		Days to 50% silking	Grain yield	Days to 50% silking	Grain yield
Locations (Loc.)	1	106.17**	1170.48**	1362.51**	2853.85**
Rep/Loc.	6	5.29	24.17	86.99	62.30
Crosses (C)	38	17.24**	126.37**	33.51**	88.38**
C × Loc.	38	2.70**	59.97**	3.83*	34.96**
Error	228 ≠	0.66	12.54	2.46	11.83

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

Line × tester analysis for days to 50% silking and grain yield of the two sets across the two locations is presented in Table (3). Mean squares due to lines (L), testers (T), L × T interaction were highly significant for the two traits of the two sets, indicating the presence of wide diversity among lines and among testers for these traits and that lines differed in their performance when crossed with two testers. Mean squares due to L × Loc and L × T × Loc interaction were highly significant for days to 50% silking and grain yield in the two sets, except L × T × Loc for days to 50% silking in Set-2. Meanwhile, mean squares due to T × Loc were significant or highly significant for grain yield in the two sets. These results are in agreement with those reported by Hosana *et al* (2015), Akula *et al* (2016), Ejigu *et al* (2017), Singh *et al* (2017) and Motawei *et al* (2019).

68

Table 3. Combined line × tester analysis of variance for days to 50% silking and grain yield for Set-1 and Set-2 across the two locations.

S.O.V	df	Set-1		Set-2	
		Days to 50% silking	Grain yield	Days to 50% silking	Grain yield
Lines (L)	17	28.80**	173.29**	42.43**	129.53**
Testers (T)	1	28.13**	844.61**	148.78**	198.50**
L x T	17	2.57**	50.15**	7.13**	42.66**
L x Loc.	17	3.26**	55.24**	5.06**	29.11**
T x Loc.	1	0.68	361.81**	2.92	61.33*
L x T x Loc.	17	2.54**	47.99**	2.09	23.82*
Error	210	0.67	12.55	2.29	12.02

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

Mean performances of crosses as well as the three checks and superiority relative to the best check for days to 50% silking and grain yield for each of Set-1 and Set-2 across the two testing locations are presented in Table (4). In set-1 for days to 50% silking, crosses ranged from 58.8 days for L-8×Sk-2 to 63.5 days for L-6×Sk-1. Seventeen single crosses were significantly earlier than the earliest check SC-168 for days to 50% silking, the earliest crosses among them were L-8×Sk-2, L-10×Sk-2 and L-11×Sk-1. Meanwhile, crosses of Set-2 for days to 50% silking ranged from 56.5 days for L-27×Gz-658 to 63.1 days for L-21× Gz-658. Twenty single crosses were superior for earliness compared to the earliest check SC-168, the earliest crosses among them were L-20×Sk-11, L-26×Sk-11, L-27×Gz-658 and L-31×Sk-11.

For grain yield in set-1, crosses ranged from 30.2 ard/fed for L-8×Sk-1 and L-8×Sk-2 to 45.5 ard/fed for L-12×Sk-1. Three single crosses (L-12×Sk-1, L-13×Sk-1 and L-16×Sk-1) significantly outyielded the best check SC-3444. Meanwhile, yield of crosses of Set-2 ranged from 24.4 (ard/fed) for L-29×Sk-11 to 37.1 ard/fed for L-23×Sk-11. Three single crosses (L-23×Sk-11, L-35×Gz-658 and L-36×Gz-658) were not significantly superior to the best check SC-168.

Above results exhibited that hybrid: L-13×Sk-1 in Set-1 and L-23×Sk-11 in Set-2 were superior for grain yield and earliness. These hybrids could be considered as promising ones in the hybrid breeding programs and require further testing.

Table 4. Mean performance of crosses along with checks and superiority relative to best check for days to 50% silking (DS) and grain yield (GY) for Set-1 and Set-2 across the two locations.

