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Evaluation and Classification of Yellow Maize Inbred Lines Using Line X Tester Analysis Across Two Locations

Ibrahim, Kh. A. M.[1]; A. A. Said[2*] and M. M. Kamara[3]

[1]Agronomy Department, Faculty of Agriculture, New Valley University, El-Kharga 72511, Egypt.
[2]Agronomy Department, Faculty of Agriculture, Sohag University, Sohag 82749, Egypt.
[3]Department of Agronomy, Faculty of Agriculture, Kafrelsheikh University, Kafr El-Sheikh 33516, Egypt.

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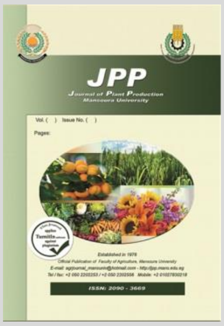

ABSTRACT

Ten yellow maize inbred lines and three testers were top crossed in line × tester scheme in 2019 season. The resulted 30 top crosses with two check hybrids were evaluated at two locations in 2020 growing season to assess mean performance, general and specific combining ability and their interaction with locations as well as elucidate type of gene action. The recorded data were days to 50% silking, plant height, ear height, ear length, ear diameter, No. of rows/ear, No. of kernels/row and grain yield (ardab/fed). The results showed that, the mean squares due to locations (Loc), genotypes (G), crosses (Cr.), G × Loc and Cr. × Loc interactions were significant for all the studied traits. Highly significant differences were observed among the evaluated lines (L), testers (T) and its corresponding hybrids for all traits. non-additive gene action gave an important role in the inheritance of all the studied traits. The inbred lines L2, L4 and L6 showed the best desirable GCA effects for earliness, L6, L7 and L10 for shortness and L4, L5, L6, L7 and L9 for lower ear placement. Whereas the inbreeds L3, L6 and L7 were the best general combiners for grain yield. The crosses L2×T1, L8×T1, L1×T2, L7×T2, L3×T3, L6×T3 and L10×T3 had the best SCA effects for grain yield. The ten inbred lines were classified into three different heterotic groups using HSGCA method. These groups could be used for selecting the best parents for making crosses in maize breeding programs.

Keywords: Maize, Locations, Combining ability, heterotic group, Gene action.

INTRODUCTION

Maize (*Zea mays* L.) is important cereal crop that is widely used for human food, animal feed and raw material for industrial products such as oil, starch and carbohydrates (Eisele *et al.* 2021). It is play a core role of Egyptian agriculture and food economy (El-Hosary 2020). The current total production of maize is insufficient to meet the needs of a rapidly growing population. As a result, increasing the productivity of such a crop is the primary goal of Egyptian maize breeders in order to reduce imports and react to high consumption (Abd El-Aty *et al.* 2018) .

Combining ability is crucial for selecting appropriate parents for hybridization and identifying superior hybrids in breeding programs (Oyekunle *et al.* 2015). Line × tester analysis method is a useful for estimating general and specific combining ability (GCA and SCA) effects as well as identifying the best parents (Kempthorne 1957). Furthermore, it determines gene action controlling the inheritance of the desired traits even with a limited sample size. Many studies have shown that the additive gene effects were more important in the genetic expression of maize grain yield (Abd El-Mottalb *et al.* 2013, Abo El-Haress 2015, El-Hosary *et al.* 2018, Mutimaamba *et al.* 2019, Olayiwola *et al.* 2021). Other researchers, however, reported that non-additive genetic effects were predominates in the inheritance of maize grain yield and the majority of its components (Makumbi *et al* 2011, Attia *et al* 2015, Kamara 2015, Wani *et al* 2017, El-Hosary 2020, Mohamed 2020, El-Shahed *et al* 2021). There is no consensus among different genetic studies on nature of the inheritance controlling maize yield or its related characters .

Heterotic groups are important in hybrid breeding, and it has been defined as a set of related or unrelated genotypes from the same or different populations, which exhibit similar combining ability and heterotic response when crossed with genotypes from other genetically distinct germplasm groups (Melchinger and Gumber 1998). Fan *et al.* (2009) argued that the HSGCA method is a simple and practical method for classifying maize inbred lines into known heterotic groups. This method has proven to be more effective than other methods (Legesse *et al.*2014).

The aims of this study were to (1) determination of the effects GCA and SCA and their interactions with locations, (2) elucidation of the inheritance of grain yield and other studied traits, (3) identification of the superior three way crosses and (4) classification of the inbred lines into heterotic groups using HSGCA method.

MATERIALS AND METHODS

Plant materials

Ten yellow maize inbred lines (*Zea mays* L.) were used as parents in this study. The parental codes, sources and names of these inbred lines are presented in Table 1.

In 2019 growing season, the ten inbred lines were topcrossed with the three single cross testers; SC162 (T1), SC167 (T2) and SC178 (T3), using line × tester mating design at the Experimental Farm, Faculty of

*** Corresponding author.**
E-mail address: tentawy@gmail.com
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Agriculture, New Valley University, El-Kharga, Egypt. In 2020 growing season, the resulted 30 test crosses and two commercial check hybrids TWC353 and TWC360 were evaluated at two different locations. The first location was the Experimental Farm, Faculty of Agriculture, Kafrelsheikh University, Egypt and the second one was the Experimental Farm, Faculty of Agriculture, New Valley University, El-Kharga, Egypt. The experimental design was randomized complete block design (RCBD) with three replications in each location. Each plot comprised of two ridges, 5 m long and 0.70 m width. Planting was made in hills spaced at 0.25 m with three kernels per hill on one side of the ridge, later thinned to one plant/hill. All other agricultural practices were carried out according to standard commercial recommendations for maize production in each location.

Table 1. The code, name and pedigree of the used parental maize inbred lines.

