UTILIZATION OF NARROW BASE TESTERS FOR EVALUATING COMBINING ABILITY OF NEWLY DEVELOPED YELLOW MAIZE INBRED LINES
(*Zea mays* L.)

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ABSTRACT

Fourteen S_3 yellow maize inbred lines, derived from the wide genetic base population Giza-45 (EV-3), were topcrossed to each of three yellow maize inbred testers, i.e. Gz 638, Gm 1002 and Gm 1021. The 42 topcrosses were evaluated in 1999 at Sakha, Gemmeiza and Sids Agric. Res. Stations for grain yield, resistance to late wilt disease, silking date, plant height and ear position. Testers contributed much more than the lines to the total genetic variation and were more affected by the environmental conditions. The inbred testers ranked the 14 inbreds differently. Parental females L-2, L-4, L-7 and L-10 were found to be the best general combiner for high yielding ability. Parental lines L-2, L-4, L-6, L-13 and L-14 were good donors for resistance to late wilt disease. L-4, L-5, L-7, L-9 and L-12 were significantly better general combiners for earliness. Inbred tester Gm 1021 manifested highest average performance of grain yield compared to testcrosses of Gz 638 or Gm 1002. Results showed that Gm 1021 crossed to inbreds L-10, L-2 and L-7 would produce the best single crosses which significantly outyield the yellow commercial check hybrid SC 161 (30.60 ard/fed) by 7.03, 5.61 and 5.14 ard/fed, respectively. The cross (L-10 x Gm 1021) significantly outyielded the best white check SC 10 (33.24 ard/fed) by 4.39 ard/fed. and showed positive significant SCA effects for grain yield. The greatest inter and intra allelic interaction in terms of SCA were observed in 9 out of 42 topcrosses for grain yield. 4 crosses for late wilt resistance and one cross for earliness.

The magnitude of the ratio of general to specific combining ability variances (σ^2 GCA to σ^2 SCA) revealed that the additive component of gene action had the major role in the inheritance of all traits, except late wilt resistance. However, the magnitude of the interactions between σ^2 SCA X location was generally higher than that of σ^2 GCA x location for the studied traits, except grain yield.

Key words: *Yellow maize, Inbred, Testers, Combining ability, Narrow base testers.*

INTRODUCTION

The increased demand for yellow maize (*Zea mays* L.) grains to provide the requirements of growing poultry industry and animal feed has emphasized the need for breeding yellow inbred lines of maize for developing superior yellow grain maize hybrids. Successful development of improved maize hybrids is dependent upon accurate evaluation of performance of inbred lines in crossing. The standard topcross procedure as

suggested by Davis (1927) has been widely used to evaluate the general combining ability of inbred lines in hybrid maize-breeding programs. Inbreds of high general combining ability are crossed to detect particular combinations that result in superior single cross, two-line, combinations for commercial use.

The choice of a tester to test the developed inbred lines is an important decision. Matzinger (1953) showed that a narrow genetic-base tester contributes more to line x tester interaction than does a heterogeneous one. Moreover, he defined a desirable tester as one that combines the greatest simplicity in use with the maximum information on performance to be expected from tested lines when used in other combinations. Also, Rawlings and Thompson (1962) and Hallauer (1975) indicated that a suitable tester should include simplicity in use, provide information that correctly classifies the relative merit of lines and maximize genetic gain. Russell *et al* (1973) and Zambezi *et al* (1986) suggested that inbred testers could be used for evaluation of both specific and general combining ability. Furthermore, Hallauer and Lopez-Perez (1979), Mahgoub *et al* (1996) and Shehata *et al* (1997) suggested that narrow genetic base tester can be effectively used to identify lines having good GCA and the most efficient is one having a low frequency of favorable alleles. Darrah *et al* (1972), Horner *et al* (1973) and Russell and Eberhart (1975) indicated the use of inbred lines as testers instead of broad genetic base testers because of the increased genetic variance among testcross progenies to about towice the case for broad-base testers. However, despite the definite advantage of inbred testers, there has been little available information on the relationship of the performance of the tester and its ability to expose differences in combining ability among tested inbred.