Cross	Set-1				Cross	Set-2			
	Mean		Superiority			Mean		Superiority	
	DS	GY	DS	GY		DS	GY	DS	GY
L-1×Sk-1	61.4	40.3	-0.65	-2.89	L-19×Sk-11	59.4	29.5	-4.81**	-18.06**
L-1×Sk-2	59.8	34.1	-3.24**	-17.83**	L-19×Gz-658	62.0	27.5	-0.64	-23.61**
L-2×Sk-1	62.0	35.7	0.32	-13.98**	L-20×Sk-11	56.8	28.0	-8.97**	-22.22**
L-2×Sk-2	61.8	34.0	0.00	-18.07**	L-20×Gz-658	58.8	31.7	-5.77**	-12.22*
L-3×Sk-1	61.1	36.1	-1.13	-13.01**	L-21×Sk-11	62.1	34.4	-0.48	-4.44
L-3×Sk-2	61.8	35.2	0.00	-15.18**	L-21×Gz-658	63.1	35.5	1.12	-1.39
L-4×Sk-1	62.1	38.7	0.49	-6.75	L-22×Sk-11	61.4	29.3	-1.60	-18.61**
L-4×Sk-2	61.9	37.2	0.16	-10.36*	L-22×Gz-658	62.4	33.2	0.00	-7.78
L-5×Sk-1	60.0	37.9	-2.91**	-8.67*	L-23×Sk-11	59.3	37.1	-4.97**	3.06
L-5×Sk-2	59.6	37.1	-3.56**	-10.60*	L-23×Gz-658	62.1	35.1	-0.48	-2.50
L-6×Sk-1	63.5	39.9	2.75**	-3.86	L-24×Sk-11	61.0	31.6	-2.24*	-12.22*
L-6×Sk-2	62.3	36.9	0.81	-11.08**	L-24×Gz-658	61.5	35.3	-1.44	-1.94
L-7×Sk-1	59.3	42.4	-4.05**	2.17	L-25×Sk-11	57.8	31.8	-7.37**	-11.67*
L-7×Sk-2	60.4	39.1	-2.27**	-5.78	L-25×Gz-658	62.0	32.1	-0.64	-10.83*
L-8×Sk-1	59.4	30.2	-3.88**	-27.23**	L-26×Sk-11	56.9	30.5	-8.81**	-15.28**
L-8×Sk-2	58.8	30.2	-4.85**	-27.23**	L-26×Gz-658	57.8	28.9	-7.37**	-19.72**
L-9×Sk-1	63.0	37.9	1.94**	-8.67*	L-27×Sk-11	58.1	27.1	-6.89**	-24.72**
L-9×Sk-2	62.5	34.6	1.13	-16.63**	L-27×Gz-658	56.5	25.6	-9.46**	-28.89**
L-10×Sk-1	59.8	38.4	-3.24**	-7.47	L-28×Sk-11	58.9	32.0	-5.61**	-11.11*
L-10×Sk-2	58.9	41.4	-4.69**	-0.24	L-28×Gz-658	61.3	31.2	-1.76	-13.33**
L-11×Sk-1	58.9	40.4	-4.69**	-2.65	L-29×Sk-11	59.6	24.4	-4.49**	-32.22**
L-11×Sk-2	59.1	32.1	-4.37**	-22.65**	L-29×Gz-658	60.1	34.5	-3.69**	-4.17
L-12×Sk-1	63.3	45.5	2.43**	14.46**	L-30×Sk-11	57.3	29.2	-8.17**	-18.89**
L-12×Sk-2	61.3	38.2	-0.81	-7.95	L-30×Gz-658	59.3	32.6	-4.97**	-9.44
L-13×Sk-1	59.9	45.1	-3.07**	15.90**	L-31×Sk-11	56.6	31.4	-9.29**	-12.78**
L-13×Sk-2	59.6	41.7	-3.56**	0.48	L-31×Gz-658	58.6	33.7	-6.09**	-6.39
L-14×Sk-1	61.3	38.1	-0.81	-8.19	L-32×Sk-11	59.1	34.4	-5.29**	-4.44
L-14×Sk-2	60.3	36.7	-2.43**	-11.57**	L-32×Gz-658	58.6	35.8	-6.09**	-0.56
L-15×Sk-1	61.0	34.9	-1.29	-15.90**	L-33×Sk-11	59.9	30.6	-4.01**	-15.00**
L-15×Sk-2	59.4	35.9	-3.88**	-13.49**	L-33×Gz-658	60.9	28.7	-2.40	-20.28**
L-16×Sk-1	62.4	45.3	0.97	9.16*	L-34×Sk-11	59.0	28.7	-5.45**	-20.28**
L-16×Sk-2	61.8	36.1	0.00	-13.01**	L-34×Gz-658	59.9	35.5	-4.01**	-1.39
L-17×Sk-1	63.1	40.2	2.10**	-3.13	L-35×Sk-11	60.4	35.3	-3.21*	-1.94
L-17×Sk-2	62.5	33.6	1.13	-19.04**	L-35×Gz-658	62.8	36.8	0.64	2.22
L-18×Sk-1	62.1	41.7	0.49	0.48	L-36×Sk-11	59.9	35.0	-4.01**	-2.78
L-18×Sk-2	60.8	37.8	-1.62*	-8.92*	L-36×Gz-658	61.6	36.7	-1.28	1.94
Check SC-168	61.8	39.2	-	-	Check SC-168	62.4	36.0	-	-
Check SC-178	63.9	40.6	-	-	Check SC-178	63.6	32.9	-	-
Check SC-3444	62.9	41.5	-	-	Check SC-3444	63.9	35.8	-	-
LSD 0.05	0.79	3.47	-	-	LSD 0.05	1.53	3.37	-	-