Parent code	Name	Source
L_1	Inb. 236	Agricultural Research Center, Egypt
L_2	Inb. 239	Agricultural Research Center, Egypt
L_3	Inb. 247	Agricultural Research Center, Egypt
L_4	Inb. 209	Agricultural Research Center, Egypt
L_5	Inb. 207	Agricultural Research Center, Egypt
L_6	CML285	CIMMYT, Mexico
L_7	CML121	CIMMYT, Mexico
L_8	CML122	CIMMYT, Mexico
L_9	CML223	CIMMYT, Mexico
L_{10}	CML224	CIMMYT, Mexico

The collected data were days to 50% silking, plant height (cm), ear height (cm), ear length (cm), ear diameter (cm), number of rows/ear, number of kernels/row and grain yield ardab/feddan adjusted to 15.5% moisture content (one ardab = 140 kg, one feddan = 4200 m2). The obtained data were statistically analyzed for the analysis of variance according to Steel and Torrie (1980). The combined analysis was done whenever the homogeneity test was not significant. The GCA effects of the lines and testers and SCA effects of the hybrids were calculated using line × tester analysis according to Kempthorne (1957).

Heterotic groups using specific and general combining ability (HSGCA) method were estimated according to Fan *et al.* (2009) as follows:

$$\textbf{HSGCA} = \textbf{Cross mean } X_{ij} - \textbf{Tester mean } (X_i) = \textbf{GCA} + \textbf{SCA}$$

Where, **X_{ij} = mean yield of the cross between i^{th} tester and j^{th}**
Xi = mean yield of the i^{th} tester

RESULTS AND DISCUSSION

Analysis of variance

The combined analysis of variance showed highly significant mean squares due to locations (Loc) for all the studied traits (Table 2), indicating the presence of a clear variation between the two locations in climatic and soil conditions for these traits. These results agreed with those reported by El Hosary *et al.* (2018), Gamea *et al.* (2018), El-Shahed *et al.* (2021) and Mousa *et al.* (2021).

Genotypes (G) and crosses (Cr.) mean squares were found to be highly significant for all the studied traits, indicating a wide diversity among the genetic materials used in the present study. Hence, the selection is possible to identify the most desirable crosses. These results are in harmony with those obtained by Murtadha *et al.* (2016), Sadek *et al.* (2017), Abdel-Moneam *et al.* (2020), El-Shamarka *et al.* (2020) and Ismail *et al.* (2020). The differences between the check hybrids were not significant for all the studied traits, except days to 50% silking, plant height and No. of kernels/row. Significant crosses vs. check (Cr. vs. Ch) mean squares were observed for all the studied traits, except ear height and ear diameter. The variance due to the interactions of G × Loc, Cr. × Loc and Cr. vs. Ch were significant for all the studied traits, except Cr. vs. Ch for days to 50% silking and No. of rows/ear. Such results revealed that the ranks of maize hybrids differed from one location to another for all measured traits. Insignificant interaction mean squares between checks and locations were observed for all the studied traits, except ear height. This result suggests that the performance of the check hybrids were nearly similar in magnitude at the two locations. Abd El-Aty *et al.* (2018) and Mohamed (2020) reached to the same conclusion for grain yield and most of its components.

Table 2. Combined analysis of variance for all the studied traits across two locations.

SOV	df	Days to 50% silking	Plant height (cm)	Ear height (cm)	Ear length (cm)	Ear diameter (cm)	No. of rows/ear	No. of kernels/ row	Grain yield (ard/fed)
Locations (L)	1	21.33*	193992.8**	178547.01**	68.28**	7.84**	289.84**	2275.63*	126.31*
Rep/L	4	1.68	94.71	83.71	0.78	0.12	2.24	137.09	7.43
Genotypes (G)	31	41.18**	775.81**	679.92**	12.87**	0.55**	9.48**	58.34**	60.45**
Crosses (Cr.)	29	43.21**	766.54**	722.93**	13.48**	0.58**	9.89**	60.34**	59.46**
Checks (Ch)	1	16.33**	468.75*	60.75	0.33	0.07	2.08	13.23*	4.08
Cr. *vs.* Ch	1	7.20*	1351.64**	52.00	7.70**	0.06	4.99*	45.60**	145.44**
G × L	31	11.57**	597.56**	499.54**	12.61**	0.68**	3.69**	55.48**	26.19**
Cr. × L	30	12.21**	604.45**	401.79**	13.06**	0.71**	3.88**	52.81**	25.80**
Ch × L	1	1.33	168.75	1474.08**	1.33	0.07	0.08	6.16	0.08
Cr. *vs.* Check × L	1	3.20	826.68**	2359.88**	11.06**	0.40*	1.61	182.31**	63.53**
Error	124	1.40	81.40	57.17	0.66	0.08	0.80	3.08	3.36

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

Line × tester analysis

Highly significant mean squares were detected for Lines (L), Testers (T) and L × T interaction for all the studied traits (Table 3). These results suggest that a wide range of variability existed among parental lines and testers and the inbred lines behaved differently according to the tester which they crossed. These results are similar with those reported by Kustanto *et al.* (2012), Kamara *et al.* (2014), Gamea *et al.* (2018), Abdel-Moneam *et al.* (2020), El-Shamarka *et al.* (2020) and Ismail *et al.* (2020).

Significant interaction between L×Loc, T×Loc and L×T× Loc were obtained for all traits, except T×Loc for plant height and ear length. This indicates that the tested inbred lines, testers and their crosses behaved differently from one location to another. These results corroborate the findings of Gamea *et al.* (2018), Abd El-Aty *et al.* (2018), Darshan and Marker (2019), Mohamed (2020) and Mousa *et al.* (2021).

Variance Components

The estimates of variances due to GCA, SCA and their interactions with locations (Table 3) showed that the SCA variance was higher than GCA variance for all studied traits, indicating that the non-additive effects had an important role in the inheritance of these traits. These results are in harmony with the findings of Abdel-Moneam *et al.* (2020), El-Hosary (2020), Mohamed (2020), El-Shahed *et al* (2021) and Mousa *et al.* (2021).

