COMBINING ABILITY OF NEW YELLOW MAIZE INBRED LINES USING LINE X TESTER ANALYSIS
BY

Mousa, S.Th. M. and Abd El-Azeem, M. E.M.
Maize Research Program, FCRI, ARC, Egypt

ABSTRACT

Fourteen yellow maize inbred lines derived from different local and exotic sources were crossed to each of two inbred lines testers, i.e. Giza-638 and Gemmeiza-1004 during summer season of 2006 at Sids Agricultural Research Station. In 2007, the 28 testcrosses in addition to two commercial single cross hybrids; SC-155 and SC-3084 were evaluated at two locations i.e. Sakha and Sids Agricultural Research Stations. Highly significant differences were found between the two locations(Loc.) for all studied traits. Mean squares due to crosses (C) and their partitions; lines (L), testers (T) and L x T were either significant or highly significant for all studied traits except for plant height and ear height of the testers. Mean squares due to C x Loc. interaction were significant for all studied traits except for grain yield. Line x Loc. interaction mean squares were significant for silking date, plant height and infection of late wilt disease. Results revealed that the non additive gene action played more important role than additive gene action in the inheritance of all traits, except for silking date. Interaction of σ^2GCA x location were higher than those of σ^2SCA x location for days to 50% silking and plant height, indicating that the additive genetic variance component was more influenced and interacted by locations than the non additive component. While, the non additive genetic variance component was more sensitive to location conditions than the additive component for ear height, infection % of late wilt disease and grain yield. The best desirable GCA effects for grain yield and most studied traits were obtained by L-6, L-7 and L-13. While, lines L-1, L-7, L-9 and L-11 showed desirable GCA effects toward earliness, shorter plants and lower ear placement. Meanwhile, high desirable GCA effects were obtained from T1 for grain yield and earliness traits. Results showed that eight topcrosses; i.e., L_1 x T_2 (31.05 ard/fed), L_1 x T_1 (30.93 ard/fed), L_6 x T_1 (31.25 ard/fed), L_6 x T_2 (31.38 ard/fed), L_7 x T_1 (32.28 ard/fed), L_4 x T_1 (32.89 ard/fed), L_{12} x T_1 (31.01 ard/fed) and L_{13} x T_1 (31.28 ard/fed) significantly outyielded the commercial single cross SC 155 (28.25 ard/fed).

Key words: maize, *Zea mays*, line x tester, combining ability, simple correlation

INTRODUCTION

The evaluation of new maize inbred lines can be accomplished through topcross test. Topcross procedure was first suggested by Davis (1927) to test the superiority of inbred lines for hybrid development programs. Ali and Tepora (1986) and Al-Naggar *et al.* (1997) used three way crosses, single crosses and inbred lines as testers to evaluate the combining ability and found that inbred lines with narrowest genetic base and lowest yield potential exhibited the highest genetic variation in the test cross progenies for most of the studied traits. They recommended that such inbred lines could be considered as the tester of choice for distinguishing the new inbred lines for their combining abilities.

Variance components due to specific combining ability (SCA) for grain yield and other agronomic traits were larger than variance components due to general combining ability (GCA), indicating the importance

of non-additive gene action in the inheritance of these traits (El-Morshidy *et al.,*2003; Aly 2004 and Aly and Mousa 2008). Interaction due to σ^2SCA x location were more affected by environmental conditions than those due to σ^2GCA x location for grain yield (El-Morshidy *et al.,* 2003). While, the σ^2 GCA x location interactions was more affected by environmental conditions than σ^2SCA x location interactions for plant height (Aly and Mousa 2008).

The present investigation was carried out with the following objectives: 1). Determining the combining ability effects for fourteen new maize inbred lines, 2) Learning about the most important mode of gene action controlling yield and some other traits, and 3) Identifying the most superior maize inbred lines in grain yield and quality to be utilized in maize breeding programs.