General combining ability effects of 18 inbred lines and two testers in Set-1 and Set-2 for days to 50% silking and grain yield across the two locations are presented in Table (5).

Table 5. General combining ability effects of 18 inbred lines and two testers for days to 50% silking (DS) and grain yield (GY) for Set-1 and Set-2 across the two locations.

Set-1			Set-2		
Inbred line	DS	GY	Inbred line	DS	GY
L-1	-0.424*	-0.732	L-19	0.899*	-3.434**
L-2	0.889**	-3.113**	L-20	-2.038**	-2.134**
L-3	0.451*	-2.294**	L-21	2.837**	2.973**
L-4	1.014**	0.037	L-22	2.087**	-0.734
L-5	-1.174**	-0.419	L-23	0.899*	4.141**
L-6	1.889**	0.462	L-24	1.462**	1.491
L-7	-1.174**	2.806**	L-25	0.087	-0.021
L-8	-1.924**	-7.726**	L-26	-2.476**	-2.259**
L-9	1.764**	-1.713	L-27	-2.476**	-5.646**
L-10	-1.674**	1.999*	L-28	0.274	-0.371
L-11	-1.986**	-1.701	L-29	0.087	-2.490**
L-12	1.264**	4.906**	L-30	-1.538**	-1.096
L-13	-1.236**	6.956**	L-31	-2.163**	0.591
L-14	-0.236	-0.507	L-32	-0.913*	3.166**
L-15	-0.799**	-2.513**	L-33	0.587	-2.334**
L-16	1.076**	2.774**	L-34	-0.351	0.135
L-17	1.826**	-0.994	L-35	1.774**	4.098**
L-18	0.451*	1.774*	L-36	0.962*	3.923**
Tester Sk-1	0.313**	1.713**	Tester Sk-11	-0.719**	-0.830**
Tester Sk-2	-0.313**	-1.713**	Tester Gz-658	0.719**	0.830**
LSD g_i (L) 0.05	0.40	1.73	LSD g_i (L) 0.05	0.74	1.69
0.01	0.52	2.28	0.01	0.97	2.23
LSD gi-gj (L) 0.05	0.57	2.45	LSD gi-gj (L) 0.05	1.05	2.40
0.01	0.74	3.22	0.01	1.38	3.15
LSD g_i (T) 0.05	0.13	0.57	LSD g_i (T) 0.05	0.24	0.56
0.01	0.17	0.76	0.01	0.32	0.74
LSD gi-gj (T) 0.05	0.19	0.82	LSD gi-gj (T) 0.05	0.34	0.80
0.01	0.25	1.07	0.01	0.46	1.05