The magnitude of SCA× Loc interaction was higher than those of GCA× Loc interaction for all evaluated traits (Table 3). This finding showed that non-additive type of gene action was more affected by locations than the additive ones. These results are in agreement with the findings of Ibrahim *et al*. (2010), Abd Allah *et al*. (2011), Mousa and Aly (2012), Abdel-Moneam *et al.* (2014) and Mousa *et al.* (2021). They found that the non-additive genetic effects were more sensitive to environmental changes than the additive genetic effects. On the other hand, Mousa and Aly (2011) and Darshan and Marker (2019) reported that the additive types of gene action were more affected by the environment than non-additive ones.

Table 3. Line × tester analysis of the F_1 topcrosses for all studied traits across two locations

SOV	df	Days to 50% silking	Plant height (cm)	Ear height (cm)	Ear length (cm)	Ear diameter (cm)	No. of rows/ear	No. of kernels/ row	Grain yield (ard/fed)
Lines (L)	9	59.77**	1106.03**	827.65**	24.26**	0.63**	8.24**	121.82**	78.46**
Testers (T)	2	25.55**	460.44**	240.52**	2.63**	0.66**	5.25**	21.70**	66.63**
L × T	18	36.90**	630.80**	724.16**	9.30**	0.55**	11.23**	33.89**	49.16**
L × Loc	9	17.29**	705.22**	436.82**	12.50**	0.89**	3.86**	31.66**	30.03**
T × Loc	2	10.05**	250.61	911.52**	0.47	0.55**	8.11**	23.36**	10.73*
L × T × Loc	18	9.91**	593.38**	327.63**	14.73**	0.63**	3.43**	66.66**	25.36**
Error	116	1.48	85.05	41.92	0.53	0.09	0.77	2.85	3.24
K^2 GCA		1.06	17.90	12.62	0.33	0.01	0.15	1.77	1.78
K^2 SCA		5.90	90.96	113.71	1.46	0.08	1.74	5.17	7.65
K^2 GCA × Loc		0.63	20.15	32.42	0.31	0.03	0.27	1.26	0.88
K^2 SCA × Loc		2.81	169.44	95.24	4.74	0.18	0.88	21.27	7.37

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

Mean performance

Mean performance of the 30 test crosses and the two check hybrids TWC 353 and TWC360 for all the studied traits across two locations are shown in Table 4. The mean values of days to 50% silking varied from 59.0 (L1×T3) to 66.33 days (L8×T3) with value of 62.87 days. The crosses L4 × T1, L6 × T1, L7 × T1, L9 × T1, L6 × T2, L10 × T2, L1 × T3 and L4 × T3 were significantly earlier than check hybrid TWC 353 (the earliest check) . Regarding plant height the crosses means varied from 196.67 cm (L1×T3) to 243.67 cm (L8×T3) with an average of 222.79 cm. Ten top crosses L4×T1, L5×T1, L7×T1, L6×T2, L9 × T2, L4 × T3, L4 × T3, L5 × T3, L6 × T3 and L9 × T3 were significantly shorter than check hybrid TWC 353 (the shortest check hybrid). As for ear height nine crosses L5×T1, L7×T1, L6×T2, L8×T2, L4×T3, L6×T3, L9×T3 and L10×T3 possessed significantly low ear position compared with the lowest check hybrid TWC353, and the crosses means ranged from 88.50 cm (L7×T2) to 145.83 cm. (L8×T3) with an average of 116.94 cm.

Concerning ear length, the cross L8×T3 recorded the lowest value (13.13 cm), while L3×T1 recorded the highest value (18.40 cm). Furthermore, the crosses L2×T1, L7×T2, L1×T3 and L2×T3 significantly surpassed the best check hybrid (TWC 360). The average of ear diameter was 4.65 cm ranging from 4.10 cm (L9×T1) to 5.22 (L3×T2). Five crosses L1×T1, L2 × T2, L3 ×T2, L7 × T3 and L8 × T3 exhibited significantly higher values than the best check hybrid TWC 360. Number of rows/ear differed significantly among the tested crosses and it ranged from 11.77 (L4×T3) to 16.20 (L4×T2) with an average of 14.42. Five crosses L1 × T1, L10 × T1, L4 × T2, L7 × T2 and L7 × T3 significantly surpassed the check TWC 353. The highest number of kernels/row was assigned for L7×T2 (40.50), whereas the cross L9×T2 (27.50) gave the lowest value. The crosses L7×T2 and L3 ×T3 had higher values than the best check hybrid TWC 360. Grain yield ranged from 14.33 (ard/fed) for the cross L1×T3 to 25.64 (ard/fed) for the cross L7×T2 with an average of 18.82 (ard/fed).

Three crosses L8×T1, L7×T2 and L3×T3 expressed significant and positive superiority percentages relative to the check hybrid TWC 353 reached to 9.76%, 17.45%, and 13.76%, respectively. While, only the topcross L7×T2 recorded significant positive superiority relative the highest yielding check hybrid TWC 360 being 11.49%. Hence, these crosses showed good potential for improving maize grain yield. Several investigators reported the same results (Osman 2014; Aslam *et al.* 2017 and Shushay *et al.*, 2017 El-Hosary *et al.* 2018, Abdel-Moneam *et al.* 2020)

General combining ability (GCA) effects

Estimates of general combining ability ($\hat{g}_i$) effects of the ten inbred lines and the three testers across the two locations are shown in Table 5. The results revealed that three lines i.e., L2, L4 and L6 had negative significant ($\hat{g}_i$) effects for days to 50% silking. In the same vein, significant and negative ($\hat{g}_i$) effects of plant height was recorded by the inbred lines L6, L7 and L10. Furthermore, inbred lines L4, L5, L6, L7 and L9 seemed to be suitable combiners for developing lower ear placement hybrids. On the contrary, the highest significant and positive ($\hat{g}_i$) effects were expressed by the inbred lines L1, L2, L3 and L7 for ear length; L2, L3 and L8 for ear diameter; L1, L7 and L10 for No. of rows/ear; L1, L2, L3 and L7 for No. of kernels/row and L3, L6 and L7 for grain yield. These findings suggested that these inbred lines had favorable genes, and that improvement in respective traits could be achieved if they are included in maize hybridization program. Abd El-Aty *et al.* (2018), El-Hosary *et al* (2020), Gamea (2020) and El-Shahed *et al.* (2021) reported desirable and significant that ($\hat{g}_i$) effects for earliness, grain yield and its components.