The inbred testers (Gz 638 Gm 1002 and Gm 1021) used in this study, had been found to have high GCA and contribute to the high yield potential of their crosses. The inbred lines Gm 1002 and Gm 1021 were found to contribute earliness genes to their hybrids (Soliman 2000), whereas, Gz 638 contribute genes for late wilt resistance in testcrosses (Mahgoub *et al* 1996). Testcross procedure is practiced commonly in the Egyptian maize breeding program to develop new inbred lines highly tolerant to late wilt (*Cephalosporium maydis*) disease and to study the combining ability pattern between lines and testers for the final goal of developing high yielding single cross hybrids.

The objectives of this study were to: (i) assess the value of three inbred line testers in the evaluation of combining ability between fourteen newly developed yellow inbred lines and three inbred testers, (ii) determine the

type of gene action involved in the manifestation of grain yield and some other traits and (iii) identify the most superior line(s) and single crosses for further use in the breeding program.

MATERIALS AND METHODS

Fourteen S_3 yellow maize lines derived from a wide genetic base population Giza-45 (Ev-3) through selection from segregating generations in the disease nursery field at Sids Agric. Res. station, were used for the purpose of this study. Population 45 namely "Amarillo Bajio" was developed at the International Maize and Wheat Improvement Center (CIMMYT), Mexico. It is a subtropical, yellow dent kernels, has a broad genetic base and found to be resistant to late wilt disease, caused by *Cephalosporium maydis* (Abo El-Saad *et al* 1994). In 1998 growing season, the 14 S_3 lines were topcrossed to each of three yellow narrow base inbred testers *viz.* Gz 638, Gm 1002 and Gm 1021 at Sids Experimental Station. The three testers are being used in seed production of commercial single and three way cross hybrids . In 1999 season, the 42 resultant testcross, 14 parental lines and 3 testers along with two commercial check hybrids, SC 10, a white grain hybrid and SC 161 a yellow-grain hybrid, were evaluated in replicated yield trials conducted at three locations; Sakha ,Gemmeiza and Sids Agric. Res. Stations.

A randomized complete block design with three replications was used in each location. plots consisted of a single row, 6m long and 0.8m apart, and hills were spaced 0.25m along the row. Two kernels were planted per hill, and thinned later to one plant per hill to provide a population of approximately 22,000 plants/feddan (Feddan = 4200 m^2). All cultural practices were applied as recommended. Data were recorded for number of days to mid silking, plant height, ear position, resistance to late wilt disease and grain yield adjusted to 15.5 % grain moisture and converted to ardab/feddan (ardab = 140 kg). Analysis of variance was performed for the combined data over locations according to Steel and Torrie (1980), and Kempthorne (1957) procedure as outlined by Singh and Chaudhary (1979) was followed to obtain information about the combining ability of the lines and the testers and to also estimate types of gene effects controlling grain yield and other studied traits in the tested lines.

RESULTS AND DISCUSSION

The combined analysis of variance for the five studied traits is presented in Table (1). Highly significant differences were detected among locations for all studied traits, indicating that the three locations differed in

their environmental conditions. Mean squares among crosses were highly significant for all traits. Partitioning the sum of squares due to crosses into its components (Singh and Chaudhary 1979) showed that mean squares due to lines and testers were highly significant for all traits, revealing that greater diversity existed among testers and lines. At the same time, mean squares of the lines x testers interaction were highly significant for all the traits, except ear position, indicating that the lines (females) differed in order of performance in crosses with each of the testers (males). Mean squares due to the interaction of both lines and testers with locations were highly significant for grain yield and late wilt resistance. Also, the testers x locations interaction was significant for plant height. These interactions with locations were indicative of different ranking of genotypes of lines and testers from one location to another. Significant lines x testers x locations mean squares were detected for grain yield and late wilt resistance, revealing that the hybrids between lines and testers behaved somewhat differently form location to location. These results are in agreement with those obtained by El-Itriby *et al* (1990), Shehata *et al* (1997), Sadek *et al* (2000), Gado *et al* (2000) and Soliman (2000).

Table 1. Analysis of variance for grain yield and other traits of 14 inbred lines topcrossed with three inbred testers, combined over three locations, 1999 season.