MATERIALS AND METHODS

Fourteen yellow maize inbred lines derived from three different populations i.e. L-1 and L-2 selected from segregating generations of the bank accession no.350 Y (originally Puerto Rico 23D # 213, Indian), L-3, L-4, L-5, L-6 and L-7 selected from segregating generations of the bank accession no.354 Y (originally Puerto Rico group # 218, Indian) and L-8, L-9, L-10, L-11, L-12, L-13 and L-14 (derived from maize breeding program) were topcrossed with two inbred testers, i.e. Giza-638 (T1) and Gemmeiza-1004 (T2) during 2006 summer season at Sids Agricultural Research Station. In 2007 summer season the 28 testcrosses in addition to two commercial hybrids; SC-155 and SC-3084 were evaluated in a yield trail carried out at two locations i.e. Sakha and Sids Agric. Res. Stations. The experimental design was a randomized complete blocks (RCB) with 4

replications. Plot size was one row, 6 m long and 80 cm apart. Planting was made in hills, evenly spaced at 25 cm along the row. Data were recorded for no. of days to 50% silking, plant height (cm), ear height (cm), infection with late wilt disease (%) and grain yield (ardab/feddan) adjusted to 15.5% moisture content. Combined analysis of data across two locations after testing homogeneity of error mean squares was performed according to Steel and Torrie (1980). Combining ability analysis was computed according to Kempthorne (1957). Hybrid (topcrosses) effects were considered as fixed and locations as random in the analysis of variance. Data on percentage of late wilt disease infection were subjected to arcsine transformation before statistical analysis, as devised by Steel and Torrie (1980).

RESULTS AND DISCUSSION

The combined analysis of variance over two locations for five traits, i.e. no. of days to 50% silking, plant and ear heights, infection of late wilt disease % and grain yield is given in Table (1). Results revealed that mean squares due to locations(Loc.) were highly significant for all studied traits, indicating that these traits differed in performance from one location to another. This is in agreement with findings reported by Soliman *et al.* (1995), Shehata *et al.* (1997), El-Zeir (1990), El-Zeir *et al.* (2000), Amer *et al.*(2003), Aly and Mousa (2008). Mean squares due to crosses (C) and their partitions; lines (L), testers (T) and L x T were significant and highly significant for all studied traits, except

for plant and ear heights of testers. Furthermore, C x Loc interactions mean squares were significant for all studied traits except for grain yield, L x Loc interactions mean squares were significant for days to 50% silking, plant height and infection of late wilt disease. On the other hand, all interactions of T x Loc and L x T x Loc were not significant, except for days to 50% silking of T x Loc and for ear height and infection of late wilt disease of L x T x Loc, indicating different ranks of interaction of inbred lines in their topcrosses from one location to another in most studied traits. These findings agree with those reported by Amer *et al.*(2003), Aly (2004) and Aly and Mousa (2008).

Table (1): Combined analysis of variance across two locations for the five traits, i.e. days to 50% silking, plant and ear heights, infection of late wilt and grain yield, 2007.

S.O.V.	D.F.	50% Silking (days)	Plant height (cm)	Ear height (cm)	Infection of late wilt disease %	Grain yield (ard/fed)
Locations (Loc.)	1	206.362**	34825.219**	17785.786**	236.161**	318.223**
Reps/Loc.	6	7.487	274.754	129.592	1.158	21.301
Crosses (C)	27	16.5**	1329.447**	876.207**	33.856**	275.588**
Lines (L)	13	25.775**	2481.732**	1619.67*	40.365**	35.591**
Testers (T)	1	69.754**	222.004	132.071	47.398**	72.617**
Lines x Testers	13	3.129**	262.351**	189.985**	26.305**	16.122**
C x Loc.	27	2.213**	151.006*	113.221*	33.704**	8.573
Lines x Loc.	13	2.64**	186.084*	83.411	41.026**	8.191
Testers x Loc.	1	9.862**	246.54	33.018	26.924	14.913
L x T x Loc	13	1.198	108.579	149.201*	26.904**	8.468
Pooled error	162	0.863	97.165	71.209	7.16	7.171

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

Mean performance of the tested materials combined over two locations for all studied traits; days to 50% silking, plant and ear heights, infection % of late wilt disease and grain yield are presented in Table (2). Results showed that eight top crosses; L_1 x T_2 (31.05 ard/fed), L_3 x T_1 (30.93 ard/fed), L_6 x T_1 (31.25 ard/fed), L_6 x T_2 (31.38 ard/fed), L_7 x T_1 (32.28 ard/fed), L_8 x T_1 (32.89 ard/fed), L_{12} x T_1 (31.01 ard/fed) and L_{13} x T_1 (31.28 ard/fed), significantly outyielded than the higher yielding commercial single cross hybrid SC 155 (28.25 ard/fed). Furthermore, most of top crosses exhibited similar productivity to that of the best check SC-155 since no significant differences existed. Number of days from planting to 50% silking was taken as indicator to maturity. Based on the results eight top crosses were significantly earlier maturity than the earlier check hybrid (SC 155). For plant and ear heights, all topcrosses of the two testers were significantly of shorter plants and lower ear placement than the higher yielding check hybrid (SC 155), except plants of the top crosses (L_1 x T_1), (L_1 x T_2), (L_2 x T_1) and (L_2 x T_2) which were taller and higher than those of the check hybrid . Considering the infection % of the late wilt disease, all top crosses along with the two check hybrids exhibited very low values of infection, except the top cross ($L10$ x $T1$) which recorded