For the testers, the highest significant and desirable GCA effects were detected from T1 (SC 168) for days to 50% silking, ear height and No. of kernels/row and T3 (TWC-352) for plant height and ear diameter. Horner *et al.* (1976), El- Shenawy and Mosa (2005) and Aly (2013) suggested the effectiveness of the single crosses as good testers.

Table 4. Mean performance of the 32 evaluated materials for all the studied traits over the two locations as well as superiority percentages relative to check hybrids for grain yield trait.

Cross	Days to 50% silking	Plant height (cm)	Ear Height (cm)	Ear Length (cm)	Ear diameter (cm)	No. of rows /ear	No. of kernels /row	Grain yield (ard/fed)	Superiority % for grain yield	
									TWC-353	TWC-360
L1×T1	63.50	225.50	124.33	14.87	5.10	16.00	38.17	18.50	-15.27**	-19.57**
L2×T1	63.50	239.00	130.00	18.75	4.70	13.23	34.90	21.88	0.19	-4.89
L3×T1	62.00	225.00	124.33	17.60	4.70	12.63	36.80	17.83	-18.32**	-22.46**
L4×T1	58.50	212.50	106.00	15.60	4.60	15.63	36.30	17.27	-20.92**	-24.93**
L5×T1	64.00	211.67	101.67	15.95	4.30	13.58	35.00	19.44	-10.97*	-15.49**
L6×T1	61.00	225.83	119.17	16.33	4.25	15.43	33.30	21.69	-0.67	-5.71
L7×T1	60.50	196.67	101.67	14.87	4.50	13.67	36.35	21.04	-3.64	-8.53
L8×T1	66.00	226.00	114.50	18.03	4.90	15.00	38.20	23.97	9.76*	4.20
L9×T1	59.00	225.67	120.17	14.43	4.10	14.27	32.65	19.15	-12.28*	-16.73**
L10×T1	65.50	233.33	121.67	15.43	4.67	16.20	34.10	14.75	-32.45**	-35.88**
L1×T2	65.00	243.67	131.50	17.37	4.40	15.77	39.97	16.83	-22.90**	-26.81**
L2×T2	62.00	230.83	120.00	17.20	5.15	14.37	35.80	17.55	-19.64**	-23.72**
L3×T2	63.00	222.50	128.33	16.70	5.22	15.83	38.90	17.67	-19.08**	-23.19**
L4×T2	64.00	231.67	123.33	15.60	4.20	16.20	34.65	18.70	-14.37**	-18.71**
L5×T2	65.50	235.83	121.67	15.70	4.60	12.27	34.50	16.51	-24.40**	-28.24**
L6×T2	58.50	204.00	103.00	13.60	4.50	12.97	33.35	15.33	-29.80**	-33.36**
L7×T2	65.00	217.50	120.00	18.10	4.65	16.00	40.50	25.64	17.45**	11.49*
L8×T2	66.00	219.00	105.00	14.33	4.50	14.03	35.80	15.23	-30.24**	-33.78**
L9×T2	66.00	214.17	114.17	14.20	4.10	14.67	27.50	16.83	-22.90**	-26.81**
L10×T2	61.00	239.17	135.83	14.97	4.60	14.00	32.10	15.85	-27.42**	-31.10**
L1×T3	58.00	227.50	125.83	18.30	4.80	14.10	37.45	14.33	-34.35**	-37.68**
L2×T3	58.50	226.67	120.00	17.30	4.50	13.47	37.45	15.20	-30.40**	-33.93**
L3× T3	64.67	218.33	125.83	18.52	4.78	14.77	40.27	24.84	13.76**	7.99
L4×T3	59.50	211.67	106.67	15.80	4.70	11.77	31.55	19.81	-9.28	-13.88**
L5×T3	64.50	215.00	119.17	14.53	4.90	14.53	33.30	16.00	-26.73**	-30.45**
L6×T3	61.00	205.00	101.67	14.23	4.50	13.90	29.65	22.67	3.82	-1.45
L7×T3	65.00	225.83	115.00	17.23	5.15	16.17	36.80	23.87	9.31	3.77
L8×T3	66.33	237.50	145.83	14.77	5.10	12.50	29.70	19.60	-10.23*	-14.78**
L9×T3	65.00	212.50	107.50	14.77	4.90	13.97	33.70	17.50	-19.87**	-23.93**
L10 ×T3	64.00	224.17	109.17	15.10	4.35	15.60	34.40	19.20	-12.05*	-16.51**
TWC-353	62.50	227.50	118.00	16.67	4.50	14.67	36.07	21.83	-	-
TWC-360	64.83	240.00	122.50	17.00	4.65	15.50	38.17	23.00	-	-
LSD 0.05	1.34	10.21	8.56	0.92	0.32	1.01	1.99	2.07	-	-
LSD 0.01	1.76	13.42	11.24	1.21	0.42	1.33	2.61	2.73	-	-

Table 5. General combining ability ($\hat{g}_i$) effects of the ten inbred lines and three testers for all the studied traits across two locations.