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

Results revealed that, eight yellow inbred lines (L-1, L-5, L-7, L-8, L-10, L-11, L-13 and L-15) in set-1 and five yellow inbred lines (L-20, L-26, L-27, L-30 and L-31) in set-2 exhibited negative and significant estimates of GCA effects for days to 50% silking, indicating that these

inbred lines have favorable alleles for earliness. While, six yellow inbred lines (L-7, L-10, L-12, L-13, L-16 and L-18) in set-1 and five yellow inbred lines (L-21, L-23, L-32, L-35, and L-36) in set-2 exhibited positive and significant estimates of GCA effects for grain yield. These inbred lines could be utilized in maize improvement program for both grain yield and earliness.

From the previous results, it could be concluded that inbred lines L-7, L-10, L-13 and L-32 are good combiners for earliness and yielding ability simultaneously. Therefore, these lines could be utilized as promising inbred lines in a hybridization programs to develop high yielding and early maturity yellow maize hybrids in the same time. In set-1, tester SK-2 showed desirable GCA effects for days to 50% silking while, tester inbred line Sk-1 exhibited positive and significant estimates of GCA effects for grain yield. In Set-2 tester Sk-11 showed desirable GCA effects for days to 50% silking and tester Gz-658 exhibited positive and significant estimates of GCA effects for grain yield. This results are in agreement with other investigations (Meseka and Ishaaq 2012, Dar *et al* 2017, Hundera 2017 and Motawei *et al* 2019), who reported significant positive GCA effects for grain yield and negative significant GCA for days to 50% silking.

Specific combining ability effects of 36 top crosses at each set across the two locations are presented in Table (6). In set-1 the best SCA effects were exhibited by the crosses L-3×Sk-1 and L-12×Sk-2 for earliness and L-10×Sk-2, L-11×SK-1, L-12×Sk-1 and L-16×Sk-1 for grain yield. Meanwhile, in set-2, the two crosses L-25×Sk-11 and L-27×Gz-658 possessed negative and significant SCA effects toward earliness while, crosses L-29×Gz-658 and L-34×Gz-658 expressed positive and significant SCA effects for grain yield. The promising crosses are selected based on desirable SCA effects had also high mean performance for grain yield especially the two crosses L-12×Sk-1 and L-16×Sk-1 which had outyielded significantly the standard check SC-3444. These crosses could be utilized in maize breeding program. The current results are in general agreement with the findings of many researchers (Meseka and Ishaaq 2012, Hundera 2017, Larièpe *et al* 2017, Dar *et al* 2017 and Motawei *et al* 2019).

Table 6. Specific combining ability effects of 36 top crosses for days to 50% silking (DS) and grain yield (GY) for each of set-1 and set-2 across the two locations.