S.O.V	DF	Grain yield	Days to mid silking	Plant height	Ear position %	L. W. resistance %
Locations(Loc.)	2	3124.8**	251.6**	43567.6**	3618.1**	2063.7**
Rep/(Loc.).	6	27.0	6.9	2338.7	254.0	119.3
Crosses+Checks	43	212.0**	19.3**	2926.4**	66.6**	189.8**
Crosses (Cr.)	41	216.7**	10.5**	2241.9**	68.0**	191.8**
Checks (Ch)	1	31.3	53.4**	8406.7**	4.8	282.4**
Cr. Vs. Ch	1	198.1**	346.3**	25509.8**	71.5*	16.0
Lines (L)	13	197.3**	21.4**	2689.2**	108.6**	342.7**
Testers (T)	2	2031.7**	38.1**	22951.9**	464.0**	409.1**
L x T	26	86.9**	2.9**	425.2**	17.2	99.6**
(Cr+Ch) x Loc.	86	30.6**	1.9**	134.1	18.9**	150.9**
Cr. X Loc.	82	30.3**	1.7*	132.9	14.9	151.9**
Ch x Loc.	2	60.0**	1.6	248.7	59.1**	234.4**
Cr. X Loc. *Vs* Ch x Loc	2	34.2*	15.6**	136.4	288.6**	28.7
L x Loc.	26	28.5**	2.0	140.2	14.5	225.0**
T x Loc.	4	227.7**	2.3	270.8*	22.2	433.0**
L x T x Loc.	52	16.0*	1.6	118.7	14.6	93.7**
Pooled error	258	11.2	1.2	105.9	11.4	38.9
CV. %		11.65	1.91	4.38	6.05	6.47

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

The magnitude of the variances due to testers and testers x locations interaction for all studied traits was higher than variance of lines and lines x locations interaction, respectively. This indicates that the testers contributed much more to the total variation and were more affected by the environmental conditions than the lines. Similar findings were obtained by El-Itriby *et al* (1990), Gado *et al* (2000) and Soliman (2000).

Considering grain yield, the obtained data presented in (Table 2) showed that over all parental lines, tester line Gm 1021 produced the highest grain yield (32.31 ard/fed) followed by Gm1002 (28.96 ard/fed), whereas the inbred tester Gz 638 gave the lowest grain yield (24.31 ard/fed). This result was reflected in the combining ability effects (Table 3), where Gm1021 was the best tester line in GCA effect; which had a good yield in its crosses with all tested lines (female lines), except line L-9. These results indicate that the inbred tester Gm 1021 possesses a high frequency of favorable dominant alleles, which contributed to the grain yield of the testcrosses. On the contrary, the tester line Gz 638 had a high negative GCA effect. Similar results were obtained by Soliman (2000) for Gm 1021 and Gm 1002 and Mahgoub *et al* (1996) for Gz 638.

Grain yield of the 14 lines across the three testers (Table-2) ranged from 21.39 to 32.07 ard/fed for testcrosses with lines L-9 and L-2, respectively. The most preferable lines were L-2, L-4, L-7 and L-10. These lines produced the highest average grain yield (ranging from 29.85 to 32.07ard/fed), and exhibited the best significantly positive GCA effects (Table-3). In other words, these lines in addition to the inbred tester Gm1021 had accumulated favorable alleles for grain yield and contributed to upgrading grain yield of all crosses involving these lines. On the other hand, L-9, L-11 and L-12 gave the lowest grain yield (ranged from 21.39 to 26.81 ard/fed) and had a high negative GCA effects (Tables-2&3). The results reported herein are in accordance with those previously reached by Rawlings and Thompson (1962), Liakat and Teparo (1986), El-Hosary (1988), Mahgoub *et al* (1996), Al-Naggar *et al* (1997), Shehata *et al* (1997) and Soliman (2000),who reported that the inbred tester method was more effective to select lines which combine well with unrelated tester. They emphasized that inbred testers were more effective in detecting small differences in combining ability than the wide genetic base testers.