Genotypes	Days to 50% silking	Plant height (cm)	Ear height (cm)	Ear length (cm)	Ear diameter (cm)	No. of rows/ear	No. of kernels/row	Grain yield (ard/fed)
Inbred Lines								
L1	-0.70*	9.43**	9.12**	0.84**	0.12	0.87**	3.42**	-2.27**
L2	-1.53**	9.38**	5.23**	1.74**	0.14*	-0.73**	0.95*	-0.62
L3	0.36	-0.84	8.07**	1.60**	0.25**	-0.01	3.55**	1.29**
L4	-2.20**	-4.18	-6.10**	-0.34*	-0.15*	0.12	-0.94*	-0.23
L5	1.80**	-1.96	-3.93**	-0.61**	-0.05	-0.96**	-0.84*	-1.51**
L6	-2.70**	-11.18**	-10.16**	-1.28**	-0.23**	-0.32	-3.00**	1.07*
L7	0.63*	-9.46**	-5.88**	0.73**	0.12	0.86**	2.78**	4.70**
L8	3.24**	4.71*	3.68*	-0.29	0.19**	-0.57**	-0.54	0.78
L9	0.47	-5.34*	-4.16**	-1.54**	-0.28**	-0.12	-3.82**	-0.99*
L10	0.63*	9.43**	4.12**	-0.84**	-0.11	0.85**	-1.57**	-2.22**
LSD (gi) 0.05	0.56	4.26	2.99	0.34	0.14	0.41	0.78	0.83
LSD (gi) 0.01	0.74	5.60	3.93	0.44	0.18	0.53	1.02	1.09
Testers								
T1 (SC-168)	-0.52**	-0.67	-1.75**	0.18*	-0.07 *	0.15	0.47**	0.73**
T2 (SC-176)	0.73**	3.04*	2.18**	-0.23*	-0.06	0.19	0.20	-1.21**
T3 (TWC-352)	-0.22	-2.37*	-0.43	0.05	0.12**	-0.34**	-0.68**	0.48*
LSD (gi) 0.05	0.31	2.33	1.64	0.18	0.07	0.22	0.43	0.46
LSD (gi) 0.01	0.40	3.07	2.15	0.24	0.10	0.29	0.56	0.60

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

Specific combining ability (SCA) effects

Estimates of specific combining ability ($\hat{S}_{ij}$) effects of the 30 F_1 crosses for all the studied traits across the two locations are shown in Table 6. The most desirable and significant ($\hat{S}_{ij}$) effects obtained by the crosses; L4×T1, L7×T1, L9×T1, L9×T1, L6×T2, L10×T2, L1×T3 and L2×T3 for days to 50% silking (towards earliness); L5×T1, L7×T1, L6×T2 and L8×T2 for plant height (towards shorter plants); L5×T1, L7×T1, L8×T1, L2×T2, L6×T2, L8×T2, L6×T3 and L10×T3 for ear height (towards lower ear placement); L2×T1, L6×T1, L8×T1, L1×T2, L7×T2, L1×T3 and L3×T3 for ear length; L1×T2, L2×T2, L3×T2, L7×T3 and L9×T3 for ear diameter; L4×T1, L6×T1, L8×T1, L10×T1, L3×T2, L4×T2, L5×T3 and L7×T3 for No. of rows/ear; L4×T1, L8×T1, L7×T2, L2×T3, L3×T3, L9×T3 and L10×T3 for No. of kernels/row and L2×T1, L8×T1, L1×T2, L7×T2, L3×T3, L6×T3 and L10×T3 for grain yield. These test-crosses could be useful in breeding programs as most of them consisted of at least one high GCA parent for the concerned traits. Furthermore, it could be important to obtain synthetic varieties or produced inbred lines (EL-Hosary, 2020). It's worth noting that crosses with high SCA effects for grain yield also had high SCA effects for one or more of its components. For instance, the cross L8×T1that had high SCA effects for grain yield, also expressed high SCA effects for ear length, No. of rows/ear and No. of kernels/row.

Table 6. Estimates of specific combining ability ($\hat{S}_{ij}$) effects of the 30 F_1 crosses for all the studied traits over two locations.