infection value of 10.52%, and was considered of high infection value. Actually, it is not permitted to cultivate maize hybrids in Egypt exhibiting more than 10% infection of late wilt disease at any location. Based on these results, only four top crosses; i.e., ($L6$ x $T1$), ($L6$ x $T2$), ($L7$ x $T1$) and ($L13$ x $T1$) significantly out yielded the best check hybrid (SC 155), and showed better performance than that of SC.155 regarding all other agronomic traits.

General combining ability (GCA) effects for studied traits combined across two locations are illustrated in Table (3). Results revealed that the best inbred lines, which possessed significant desirable GCA effects were; L-6, L-7 and L-13 for grain yield; L-1, L-6, L-7 and L-11for earliness; L-4, L-6, L-7, L-9,L-10, L-11 and L-12 for shorter plant and lower ear placement. Meanwhile, high desirable GCA effects for the testers were obtained from the T_1 for grain yield and earliness traits. These results indicated that the inbred line tester T_1 had a high frequency of favorable dominant alleles, which contributed to the yield of its topcrosses. Amcha (1977), Al-Naggaar *et al.*(1997), Abd El-Azeem (2000) and Amer *et al.*(2003) reported that most efficient testers for grain yield were inbred lines since they are of narrow genetic base and low yield potential.

Table (2): Mean performance for all studied traits combined across the two locations.

Lines	50% Silking (days)		Plant height (cm)		Ear height (cm)		Infection of late wilt disease %		Grain yield (ard/fed)	
	T_1	T_2	T_1	T_2	T_1	T_2	T_1	T_2	T_1	T_2
line - 1	60.25	60.75	260.00	262.00	141.88	149.25	1.50	1.50	29.38	31.05
line - 2	60.63	62.00	267.88	260.50	144.00	143.00	0.00	0.00	28.03	27.81
line - 3	63.13	63.50	255.88	247.63	138.50	137.50	0.00	0.00	30.93	27.10
line - 4	60.88	63.25	224.38	233.50	119.00	127.50	0.00	2.00	25.96	28.13
line - 5	61.75	62.75	256.50	247.25	140.25	134.75	0.00	0.00	29.94	29.93
line - 6	59.00	60.00	234.25	241.63	120.25	130.50	3.20	0.50	31.25	31.38
line - 7	58.38	59.00	227.88	223.63	116.25	115.13	2.07	0.50	32.28	29.37
line - 8	61.88	62.38	257.13	252.63	149.50	139.00	0.00	0.00	32.89	28.63
line - 9	59.75	62.63	235.38	246.13	119.63	132.50	0.00	0.00	30.70	29.76
line - 10	60.75	62.38	237.88	234.00	130.50	128.50	10.52	1.50	27.94	24.90
line - 11	60.13	61.00	236.88	224.38	124.13	120.75	1.60	2.02	30.41	29.20
line - 12	61.88	61.63	244.13	229.88	126.88	122.25	2.02	1.00	31.01	27.79
line - 13	60.88	63.13	250.50	255.63	141.00	145.25	0.00	0.00	31.28	31.03
line - 14	62.75	63.25	253.38	255.38	138.13	145.50	1.50	0.50	29.35	29.13
$\overline{X}$	60.86	61.97	245.86	243.87	132.13	133.67	1.60	0.68	30.10	28.94
SC-155	61.50		265.37		150.00.		0.50		28.25	
SC-3084	64.88		274.75		140.75		0.00		26.16	
LSD 0.05	0.910		9.660		8.270		2.622		2.624	
0.01	1.197		12.706		10.877		3.449		3.452	

Table (3): General combining ability (GCA) effects for studied traits combined across two locations.