Grain yield of the 42 topcrosses (Table 2) ranged from 15.86 to 37.63 ard/fed for L-12 x Gz 638 and L-10 x Gm 1021, respectively. 16 out of the 42 topcrosses were superior. These crosses outyielded the yellow commercial check hybrid SC 161 (30.60 ard/fed) with minimum of 0.05 ard/fed and maximum of 7.03 ard/fed (23 %). Furthermore, the three top

Table 2. Mean performance of 42 line x tester crosses and two checks, combined over three locations,1999 season.

Line	Grain yield (ard/fed)				Number of days to mid silking				Plant height (cm)			
	Gz-638	Gm-1002	Gm-1021	Mean	Gz-638	Gm-1002	Gm-1021	Mean	Gz-638	Gm-1002	Gm-1021	Mean
L-1	26.78	26.60	30.52	27.97	58.2	56.3	57.7	57.4	230.2	217.6	247.4	231.7
L-2	30.42	29.57	36.21	32.07	57.1	56.4	57.3	57.0	229.6	248.2	266.6	248.1
L-3	25.57	29.49	32.75	29.27	57.8	57.1	58.7	57.9	230.9	229.4	255.8	238.7
L-4	30.65	27.38	31.53	29.85	56.7	56.4	57.0	56.7	230.8	235.7	251.8	239.4
L-5	21.14	30.75	30.83	27.58	57.2	56.2	55.9	56.4	210.9	217.8	235.8	221.5
L-6	26.25	28.87	31.38	28.83	58.6	56.9	58.1	57.9	233.9	227.7	248.4	236.7
L-7	27.33	28.89	35.74	30.65	57.1	56.4	56.4	56.7	237.2	233.1	261.2	243.9
L-8	24.86	29.97	32.92	29.25	57.8	56.4	57.6	57.3	227.9	222.8	253.8	234.8
L-9	16.01	23.87	24.29	21.39	55.7	55.8	55.7	55.7	214.1	226.9	238.2	226.4
L-10	25.45	30.32	37.63	31.13	58.4	57.2	58.1	57.9	216.6	213.4	243.6	224.5
L-11	16.66	31.31	32.45	26.81	59.6	56.3	57.3	57.7	228.1	244.8	256.7	243.2
L-12	15.86	28.97	31.01	25.28	57.2	54.9	55.3	55.8	185.7	211.9	234.4	210.7
L-13	23.47	32.70	32.89	29.69	58.2	58.2	58.2	58.2	223.4	239.7	239.9	234.3
L-14	29.95	26.69	32.20	29.61	59.0	58.4	58.7	58.7	219.6	228.2	244.6	230.8
Average	24.31	28.96	32.31	28.53	57.8	56.7	57.3	57.3	222.8	228.4	248.4	233.2
Checks SC10	33.24				63.4				293.3			
SC161	30.60				60.0				250.1			
LSD for	5%	1%			5%	1%			5%	1%		
Lines (L)	1.79	2.35			0.58	0.77			5.49	7.23		
Testers (T)	0.83	1.09			0.27	0.36			2.54	3.35		
Crosses & checks	3.09	4.07			1.01	1.33			9.51	12.52		

Table 2. Cont.

Line	Ear position (%)				Late wilt resistance %			
	Gz-638	Gm-1002	Gm-1021	Mean	Gz-638	Gm-1002	Gm-1021	Mean
L-1	55.9	53.3	58.0	55.7	93.1	97.0	89.7	93.3
L-2	58.9	55.0	59.8	57.9	99.5	99.6	99.5	99.5
L-3	57.8	57.2	61.8	58.9	97.4	97.4	96.4	97.1
L-4	54.6	54.1	59.8	56.2	98.6	100.0	99.5	99.4
L-5	52.8	54.2	56.1	54.3	93.5	96.7	79.7	90.0
L-6	53.4	52.5	56.9	54.3	100.0	100.0	99.1	99.7
L-7	53.9	54.0	57.5	55.1	96.7	98.3	99.4	98.2
L-8	57.5	56.8	61.6	58.7	95.7	99.6	99.5	98.3
L-9	51.2	54.6	53.2	53.0	86.2	96.6	84.2	89.0
L-10	59.6	55.0	60.6	58.4	95.5	99.1	90.5	95.0
L-11	54.3	52.8	58.1	55.1	93.8	98.5	97.0	96.5
L-12	52.4	52.7	55.1	53.4	90.7	97.7	98.4	95.6
L-13	52.4	54.3	56.6	54.4	99.5	99.5	99.5	99.5
L-14	58.7	55.2	58.2	57.4	99.5	99.7	100.0	99.8
Average	55.3	54.4	58.1	55.9	95.7	98.6	95.2	96.5
Checks SC.10		53.4				99.5		
SC 161		54.4				91.5		