Cross	Days to 50% silking	Plant height (cm)	Ear height (cm)	Ear length (cm)	Ear diameter (cm)	No. of rows/ear	No. of kernels/row	Grain yield (ard/fed)
L1×T1	1.85**	-6.05	-1.14	-2.16**	0.40**	0.56	-0.83	1.22
L2×T1	2.68**	7.51*	8.42**	0.82**	-0.02	-0.60	-1.62*	2.94**
L3×T1	-0.71	3.73	-0.08	-0.19	-0.13	-1.93**	-2.33**	-3.01**
L4×T1	-1.65**	-5.44	-4.25	-0.25	0.17	0.95**	1.66*	-2.05**
L5×T1	-0.15	-8.49*	-10.75**	0.38	-0.23	-0.03	0.26	1.40
L6×T1	1.35**	14.89**	12.97**	1.43**	-0.10	1.19**	0.73	1.06
L7×T1	-2.48**	-15.99**	-8.81**	-2.05**	-0.20	-1.76**	-2.01**	-3.21**
L8×T1	0.41	-0.83	-5.53*	2.14**	0.13	1.01**	3.16**	3.64**
L9×T1	-3.82**	8.89*	7.97**	-0.21	-0.20	-0.18	0.89	0.60
L10×T1	2.52**	1.78	1.19	0.09	0.19	0.79*	0.09	-2.58**
L1×T2	2.10**	8.40*	2.09	0.75*	-0.31**	0.28	1.24	1.49*
L2×T2	-0.07	-4.38	-5.52*	-0.32	0.42**	0.49	-0.45	0.55
L3×T2	-0.96	-2.49	-0.02	-0.68*	0.37**	1.23**	0.04	-1.24
L4×T2	2.60**	10.01**	9.15**	0.16	-0.24*	1.47**	0.28	1.31
L5×T2	0.10	11.96**	5.32*	0.54	0.06	-1.39**	0.03	0.40
L6×T2	-2.40**	-10.66**	-7.13**	-0.89**	0.14	-1.33**	1.05	-3.36**
L7×T2	0.77	1.12	5.59*	1.60**	-0.06	0.53	2.41**	3.34**
L8×T2	-0.84	-11.54**	-18.96**	-1.15**	-0.28*	0.00	1.03	-3.16**
L9×T2	1.93**	-6.32	-1.96	-0.04	-0.21	0.17	-3.99**	0.21
L10×T2	-3.23**	3.90	11.43**	0.03	0.12	-1.46**	-1.64*	0.46
L1×T3	-3.95**	-2.35	-0.96	1.41**	-0.09	-0.85*	-0.40	-2.70**
L2×T3	-2.62**	-3.13	-2.90	-0.50	-0.40**	0.12	2.08**	-3.49**
L3× T3	1.66**	-1.24	0.10	0.86**	-0.24*	0.70	2.29**	4.25**
L4×T3	-0.95	-4.57	-4.90	0.08	0.08	-2.43**	-1.94**	0.74
L5×T3	0.05	-3.46	5.43*	-0.91**	0.18	1.41**	-0.29	-1.80*
L6×T3	1.05*	-4.24	-5.84*	-0.54	-0.04	0.14	-1.77*	2.29**
L7×T3	1.72**	14.87**	3.21	0.45	0.26*	1.23**	-0.41	-0.13
L8×T3	0.44	12.37**	24.49**	-0.99**	0.15	-1.00**	-4.19**	-0.48
L9×T3	1.88**	-2.57	-6.01*	0.25	0.41**	0.01	3.09**	-0.81
L10 ×T3	0.72	-5.68	-12.62**	-0.12	-0.31**	0.67	1.54*	2.12**
LSD 5% (s_{ij})	0.97	7.38	5.18	0.58	0.23	0.70	1.35	1.44
LSD 1% (s_{ij})	1.28	9.70	6.81	0.76	0.31	0.93	1.77	1.89

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

Heterotic groups

Heterotic groups estimates based on specific and general combining ability effects (HSGCA) for grain yield are shown in Table 7. The results showed that the ten inbred lines were placed into three heterotic groups. Group I (tester SC162) consisted of the L3, L4 and L10. While, group 2 (tester SC167) included the inbreds; L6 and L8. Moreover, group 3 (tester SC178) contained the inbreds L1, L2, L5and L9. However, the method was not able to classify the inbred line L7 in any group. The above results could be recommended for breeding programs in selecting the best parents for making crosses. The placement of the inbred lines into different heterotic groups increased the chances of developing high yielding hybrids through crossing of inbred lines belonging to different heterotic groups (Legesse *et al.* 2014). Maximum genetic variability and hybrid vigor (heterosis) can be exploited by crossing inbred lines from different heterotic groups. Lu *et al.* (2009) pointed out that the crossing inbred lines between dissimilar groups produces better performing hybrids, as compared to crossing lines from within groups.

Table 7. Estimates of heterotic groups using specific and general combining ability (HSGCA) for grain yield across two locations.

Inbred lines	T1 (SC 162)	T2 (SC 167)	T3(SC 178)
L1	-1.05	-0.78	-4.97#
L2	2.32	-0.07	-4.10#
L3	-1.72#	0.05	5.54
L4	-2.28#	1.08	0.51
L5	-0.11	-1.11	-3.30#
L6	2.14	-2.29#	3.37
L7	1.49	8.03	4.57
L8	4.41	-2.38#	0.30
L9	-0.40	-0.78	-1.81#
L10	-4.80#	-1.77	-0.10

 # means that this inbred line belongs to tester group

REFERENCES

Abd Allah, T.A.E., Kh. A.M. Ibrahim and M.A.A. Mostafa (2011). Combining Ability Evaluation of Yellow Maize Inbred Lines Derived from Different Sources. Egypt. J. Plant Breed. 15(5), 171-186.

Abd El-Aty, M.S., Abd El-Hameed, A.E.W. El-Sayed, E.A.E.F. Amer, M.S.R. (2018). Evaluation and classification of sixteen new yellow maize inbred lines using line × tester analysis in different locations under Egyptian environment. Fresenius Environ. Bull., 27, 4986-4994.

Abd El-Mottalb, A.A. and H.A.A. Gamea (2014). Combining ability analysis in new white maize inbred lines (Zea mays L.). Minufiya J. Agric.Res. 39 (1),143-151.

Abdel-Moneam, M. A., M.S. Sultan, W.A. Abido, A. Hadházy, S.A. Sadek, and M.S Shalof (2020). Investigation of combining ability and superiority percentages for yield and some related traits in yellow maize using line× tester analysis. Acta Agraria Debreceniensis, (1), 5-14.

Abdel-Moneam, M., M. Sultan, S. Salama and A. El Oraby (2014). Evaluation of combining ability and heterosis for yield and its components traits of five maize inbreds under normal and stress nitrogen fertilization. Asian J. Crop Sci., 6, 142-149.

Abo El-Haress, S.M. (2015). Diallel analysis for yield, downy mildew and agronomic characters in maize (*Zea mays* L.). Alex. J. Agric. Res. 60 (1), 25-31.

Aly, R.S.H. 2013. Relationship between combining ability of grain yield and yield components for some newly yellow maize inbred lines via line × tester analysis. Alex J Agric Res. 58(2), 115-124.

Aslam, M. Sohail, Q. Sohail, M. A. Maqbool, R. S. Shahzad (2017). Combining Ability Analysis for yield traits in diallel crosses of maize. J. of Ani. & Pl. Sci., 27(1), 136–143.

Attia, A.N., M.S. Sultan, M.A. Badawi, M.A. Abdel–Moneam and A.R.M. Al-Rawi (2015). Estimation of combining ability and heterosis for some maize inbred lines and its single crosses. J. Plant Production, Mansoura Univ. 6 (1), 83 -98.