	50% Silking (days)	Plant height (cm)	Ear height (cm)	Infection of late wilt disease %	Grain yield (ard/fed)
Line -1	-0.915**	16.139**	12.661**	0.360	0.687
Line-2	-0.103	19.326**	10.599**	-1.140	-1.603*
Line-3	1.898**	6.889**	5.099*	-1.140	-0.512
Line-4	0.648**	-15.924**	-9.652**	-0.140	-2.475**
Line-5	0.835**	7.014**	4.599*	-1.140	0.411
Line-6	-1.915**	-6.924**	-7.527**	0.710	1.790**
Line-7	-2.728**	-19.112**	-17.215**	0.143	1.280*
Line-8	0.710**	10.014**	11.349**	-1.140	1.240
Line-9	-0.228	-4.112*	-6.840**	-1.140	0.708
Line-10	0.148	-8.924**	-3.402	4.871**	-3.104**
Line-11	-0.853**	-14.237**	-10.465**	0.668	0.280
Line-12	0.335	-7.877**	-8.340**	0.371	-0.125
Line-13	0.284	8.201**	10.224**	-1.140	1.634*
Line-14	1.585**	9.514**	8.911**	-0.140	-0.210
Tester-1	-0.558**	0.996	-0.768	0.465	0.569*
Tester-2	0.558**	-0.996	0.768	-0.465	-0.569*
LSD gi (L) 0.05	0.455	4.829	4.136	1.311	1.311
0.01	0.598	6.347	5.435	1.723	1.723
LSD gi (T) 0.05	0.172	1.825	1.562	0.495	0.496
0.01	0.256	2.398	2.053	0.651	0.652

Specific combining ability (SCA) effects for days to 50% silking, plant and ear heights, infection of late wilt disease and grain yield in the combined across two locations are given in Table (4). Topcrosses which exhibited significant negative SCA effects were L_9 x T_1 and L_{12} x T_2 for days to 50% silking toward

earliness; L_8 x T_2 for ear height toward lower ear placement; L_{10} x T_2 for infection of late wilt disease toward higher resistance to late wilt. Top crosses L_4 x T_2 and L_8 x T_1 exhibited significant positive SCA effects for grain yield toward higher yield.

Table (4): Specific combining ability (SCA) effects for studied traits combined across two locations.

	50% Silking (days)		Plant height (cm)		Ear height (cm)		Infection of late wilt disease %		Grain yield (ard/fed)	
	T_1	T_2	T_1	T_2	T_1	T_2	T_1	T_2	T_1	T_2
line - 1	0.308	-0.308	-1.996	1.996	-2.920	2.920	-0.460	0.460	-1.404	1.404
line - 2	-0.130	0.130	2.692	-2.692	1.268	-1.268	-0.460	0.460	-0.460	0.460
line - 3	0.371	-0.371	3.130	-3.130	1.268	-1.268	-0.460	0.460	1.345	-1.345
line - 4	-0.616	0.616	-5.558	5.558	-3.482	3.482	-1.460	1.460	-1.856*	1.856*
line - 5	0.058	-0.058	3.630	-3.630	3.518	-3.518	-0.460	0.460	-0.561	0.561
line - 6	0.058	-0.058	-4.683	4.683	-4.342	4.342	0.890	-0.890	-0.632	0.632
line - 7	0.246	-0.246	1.130	-1.130	1.331	-1.331	0.323	-0.323	0.860	-0.860
line - 8	0.308	-0.308	1.255	-1.255	6.018*	-6.018*	-0.460	0.460	1.866*	-1.866*
line - 9	-0.880**	0.880**	-6.371	6.371	-5.670	5.670	-0.460	0.460	-0.102	0.102
line - 10	-0.230	0.230	0.942	-0.942	1.768	-1.768	4.051**	-4.051**	0.953	-0.953
line - 11	0.121	-0.121	5.255	-5.255	2.456	-2.456	-0.673	0.673	0.035	-0.035
line - 12	0.683*	-0.683*	6.130	-6.130	3.081	-3.081	0.051	-0.051	1.040	-1.040
line - 13	-0.567	0.567	-3.558	3.558	-1.357	1.357	-0.460	0.460	-0.445	0.445
line - 14	0.308	-0.308	-1.996	1.996	-2.920	2.920	0.040	-0.040	-0.533	0.533
LSD 0.05	0.643		6.831		5.847		1.854		1.856	
0.01	0.845		8.977		7.684		2.437		2.439	