	Set-1			Set-2	
Cross	DS	GY	Cross	DS	GY
L-1×Sk-1	0.500	1.344	L-19×Sk-11	-0.594	1.830
L-1×Sk-2	-0.500	-1.344	L-19×Gz-658	0.594	-1.830
L-2×Sk-1	-0.188	-0.863	L-20×Sk-11	-0.281	-0.995
L-2×Sk-2	0.188	0.863	L-20×Gz-658	0.281	0.995
L-3×Sk-1	-0.625*	-1.244	L-21×Sk-11	0.219	0.286
L-3×Sk-2	0.625*	1.244	L-21×Gz-658	-0.219	-0.286
L-4×Sk-1	-0.188	-0.938	L-22×Sk-11	0.219	-1.157
L-4×Sk-2	0.188	0.938	L-22×Gz-658	-0.219	1.157
L-5×Sk-1	-0.125	-1.281	L-23×Sk-11	-0.719	1.780
L-5×Sk-2	0.125	1.281	L-23×Gz-658	0.719	-1.780
L-6×Sk-1	0.313	-0.213	L-24×Sk-11	0.469	-1.007
L-6×Sk-2	-0.313	0.213	L-24×Gz-658	-0.469	1.007
L-7×Sk-1	-0.875*	-0.044	L-25×Sk-11	-1.406**	0.705
L-7×Sk-2	0.875*	0.044	L-25×Gz-658	1.406**	-0.705
L-8×Sk-1	0.001	-1.750	L-26×Sk-11	0.281	1.680
L-8×Sk-2	-0.001	1.750	L-26×Gz-658	-0.281	-1.680
L-9×Sk-1	-0.063	-0.075	L-27×Sk-11	1.531**	1.580
L-9×Sk-2	0.063	0.075	L-27×Gz-658	-1.531**	-1.580
L-10×Sk-1	0.125	-3.213**	L-28×Sk-11	-0.469	1.218
L-10×Sk-2	-0.125	3.213**	L-28×Gz-658	0.469	-1.218
L-11×Sk-1	-0.438	2.413*	L-29×Sk-11	0.469	-4.201**
L-11×Sk-2	0.438	-2.413*	L-29×Gz-658	-0.469	4.201**
L-12×Sk-1	0.688*	2.956*	L-30×Sk-11	-0.281	-0.870
L-12×Sk-2	-0.688*	-2.956*	L-30×Gz-658	0.281	0.870
L-13×Sk-1	-0.188	1.481	L-31×Sk-11	-0.281	-0.307
L-13×Sk-2	0.188	-1.481	L-31×Gz-658	0.281	0.307
L-14×Sk-1	0.188	-1.031	L-32×Sk-11	0.969	0.130
L-14×Sk-2	-0.188	1.031	L-32×Gz-658	-0.969	-0.130
L-15×Sk-1	0.500	-2.188	L-33×Sk-11	0.219	1.780
L-15×Sk-2	-0.500	2.188	L-33×Gz-658	-0.219	-1.780
L-16×Sk-1	0.001	2.850*	L-34×Sk-11	0.281	-2.526**
L-16×Sk-2	-0.001	-2.850*	L-34×Gz-658	-0.281	2.526**
L-17×Sk-1	0.001	1.569	L-35×Sk-11	-0.469	0.111
L-17×Sk-2	-0.001	-1.569	L-35×Gz-658	0.469	-0.111
L-18×Sk-1	0.375	0.225	L-36×Sk-11	-0.156	-0.039
L-18×Sk-2	-0.375	-0.225	L-36×Gz-658	0.156	0.039
LSD S_{ij}-S_{ik} 0.05	0.56	2.45	LSD S_{ij}-S_{ik} 0.05	1.04	2.40
0.01	0.74	3.23	0.01	1.38	3.16
LSD S_{ij}-S_{ik} 0.05	0.80	3.47	LSD S_{ij}-S_{ik} 0.05	1.48	3.40
0.01	1.05	4.55	0.01	1.94	4.46

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

Estimates of general and specific combining ability effects (additive and non-additive gene action) for days to 50% silking and grain yield in the

73

two sets are presented in Table (7). The K^2GCA or additive gene effects were the most important component controlling the inheritance of days of 50% silking and grain yield in the two sets, except for grain yield in set-2, where the K^2SCA or non-additive gene effects played the important role. These results are in agreement with those obtained by many researchers; among them Musila *et al* (2010), Wegory *et al* (2013) and Hosana *et al* (2015), who reported that additive gene action played an important role in the inheritance of grain yield and days to 50% silking. Meanwhile, Amiruzzaman *et al* (2013), Verma *et al* (2014), Akula *et al* (2016), Ejigu *et al* (2017) Singh *et al* (2017), Mosa *et al* (2017) and Motawei *et al* (2019) indicated that non-additive gene action played the main role in the inheritance of grain yield.