Darshan, S.S. and S. Marker (2019). Heterosis and combining ability for grain yield and its component characters in quality protein maize (*Zea mays* L.) hybrids. Electronic J. Plant Breed., 10 (1), 111 – 118

Eisele, T. G., D. Lazzari, T. A. da Silva, R. J. B. Pinto, R. A. Matsuzaki, M. F. D. S. D Maioli, and A. T. do Amaral Junior (2021). Combining ability and genetic divergence among tropical maize inbred lines using SSR markers. Acta Scientiarum. Agronomy, 43, 53317-53317.

El-Hosary A. A. A., M. H. Motawea and A. A. Elgammal (2018). Combining ability for yield and some of its attributes in maize across two locations. Egypt. J. Plant Breed. 22(3): 625-640.

El-Hosary, A. A. A. (2020). Estimation of genetic variability using line × tester technic in yellow maize and stability analysis for superior hybrids using different stability procedures. J. of Plant Production, Mansoura Univ., 11 (9):847-854.

El-Shahed, H. M., A. M. Abu Shosha, M. A. M. El-Ghonemy and R. H. A. Alsebaey (2021). Diallel Analysis of Eight Yellow Maize Inbred Lines for Earliness and Grain Yield. J. Plant Production, Mansoura Univ., 12 (3),329-332.

El-Shamarka SH.A., I.H. Darwish, Marwa M.El-Nahas, A.A. Afifi and A.M. Nour El-Dein (2020). Combining Abilities for Yield and Its Components through Line by Tester Analysis in Maize under Two Plant Densities. Alex. J. Agric. Sci. 65, 253-278.

El-Shenawy AA, H.E. Mosa (2005). Evaluation of new single and three way crosses for resistance to downy mildew disease and grain yield under different environments. Alex. J. Agric Res. 50, 35-43.

Fan, X.M., Y.M. Zhang; W.H. Yao; H.M. Chen; T. Tan; C.X. Xu, X.L. han, L.M. Luo and M.S. Kang (2009). Classifying maize inbred lines into heterotic group using a factorial mating design. Agron. J. 101, 106-112.

Gamea H.A.A., M.M.B. Darwich and H.A. Abo Yousef (2018). Combining ability for some inbred lines in half-Diallel crosses of maize under two different locations conditions. Archives of Agriculture Sciences Journal 1(3),14-25. Special Issue.

Gamea, H. A. A. (2020). Mean Performance, Type of Gene Action, Combining Ability and Superiority Percentage of some New White Maize Inbred Lines in Top Crosses. J. Plant Production, 11(4), 319-323.

Horner E.S., M.C. Lutrick, W.H. Chapman and F.G. Martin (1976). Effect of recurrent selection for combining ability with a single cross tester in maize. Crop Sci. 16, 5-8.

Ibrahim, Kh.A.M., M.A. Abd El-Moula and M.E.M. Abd El-Azeem (2010). Combining Ability Analysis of Some Yellow maize (*Zea mays* L.) Inbred Lines. Egypt. J. Agric. Res. 88(1), 29-46.

Ismail, M. R., El-Hosary, A. A., and EL-Badawy, M. E. M. (2020). Genetic analysis of some topcrosses of yellow maize. Electronic. J. Plant Breed, 11(04), 1099-1105.

Kamara, M. M. 2015. Diallel analysis of some yellow maize inbred lines under low and normal nitrogen levels. International J. of Plant Breeding and genetics 9(2), 32 - 43.

Kamara, M.M., I.S. El-Degwy and H. Koyama (2014). Estimation combining ability of some maize inbred lines using line x tester mating design under two nitrogen levels. *Aust.* J. Crop Sci., 8 1336-1342.

Kempthorne, O. (1957). An introduction to genetic statistics. Jonh Wiley and Sons New York: 468-472.

Kustanto H, Sugiharto AN, Basuki N, Kasno A 2012 Study on heterosis and genetic distance of S6 inbred lines of maize. J. Agric Food Tech. 2: 118-125.

Legesse, W., W. Mosisa, T. Berhanu, A. Girum, A. Wande, A. Solomon, K. Tolera, W. Andualem and A. Belayneh (2014). Genetic improvement of maize for mid-altitude and lowland subhumid agro-ecologies of Ethiopia. In Worku, M., S. Twumasi-AfriyieB. M. Prasanna, (Eds.), (Vol. 57, pp. 24–34) 18–20 April 2012. Proceedings of the Third National Maize Workshop of Ethiopia. Addis Ababa, Ethiopia.

Lu, Y., J. Yan, C.T. Guimaraes, S. Taba, Z. Hao, S. Gao and Y. Xu (2009). Molecular characterization of global maize breeding germplasm based on genome-wide single nucleotide polymorphisms. Theoretical and Applied Genetics, 120, 93–115.

Makumbi D., J.F. Betran, M. Banziger and J.M. Ribaut 2011. Combining ability, heterosis and genetic diversity in tropical maize (*Zea mays* L.) under stress and non-stress conditions. Euphytica 180, 143–162.

Melchinger, A.E. and R.K. Gumber 1998. Overview of heterotic groups in agronomic crops. 29-44. In: K.R. Lamkey and J.E. Staub (Eds.), concepts and breeding of heterosis in crop plants. CSSA, Madison, W.I., USA.

Mohamed, H. A. 2020. Combining ability of newly developed white maize (*Zea mays* L.) inbred lines via top cross analysis. Zagazig J.l of Agricultural Research, 47(3), 657-668.

Mousa, S. Th. M., H.A.A. Mohamed, R.S.H. Aly and H. A. Darwish (2021). Combining Ability of White Maize Inbred Lines Via Line X Tester Analysis. J. Plant Production, Mansoura Univ., 12 (2),109 – 113.