Estimate of the variance due to general combining ability (σ^2GCA), specific combining ability (σ^2SCA) and their interaction with locations are illustrated in Table (5). Results showed that estimates of (σ^2SCA) were higher than those of (σ^2GCA) for all studied traits except no. of days to 50% silking, indicating that the non additive gene action played more important role than the additive gene action in the inheritance of these traits. These results are in agreement with those reported by Sprague and Tatum (1942) and Rajos and Sprague (1952), Nawar and El-Hosary (1984), El Shenawy *et al.* (2003) and Mosa (2004). While for days to 50% silking estimate value of σ^2GCA exceeded that of σ^2SCA, indicating that the additive gene action was more important than the non additive one in the inheritance of such trait. Similar findings were obtained by Sokolv and

Kostyuchanco (1978), Shehata (1992), Mosa (1996), El-Zeir (1999), El-Zeir *et al.* (2000), Abd El-Azeem (2000) and Aly and Mousa (2008). On the other hand, the magnitude of σ^2GCA x location interaction was higher than that of σ^2SCA x location interaction for days to 50% silking and plant height indicating that the additive component of the genetic variance was more influenced and interacted by locations than the non additive component. Meanwhile, the non additive genetic variance component was more sensitive to the location environmental conditions than the additive component for ear height, infection of late wilt disease and grain yield. These results are in agreement with those reported by Joshi *et al.* (1998), Mahmoud (1996), El-Zeir *et al.* (2000) and Aly and Mousa (2008) for days to 50% silking and plant height; and (El-Hosary

(1988), El-Kielany (1999) and Mosa (2004) for grain yield).

Simple correlation coefficients between grain yield, days to 50% silking, plant height and ear height were computed based on the combined performance across two locations and presented in Table (6). All coefficients were highly significant except that of the correlation between days to 50% silking date and grain yield. Days to 50% silking date was negatively correlated with both plant and ear heights. While, plant height was positively correlated with ear height and grain yield. Also, ear height was positively correlated with grain yield. Similar findings were obtained by Saleem et al.(2007) and Shakoor et al. (2007).

Table (5): Estimate values of the variance due to general combining ability (σ^2GCA), specific combining ability (σ^2SCA) and their interactions with locations for the studied traits.

Genetic parameters	50% Silking (days)	Plant height (cm)	Ear height (cm)	Infection of late wilt disease(%)	Grain yield (ard/fed)
σ^2 GCA	0.697	17.024	10.717	0.274	0.593
σ^2 SCA	0.283	20.648	14.847	2.393	1.119
σ^2 GCA/σ^2 SCA	2.463	0.824	0.722	0.115	0.530
σ^2 GCA x Loc	0.158	3.367	-2.843@	0.221	0.096
σ^2 S CA x Loc	0.084	2.854	19.498	4.936	0.324
σ^2 GCA x Loc /σ^2 S CA x Loc	1.881	1.180	-0.155	0.045	0.296

@ Variance estimate preceded by negative sign is considered zero (Robinson et al. 1955)

Table (6): Simple correlation coefficients between grain yield, days to 50% silking, plant height and ear height combined across two locations.

	50% Silking (days)	Plant height	Ear height	Grain yield (ard/fed)
50% Silking (days)	-	-0.506**	-0.631**	-0.311
Plant height		-	0.939**	0.597**
Ear height			-	0.432**
Grain yield (ard/fed)				-

REFERENCES

Abd El-Azeem, M.E.M. (2000): Combining ability analysis of grain yield and its components in maize. Ph.D. Thesis, Fac. Agric., Moshtohor, Zagazig Univ., Egypt.

Ali, M.L. and Tepora, N.M. (1986): Comparative performance of four types of testers for evaluating corn inbred lines from two populations. Crop Sci., 11(3): 175-179.

Al-Naggar, A.M.; El-Sherbieny, H.Y.and Mahmoud, A.A. (1997): Effectiveness of inbreds, single crosses and populations as testers for combining ability in maize. Egypt. J. Plant Breed., 1: 35 – 46.

Aly, A.A. (2004): Combining ability and gene action of new inbred maize lines (Zea mays L.) using line x tester analysis. Egypt. J. Appl. Sci., 19(12 B): 492 – 518.

Aly, R.S.H. and Mousa, S.Th.M. (2008): Estimation of combining ability for newly developed white inbred lines of maize (Zea mays L.) via line x tester analysis. Egypt. J. of Appli. Sci., 23(2B): 554 – 564.