Table 7. **Estimates of general (K^2GCA) and specific (K^2SCA) combining ability effects for days to 50% silking (DS) and grain yield (GY) in Set-1 and Set-2 across the two locations.**

Genetic component	Set-1		Set-2	
	DS	GY	DS	GY
K^2GCA	0.35	6.20	1.17	1.90
K^2SCA	0.23	4.70	0.61	3.80

Estimates of heterotic groups based on specific and general combining ability effects (HSGCA) for days to 50% silking and grain yield in the two sets are presented in Table (8). Fan *et al* (2009) proposed a method of heterotic grouping based on specific and general combining ability effects (HSGCA). 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 HSGCA 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.

Table 8. Estimates of heterotic groups using specific and general combining ability method (HSGCA) for days to 50% silking (DS) and grain yield (GY) in Set-1 and Set-2 across the two locations.

Inbred line	Set-1				Inbred line	Set-2			
	DS		GY			DS		GY	
	Sk-1	Sk-2	Sk-1	Sk-2		Sk-11	Gz-658	Sk-11	Gz-658
L-1	0.076	-0.924≠	0.612	-2.076≠	L-19	0.305	1.493	-1.604	-5.264≠
L-2	0.701	1.077	-3.976≠	-2.250	L-20	-2.319≠	-1.757	-3.129≠	-1.139
L-3	-0.174≠	1.076	-3.538≠	-1.050	L-21	3.056	2.618	3.259	2.687
L-4	0.826	1.202	-0.901≠	0.975	L-22	2.306	1.868	-1.891≠	0.423
L-5	-1.299≠	-1.049	-1.700≠	0.862	L-23	0.180	1.618	5.921	2.361
L-6	2.202	1.576	0.249	0.675	L-24	1.931	0.993	0.484	2.498
L-7	-2.049≠	-0.299	2.762	2.850	L-25	-1.319≠	1.493	0.684	-0.726≠
L-8	-1.923	-1.925≠	-9.476≠	-5.976	L-26	-2.195	-2.757≠	-0.579	-3.939≠
L-9	1.701	1.827	-1.788≠	-1.638	L-27	-0.945	-4.007≠	-4.066	-7.226≠
L-10	-1.549	-1.799≠	-1.214≠	5.212	L-28	-0.195≠	0.743	0.847	-1.589≠
L-11	-2.424≠	-1.548	0.712	-4.114≠	L-29	0.556	-0.382≠	-6.691≠	1.711
L-12	1.952	0.576	7.862	1.950	L-30	-1.819≠	-1.257	-1.966≠	-0.226
L-13	-1.424≠	-1.048	8.437	5.475	L-31	-2.444≠	-1.882	0.284	0.898
L-14	-0.048	-0.424≠	-1.538≠	0.524	L-32	0.056	-1.882≠	3.296	3.036
L-15	-0.299	-1.299≠	-4.701≠	-0.325	L-33	0.806	0.368	-0.554	-4.114≠
L-16	1.077	1.075	5.624	-0.076≠	L-34	-0.070	-0.632≠	-2.391≠	2.661
L-17	1.827	1.825	0.575	-2.563≠	L-35	1.305	2.243	4.209	3.987
L-18	0.826	0.076	1.999	1.549	L-36	0.806	1.118	3.884	3.962

≠ means that this inbred line belongs to tester group.

In set-1, for days to 50% silking group-1 (Tester Sk-1) included inbred lines L-3, L-5, L-7, L-11 and L-13 while group-2 (tester Sk-2) included inbred lines L-1, L-8, L-10, L-14 and L-15. However, the method was not able to classify the inbred lines L-2, L-4, L-6, L-9, L-12, 16, L-17 and L-18. For grain yield, group-1(tester SK-1) included inbred lines L-2, L-3, L-4, L-5, L-8, L-9, L-10, L-14 and L-15 while group-2 (tester Sk-2)

included L-1, L-11, L-16 and L-17. Meanwhile, the method was unable to categorize the inbred lines L-6, L-7, L-12, L-13 and L-18.