LSD for	5%	1%			5%	1%		
Lines (L)	1.80	2.37			3.3	4.4		
Testers (T)	0.83	1.10			1.5	2.0		
Crosses & checks	3.12	4.11			5.8	7.6		

most outyielding crosses, i.e. L-10 x Gm 1021, L-2 x Gm 1021 and L-7 x Gm 1021, gave the highest grain yield and highly significantly outyielded the yellow check hybrid SC 161 by 7.03, 5.61 and 5.14 ard/fed, respectively. Moreover, the most outstanding topcross (L-10 x Gm 1021) highly significant surpassed the best white check hybrid SC 10 (33.24 ard/fed) by 4.39 ard/fed, and exhibited a significantly positive SCA effect (Table 4).

Concerning SCA effects, data presented in Table (4) revealed that 9 out of the 42 topcrosses showed positively significant SCA effects. Five out of those nine topcrosses (L-4 x Gz 638, L-5 x Gm1002, L-11 x Gm1002, L-13 x Gm1002 and L-10 x Gm1021) are included among the 16 superior crosses. The other 4 testcrosses, however, were lower in grain yield but not significantly less than SC 161, except (L-1 x Gz 638). It is worth noting that a cross exhibiting high SCA may come from two parents

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Table 3. General combining ability effects ($\hat{g}_i$) of 14 inbred lines and three testers for the studied traits, combined over three locations, 1999 season.

Genotypes		Grain yield	days to mid silking	Plant height	Ear position	L. W. resistance %
Lines	L-1	-0.561	0.174	- 1.450	-0.205	-3.218**
	L-2	3.541**	-0.270	14.921**	1.971**	3.051*
	L-3	0.743	0.619**	5.513**	3.007**	0.596
	L-4	1.325*	-0.529*	6.217**	0.306	2.919*
	L-5	-0.951	-0.788**	- 11.709**	-1.582*	-6.510**
	L-6	0.306	0.619**	3.476	-1.646*	3.214**
	L-7	2.124**	-0.566**	10.661**	-0.773	1.690
	L-8	0.725	0.026	1.624	2.737**	1.781
	L-9	-7.140**	-1.529**	- 6.783**	-2.917**	-7.448**
	L-10	2.608**	0.693**	- 8.672**	2.468**	-1.452
	L-11	-1.721**	0.508*	9.994**	-0.846	-0.012
	L-12	-3.246**	-1.428**	-22.524**	-2.506**	-0.855
	L-13	1.158	0.989**	1.143	-1.479*	3.024*
	L-14	1.087	1.471**	- 2.413	1.466*	3.220**
Testers	Gz-638	-4.213**	0.521**	-10.421**	-0.660*	-0.775
	Gm.1002	0.429	-0.574**	- 4.825**	-1.502**	2.059**
	Gm.1021	3.784**	0.053	15.246**	2.162**	-1.284*
SE for Lines $\hat{g}_i$		0.644	0.211	1.980	0.650	1.200
$\hat{g}_i - \hat{g}_j$		0.911	0.298	2.801	0.919	1.689
Testers $\hat{g}_i$		0.298	0.098	0.917	0.301	0.556
$\hat{g}_i - \hat{g}_j$		0.422	0.138	1.297	0.425	0.766

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

possessing good GCA or from one parent with good GCA and another with poor GCA. For example the best S_{ij} for grain yield was exhibited between parents with poor and good GCA, L-2 x Gz-638, L-4 x Gz-638, L-14 x Gz 638, L-5 x Gm 1002, L-11 x Gm 1002 and L-12 x Gm 1002. Similar findings were obtained by Nawar *et al* (1979) and Nawar and El-Hosary (1985).