Ameha, M. (1977): Comparison of S2 progeny and inbred tester methods for improving maize. Ph. D. Thesis, Fac. Agric., Iowa State Univ., USA.

Amer, E.A.; El-Shenawy, A.A. and Metawei, A.A. (2003): Combining ability of new maize inbred lines via line x tester analysis. Egypt. J. Plant Breed. 7(1): 229 – 239. Proceed Third Pl. Breed. Conf. April 26, 2003, Giza.

Davis, R.L. (1927): Report of the plant breeding. Ann. Rep. Pureto Rico Agric. Res., 48: 14 – 45.

El-Hosary, A.A. (1988): Study of combining ability in some top crosses in maize. Egypt. J. Agron. 10(1-2): 39-47.

El-Kielany, M.E.M. (1999): Evaluation of some new inbred lines of maize (Zea mays L.). Ph.D. Thesis, Fac. Agric., Zagazig Univ., Egypt.

El-Morshidy, M.A.; Hassaballa, E.A.; Abou-Elsaad, Sh.F. and Abd El-Moula, M.A. (2003): Combining ability and type of gene action in maize under favorable and water stress environments. Egypt. J. Plant Breed., 7(1): 55 – 75.

El-Shenawy, A.A.; Amer, E.A. and Mosa, H.E. (2003): Estimation of combining ability of newly developed inbred lines of maize by (line x tester) analysis. J. Agric. Res. Tanta Univ., 29(1): 50 – 63.

El-Zeir, F.A. (1990): Genetic studies on some inbred lines of maize and their single crosses. Ph. D. Thesis, Fac. Agric. Al-Azhar Univ. Egypt.

El-Zeir, F.A. (1999): Evaluating some new inbred lines for combining ability using top-crosses in maize (Zea mays L.). Minufiya J. Agric. Res. 24(5): 1609-1620.

El-Zeir, F.A.; Amer, E.A.; Abdel-Aziz, A.A. and Mahmoud, A.A. (2000): Combining ability of new maize inbred lines and type of gene action using top crosses of maize. Egypt. J. Appl. Sci., 15(2): 116 – 128.

Joshi, V.N.; Pandiya, N. and Dubey, R.B. (1998): Heterosis and combining ability for grain yield and quality in early maturing single crosses of maize. Indian J. Gene. Plant Breed., 58: 519 – 524.

Kempthorne, O. (1957): An introduction to genetic statistical. John Wiley-Sons Inc., New York U.S.A.

Mahmoud, A.A. (1996): Evaluation of combining ability of newly developed inbred lines of maize. Ph.D. Thesis, Fac. Agric. Cairo Univ., Egypt.

Mosa, H.E. (1996): Studies on corn breeding. M Sc. Thesis, Fac. of Agric. Kafer El-Sheikh, Tanta Univ., Egypt.

Mosa, H.E. (2004): Comparison between two types of testers for evaluating new white inbred lines of maize. Annals of Agric. Sci., Moshtohor, 42(2): 475 – 487.

Nawar, A.A. and El-Hosary, A.A. (1984): Evaluation of eleven testers of different genetic sources of corn. J. Genet. Cytol., 13: 227-237.

Rojas, B.A. and Sprague, G.F. (1952): A comparison of variance components in grain yield traits. III- general and specific combining ability and their interaction with locations and years. Agric. J. 44: 462-466.

Saleem, A.; Saleem, U. and Subhani, G.M. (2007): Correlation and path coefficient analysis in maize (Zea mays L.). Journal of Agric. Res. (Pakistan), 45(3): 177 – 183.

Shakoor, M.S.; Akber, M. and Hussain, A. (2007): Correlation and path coefficient studies of some morphological traits in maize double crosses. Pakistan J. of Agric. Sci., 44(2): 213 – 216.

Shehata, A.M. (1992): Breeding and genetic studies of maize. Ph.D. Thesis, Agric. Monofiya Univ. Egypt.

Shehata, A.M.; El-Zeir, F.A. and Amer, E.A. (1997): Influence of tester lines on evaluating combining ability of some new maize inbred lines. J. Agric. Mansoura Univ., 22(7): 2159-2176.

Soklov, B.P. and Kostyuchanco, V.I. (1978): Choice testers for the evaluation of combining ability in maize lines in top-crosses. S1, Skokhazyaistvennaya Biolog., 13(1): 44 – 48. (C.F. Computer search).