In set-2, for days to 50% silking group-1 (tester Sk-11) contained the inbred lines L-20, L-25, L-28, L-30 and L-31 meanwhile group-2 (tester Gz-658) contained the inbred lines L-26, L-27, L-29, L-32 and L-34 While, inbred lines L-19, L-21, L-22, L-23, L-24, L-33, L-35 and L-36 were not classified. For grain yield, group-1 (tester Sk-11) included inbred lines   L-20, L-22, L-29, L-30 and L-34. While group-2 (tester Gz-658) included L-19, L-25, L-26, L-27, L-28 and L-33. However, the method was not able to classify the inbred lines L-21, L-23, L-24, L-31, L-32, L-35 and L-36.

The above results for heterotic grouping could be recommended for breeding programs to select the best parents for developing crosses of high heterosis. Lee (1995), Mosa *et al* (2017) and Motawei *et al* (2019) 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 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) and Legesse *et al* (2009) 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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77

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تقييم وتقسيم مجموعتين من سلالات الذرة الشامية صفراء الحبوب عن طريق تحليل السلالة فى الكشاف

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

تم تكوين مجموعتين من هجن الذرة الشامية صفراء الحبوب بتهجين ١٨ سلالة جديدة مرباة داخلياً مع اثنين من الكشافات لكل مجموعة بنظام السلالة × الكشاف وذلك بمحطة البحوث الزراعية بسخا موسم ٢٠١٧. تم تقييم عدد ٣٦ هجين مع ثلاثة هجن مقارنة لكل مجموعة موسم ٢٠١٨ تحت موقعى سخا والإسماعلية للمجموعة الأولى وسخا وسدس للمجموعة الثانية. تم قياس صفة عدد الأيام اللازمة حتى خروج ٥٠% من حرائر النورات المؤنثة ومحصول الحبوب بالأردب/الفدان. أظهرت ثلاثة سلالات وهى (13-L, L-10 and L-7) فى المجموعة الأولى والسلالة (L-32) فى المجموعة الثانية قيم مرغوبة ومعنوية لتأثيرات القدرة العامة على التآلف لصفتى التبكير والمحصول العالى. ولذلك توصى هذه الدراسة بإستخدام هذه السلالات فى برامج التربية للحصول على هجن عالية المحصول ومبكرة النضج فى آن واحد. كان أفضل هجين فى القدرة الخاصة على الإئتلاف فى صفة التبكير هو (L-7×Sk-1) وفى صفة المحصول الهجين (L-10×Sk-2) فى المجموعة الأولى وفى المجموعة الثانية كان الهجين (L-29×Gz-658) لصفة التبكير والهجين (L-13×Sk-1) لصفة المحصول. كما أظهر الهجين (L-13×Sk-1) فى المجموعة الأولى و الهجين (L-23×Sk-11) فى المجموعة الثانية زيادة منعوية وتبكير عن أفضل هجن المقارنة. تبين أن الفعل الجينى المضيف له الدور الأهم والرئيسى فى وراثة صفة عدد الأيام اللازمة حتى خروج ٥٠% من حرائر النورات المؤنثة فى كلتا المجموعتين ولمحصول الحبوب فى المجموعة الأولى بينما كان للفعل الجينى غير المضيف الدور الأهم فى وراثة صفة المحصول فى المجموعة الثانية. تم تقسيم السلالات فى كل مجموعة لصفة المحصول على أساس طريقة HSGCA إلى مجموعتين هجينيتين كما يلي :- فى Set-1 تضم المجموعة الهجينية الأولى (Sk-1) السلالات أرقام (2, 3, 4, 5, 8, 9, 10, 14 and 15). بينما تضم المجموعة الهجينية الثانية (Sk-2) السلالات أرقام (1, 11, 16 and 17) بينما فى Set-2 تضم المجموعة الهجينية الأولى (Sk-11) السلالات أرقام (20, 22, 29, 30, and 34) بينما تضم المجموعة الهجينية الثانية (Gz-658) السلالات (19, 25, 26, 27, 28 and 33). وهذه المجاميع الهجينية من الممكن أن تستخدم فى برامج التربية لانتخاب أفضل الإباء لتكوين هجن جديدة ذات قوة هجين عالية.