In respect of number of days to 50% silking, Table (2) shows that in general all the topcrosses were significantly earlier than the yellow check hybrid SC 161 (60.0 days), except (L-11 x Gz 638). For GCA effects (Table 3), the parental lines L-4, L-5, L-7, L-9, L-12, as well as, the inbred tester Gm 1002 had highly significant GCA effects towards earliness. In

Table 4. Specific combining ability effects ($\hat{S}_{ij}$) of 42 top-crosses for the studied traits, combined over three locations, 1999 season.

Top crosses	Grain yield	Days to mid silking	Plant height	Ear position	L. W. resistance
L-1 x T_1	3.027**	0.294	8.902**	0.846	0.579
L-2 x T_1	2.567*	-0.373	- 8.135*	1.705	0.725
L-3 x T_1	0.512	-0.595	2.606	-0.451	1.107
L-4 x T_1	5.009**	-0.558	1.791	-0.922	0.016
L-5 x T_1	-2.220*	0.257	- 0.172	-0.926	4.299*
L-6 x T_1	1.633	0.182	7.643*	-0.227	1.090
L-7 x T_1	0.893	-0.077	3.791	-0.551	-0.648
L-8 x T_1	-0.182	-0.002	3.495	-0.472	-1.814
L-9 x T_1	-1.169	-0.558	- 1.876	-1.100	-1.999
L-10 x T_1	-1.470	-0.002	2.458	1.852	1.269
L-11 x T_1	-5.935**	1.294**	- 4.653	-0.102	-1.866
L-12 x T_1	-5.213**	0.886*	-14.579**	-0.310	-4.110*
L-13 x T_1	-2.006	-0.521	- 0.468	-1.361	0.752
L-14 x T_1	4.553**	-0.225	- 0.802	2.020	0.601
L-1 x T_2	-1.796	-0.500	- 9.360**	-0.927	1.642
L-2 x T_2	-2.927**	0.056	4.937	-1.935	-2.024
L-3 x T_2	-0.208	-0.167	- 4.434	-0.218	-1.769
L-4 x T_2	-2.904**	0.314	1.085	-0.586	-1.448
L-5 x T_2	2.747*	0.352	1.122	1.369	4.696*
L-6 x T_2	-0.392	-0.389	- 4.175	-0.254	-1.743
L-7 x T_2	-2.193*	0.351	- 5.915	0.384	-1.891
L-8 x T_2	0.293	-0.241	- 7.212*	-0.308	-0.755
L-9 x T_2	2.050	0.648	5.307	3.077**	5.507**
L-10 x T_2	-1.244	-0.130	- 6.249	-1.877	1.977
L-11 x T_2	4.079**	-0.833*	6.418	-0.792	0.010
L-12 x T_2	3.265**	-0.532	6.048	0.811	0.029
L-13 x T_2	2.586*	0.574	10.159**	1.401	-2.036
L-14 x T_2	-3.356**	0.315	2.270	-0.644	-2.194
L-1 x T_3	-1.231	0.206	0.458	0.081	-2.220
L-2 x T_3	0.361	0.317	3.198	-0.270	1.300
L-3 x T_3	-0.305	0.762*	1.828	0.670	0.662
L-4 x T_3	-2.106	0.243	- 2.876	1.509	1.432
L-5 x T_3	-0.527	-0.608	- 0.950	-0.443	-8.994**
L-6 x T_3	-1.242	0.206	- 3.468	0.482	0.653
L-7 x T_3	1.301	-0.275	2.124	0.167	2.540
L-8 x T_3	-0.111	0.243	3.717	0.780	2.569
L-9 x T_3	-0.882	-0.090	- 3.431	-1.977	-3.509
L-10 x T_3	2.714*	0.132	3.791	0.025	-3.246
L-11 x T_3	1.856	-0.460	- 1.765	0.895	1.856
L-12 x T_3	1.948	-0.534	8.532*	-0.501	4.081*
L-13 x T_3	-0.580	-0.053	- 9.690**	-0.040	1.284
L-14 x T_3	-1.197	-0.090	- 1.468	-1.376	1.593
SE $\hat{S}_{ij}$	1.116	0.365	3.430	1.125	2.079
$\hat{S}_{ij} - \hat{S}_{kl}$	1.578	0.516	4.851	1.592	2.940