Soliman, F.H.S.; EL-Shenawy, A.A.; El-Zeir, F.A. and E.A. Amer (1995): Estimates of combining ability and type of gene action in top-crosses of yellow maize. Egypt. J. Appl. Sci., 10(8): 312-329.

Sprague, G.F. and Tatum, L.A. (1942): General vs. specific combining ability in single crosses of corn. J. Amer. Soc. Agron. 34: 923 – 932.

Steel, R.G. and Torrie, J.H. (1980): Principles and procedures of statistics. Mc Grow Hill Inc., New York U.S.A

القدرة على التآلف لسلالات صفراء جديدة من الذرة الشامية باستخدام تحليل السلالة X الكشاف

سمير ثروت محمود موسى ، محمد المهدى محمد عبد العظيم

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

هجنت أربعة عشر سلالة صفراء من الذرة الشامية من مصادر مختلفة أجنبية ومحلية مع إثنين من الكشافات وهم سلالة جيزة$638(T_1)$ وسلالة جميزة $1004(T_2)$) فى موسم ٢٠٠٦ بمحطة البحوث الزراعية بسدس . قيمت الهجن الناتجة بالإضافة إلى إثنين من هجن المقارنة وهم هجين فردى-١٥٥ وهجين فردى-٣٠٨٤ فى موسم ٢٠٠٧ فى محطتى بحوث (سخا وسدس) فى تصميم القطاعات كاملة العشوائية وتم التحليل الوراثى باستخدام تحليل (السلالة x الكشاف) بغرض تقدير القدرة الإئتلافية للسلالات تحت الدراسة لصفات محصول الحبوب ، عدد الأيام حتى ظهور ٥٠ % من الحراير وإرتفاع النبات وإرتفاع الكوز ونسبة الإصابة بمرض الذبول المتأخر. وكانت أهم النتائج المتحصل عليها كما يلى:-

١ – وجدت إختلافات عالية المعنوية بين المواقع لكل الصفات تحت الدراسة.

٢ – وجدت إختلافات معنوية بين الهجن ومجزئاتها من (السلالات والكشافات والسلالة فى الكشاف) لكل الصفات ماعد تباين الكشافات لصفات إرتفاع النبات وإرتفاع الكوز.

٣ – كانت التفاعل بين الهجن والمواقع معنوية لكل الصفات تحت الدراسة ما عدا صفة المحصول بينما كان تفاعل السلالات مع المواقع معنويا لصفات التزهير وإرتفاع النبات وإرتفاع الكوز ونسبة الإصابة بمرض الذبول المتأخر.

٤ – لعب الفعل الجينى غير المضيف الدور الأكبر والأكثر أهمية فى وراثة جميع الصفات ما عدا صفة التزهير. كان تباين الفعل الجينى غير المضيف أكثر حساسية للظروف البيئية لصفات المحصول وإرتفاع النبات والإصابة بمرض الذبول بينما كان تباين الفعل الجينى المضيف أكثر تأثراً بالمواقع لصفات التزهير وإرتفاع الكوز.

٥ – أظهرت السلالات L-13, L-7, L-6 أفضل قدرة عامة على التآلف لصفات المحصول بينما كانت السلالات L-11 L-7, L-6, L-1 تمتلك أفضل قدرة إئتلاف مرغوبة فى إتجاة التبكير وقصر النبات وموقع أفضل للكوز على النبات فى حين أظهر الكشاف الأول T_1 أحسن قدرة إئتلاف عالية ومرغوبة لصفات محصول الحبوب والتبكير.

٦ – أظهرت النتائج وجود هجن قمية تفوقت على أفضل هجين المقارنة الهجين الفردى ١٥٥ (٢٥٫٢٨ أردب/فدان) فى صفة المحصول وهى:

L_6 x (٣١٫٢٥ أردب/فدان), L_6 x T_1 (٣٠٫٩٣ أردب/فدان), L_3 x T_1 (٣١٫٠٥ أردب/فدان), L_1 x T_2 T_2 (٣٢٫٨٩ أردب/فدان), L_8 x T_1 (٣٢٫٢٨ أردب/فدان), L_7 x T_1 (٣١٫٣٨ أردب/فدان), L_{12} x T_1 (٣١٫٢٨ أردب/فدان), L_{13} x T_1 (٣١٫٠١ أردب/فدان).