Mousa, S.Th.M. and R.S.H. Aly (2011). Combining ability for grain yield and some related traits of newly yellow maize (*Zea mays* L.) inbred lines. J. Agric. Chem. and Biotech., Mansoura Univ., 2 (12), 331- 341.

Mousa, S.Th.M. and R.S.H. Aly (2012). Estimation of combining ability effects of new white maize inbred lines (*Zea mays* L.) via line x tester analysis. Egypt J. Agric. Res., 90 (4), 77-90.

Murtadha, M., O. Ariyo and S. Alghamdi (2018). Analysis of combining ability over environments in diallel crosses of maize (*Zea mays*). Journal of the Saudi Society of Agricultural Sciences, 17(1), 69-78.

Mutimaamba, C., J. MacRobert, J.E. Cairns, C. Magorokosho, T. Ndhlela, C. Mukungurutse, and M. Labuschagne, (2020). Line× tester analysis of maize grain yield under acid and non-acid soil conditions. Crop Science, 60(2), 991-1003.

Olayiwola, M. O., S.O. Ajala, O.J. Ariyo, D.K. Ojo, M. Gedil, (2021). Heterotic grouping of tropical maize inbred lines and their hybrid performance under stem borer infestation and low soil nitrogen condition in West and Central Africa. Euphytica, 217(1), 1-22.

Osman, M. M. A. (2014). A diallel analysis among seven newly yellow maize inbred lines for grain yield and other agronomic traits. Egypt. J. of Appl. Sci.; 29 (1), 1–11.

Oyekunle, M., B. Badu-Apraku, S. Hearne and J. Franco (2015). Genetic diversity of tropical early maturing maize inbreds and their performance in hybrid combinations under drought and optimum growing conditions. Field Crops Res. 170, 55-65.

Sadek, M.S.E.; M. G. Balbaa and M.A.A. Mostafa (2017). Combining ability analysis of new yellow maize inbred lines for yield and some related characters. Alex. J. Agric. Sci. 62, 209– 217.

Shushay W. A., H. Z. Zeleke and D.W. Gissa (2017). Line x tester analysis of maize inbred lines for grain yield and yield related traits. Asian J. of Plant Scie. and Res., 3(5),12–19.

Steel, R.G.D. and J.H. Torrie (1980). Principles and Procedures of Statistics. A Biometrical Approach. 2nd Ed. Mc Graw Hill, N.Y., USA.

Wani, M. M. A., S. A. Wani, Z. A. Dar, A. A. Lone, I. Abedi and A. Gazal (2017). Combining ability analysis in early maturing maize inbred lines under temperate conditions, Int. J. Pure App. Biosci. 5(2), 456-466.

تقييم وتقسيم سلالات من الذرة الشامية الصفراء عن طريق تحليل السلالة × الكشاف عبر موقعين

خالدعبد الحفيظ محمد ابراهيم[١]، علاء على سعيد[٢] ومحمد محمد قمرة[٣]

[١]قسم المحاصيل- كلية الزراعة- جامعة الوادى الجديد- الوادى الجديد- مصر

[٢]قسم المحاصيل- كلية الزراعة- جامعه سوهاج- سوهاج - مصر

[٣]قسم المحاصيل- كلية الزراعة- جامعة كفر الشيخ- كفر الشيخ- مصر

تم إجراء التهجين بين ١٠ سلالات من الذرة الشامية الصفراء مع ثلاثة كشافات وهى هجين فردى ١٦٢، هجين فردى ١٦٧ وهجين فردى ١٧٨ فى موسم ٢٠١٩. تم تقييم الهجن الناتجة (٣٠ هجيناً) مع اثنين من الهجن التجارية كهجن مقارنة وهما هجين ثلاثى٣٥٣ وهجين ثلاثى ٣٦٠ فى موقعين (كفر الشيخ والخارجه) فى تصميم القطاعات الكاملة العشوائية بثلاث مكررات فى موسم ٢٠٢٠. وذلك لتقدير تأثيرات القدرة العامة والخاصة على التآلف وتفاعلهما مع المواقع ولتحديد الفعل الجينى المتحكم فى وراثة الصفات تحت الدراسة. تم دراسة الصفات التالية: عدد الأيام حتي ظهور ٥٠% من الحراير، إرتفاع النبات، إرتفاع الكوز، طول الكوز، قطر الكوز، عدد الصفوف/كوز، وعدد الحبوب/صف ومحصول الحبوب (أردب/فدان) .أظهرت النتائج أن التباين الراجع لكل من المواقع ، التراكيب الوراثية، الهجن وتفاعل كلا من التراكيب الوراثية و الهجن مع المواقع كان معنوياً لجميع الصفات تحت الدراسة.كما أوضحت النتائج وجود اختلافات عالية المعنوية بين السلالات، الكشافات، والتفاعل بين السلالات × الكشافات لجميع الصفات المدروسة. كان الفعل الجينى غير المضيف هو الاكثر اهمية فى وراثة جميع الصفات. أفضل السلالات فى القدرة العامة على التالف هى السلالات ٤،٢ و٦ لصفه التزهير، السلالات ٦، ٧ و ١٠ لصفه إرتفاع النبات والسلالات ٣، ٦ و ٧ لصفه إرتفاع الكوز.كما أظهرت السلالات ٣ ،٦ و٧ قدرة عامة على التالف معنوية ومرغوبة بالنسبة لصفة محصول الحبوب. أظهرت الهجن L10×T3, L2×T1, L8×T1, L1×T2, L7×T2, L3×T3, L6×T3 أفضل القيم لتأثيرات القدرة الخاصة على الائتلاف لصفة المحصول وواحد أو أكثر من مكوناتة. قسمت السلالات الى ثلاثه مجاميع متباعدة باستخدام تأثيرات القدرة العامة والخاصة على الائتلاف. هذه المجاميع يمكن أن يستفاد منها فى انتخاب افضل السلالات لعمل الهجن في برامج تربية الذرة الشامية.