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

other words, topcrosses involving these lines and/or Gm 1021 as a tester were earlier. This indicates that these inbreds possess favorable genes for earliness. The same trend for Gm 1002 and Gm 1021 was reported by Soliman (2000). On the contrary, parental lines L-3, L-6, L-10, L-11, L-13, L-14 and the tester line Gz 638 had positive and highly significant GCA effects marked by lateness in silking appearance. However, data of Table (4) showed that the best specific combination (negatively significant SCA effect) resulted from L-11 x Gm 1002 conforming its earliness. On the other hand, three topcrosses, i.e, L-11 x Gz 638, L-12 x Gz 638 and L-3 x Gm 1021 had positively significant SCA effects in relation to lateness.

Considering plant height, data of Table (2) revealed highly significant differences among the three testers. The inbred tester Gz 638 was the shortest tester (222.8cm) followed by Gm 1002 (228.4cm), while the tester line Gm 1021 was the tallest (248.4cm). This result was reflected in the combining ability effects (Table 3), where Gz 638 was the inbred tester exhibiting the largest GCA effect towards shortness followed by Gm 1002. On the contrary, the inbred tester Gm 1021 had positive and highly significant (undesirable) GCA effect. For the parental lines, the best general combiners were L-5, L-9, L-10 and L-12, since they had highly significant negative (desirable) GCA effects and the shortest plants (Tables 2 and 3).

Plant height of the 42 topcrosses (Table 2) ranged from 185.7 to 266.6 cm for crosses L-12 x Gz 638 and L-2 x Gm 1021, respectively. Moreover, all the topcrosses involved the lines (L-5, L-9, L-10 and L-12) and the testers Gz 638 and Gm 1002 were significantly shorter than SC 161 (250.1cm), except three testcrosses (L-2 x Gm 1002, L-11 x Gm 1002 and L-10 x Gm 1021). Five topcrosses, i.e. L-2 x Gz 638, L-12 x Gz 638, L-1 x Gm 1002, L-8 x Gm 1002 and L-13 x Gm 1021 showed negative and significant or highly significant SCA effects in direction to shortness (Table 4). On the other hand, the highest positive SCA effects, towards tallness in plant height were shown in the topcrosses L-1 x Gz 638, L-6 x Gz 638, L-13 x Gm 1002 and L-12 x Gm 1021.

Considering ear position the obtained results (Tables 2 and 3) confirmed that the inbred tester Gm 1002 was the best in GCA effect towards low ear placement, followed by the tester line Gz 638. The inbred tester Gm 1002 had the lowest ear position (54.4 %) followed by Gz 638 (55.3 %). On the contrary, most of the topcrosses involved the inbred tester Gm 1021 showed significantly the highest ear placement (58.1 %), which corresponded with its highly significant GCA effect. For the parental lines across the three testers, L-5, L-6, L-9, L-12 and L-13 ranked the best with an average of 54.3, 54.3, 53.0, 53.4 and 54.4 %, respectively, and with distinct GCA effects, (negatively significant) towards low ear placement. On the

other hand, five parental lines exhibited the highest average for ear position (57.4 to 58.9 %), with highly significant positive GCA effects.

Average ear position for the top crosses (Table 2) ranged from 51.2 to 61.8 % for L-9 x Gz 638 and L-3 x Gm 1021, respectively. The topcross L-9 x Gz 638 was significantly lower in ear placement than SC 161 (54.4 %). Other 15 topcrosses, showed insignificantly lower ear placement than SC 161. None of the topcrosses, however showed significantly negative SCA effect for ear position. Although 25 out of the 42 topcrosses exhibited negative (desirable) SCA effects but did not reach the level of significance, except L-9 x Gm 1002 which manifested positively significant SCA effect towards high ear placement.

With respect to percent of resistance to late wilt disease (Table 2) performance of the 14 lines across the three testers ranged from 89.0 % (least resistant) to 99.8 % (most resistant) for lines L-9 and L-14, respectively.

Resistance to late wilt disease of five lines: L-2, L-4, L-6, L-13 and L-14 across the three testers, six lines crossed with Gm 1002 (L-3, L-7, L-8, L-10, L-11 and L-12) and three lines crossed with Gm 1021 (L-7, L-8 and L-12), in addition to L-3 x Gz 638 was significantly higher (ranged from 97.4 to 100.0 %) than the yellow check hybrid SC 161 (91.5 %). Furthermore, four out of the above mentioned topcrosses (L-4 x Gm 1002, L-6 x Gm 1002, L-6 x Gz 638 and L-14 x Gm 1021) were higher in resistance to late wilt (100.0 %) but not significantly than the white check hybrid SC10 (99.5 %). General combining ability effects (Table 3) showed that lines L-2, L-4, L-6, L-13 and L-14 had the best significant GCA effects for late wilt resistance, suggesting that these parents are good donors for resistance to this disease. Considering SCA effects (Table 4), the highest desirable SCA effects towards resistance resulted from the topcrosses L-5 x Gz 638, L-5 x Gm 1002, L-9 x Gm 1002 and L-12 x Gm 1021, which showed significantly positive values. The three testers were significantly different in their reaction to late wilt disease (Table 1), and the inbred tester Gm 1002 across the 14 lines was significantly more resistant to late wilt (98.6 %) than the inbred testers Gz 638 (95.7 %) and Gm 1021 (95.2 %). This was reflected by GCA effects of 2.059**, -0.775 and -1.284* for the three testers, respectively. In this respect, Mahgoub *et al* (1996) found that the inbred tester Gz 638 across 20 tested lines was significantly resistant to late wilt disease and had good GCA.

The data obtained (Table 2) showed that resistance to late wilt disease ranged from 79.7 to 100.0 % for crosses with Gm 1021 and from 86.2 to 100.0 % for crosses with Gz 638. Resistance to late wilt, however, ranged

from 96.6 to 100.0 % for crosses with Gm 1002. Variation in resistance among testcrosses with Gm 1021 or Gz 638 was greater than that of testcrosses with Gm 1002. This result indicated that the lowest resistance inbred tester (Gm 1021) which might have a low gene frequency for resistance was better in differentiating among lines. On the contrary, susceptibility genes in the lines were masked in top crosses by the dominant genes of the more resistant inbred tester (Gm 1002). These results are in good agreement with Rawlings and Thompson(1962), Hallauer and Lopez-Perez (1979)and El-Itriby *et al* (1990) who concluded that narrow genetic base testers can be effectively used to identify lines having good GCA, and the most efficient tester is the one having a low frequency of favourable alleles.

The estimates of combining ability variances (σ^2 GCA and σ^2 SCA) and its interaction with locations (σ^2GCA x loc and σ^2 SCA x loc) for grain yield, late wilt resistance and other studied traits (Table 5) showed that GCA played the major role in determining the inheritance of all traits, except late wilt resistance. This indicates that the largest part of the total genetic variability associated with these traits was the result of additive gene action. On the other hand, non-additive genetic variance was predominant and played an important role in the inheritance of late wilt resistance. Similar findings were also obtained by Comstock and Robinson (1963), Eberhart *et al* (1966) and Darrah and Hallauer (1972). Also, Russell *et al* (1973), Hallauer and Mirinda (1981) and El-Itriby *et al* (1990) indicated the importance of additive gene action in affecting grain yield of maize. For late wilt, Shehata (1976), El-Itriby *et al* (1984) and Sadek *et al* (2000) found that SCA variance was more important in conditioning resistance than GCA variance. The non-additive gene action, however interacted more with different environmental conditions prevailing in the three locations than the additive gene effects for all studied traits, except for grain yield, where the opposite was true (Table5). This finding indicates non-additive types of gene action to be more affected by environment than additive and additive x additive types of gene action. This result is in agreement with the finding of several investigators who reported specific combining ability to be more sensitive to environmental changes than general combining ability (Gilbert 1958), Shehata and Dhawan (1975) and Sadek *et al* (2000) also found that the non-additive genetic variation interacted more with the environment than the additive component. Though, El-Itriby *et al* (1990) and El-Zeir *et al* (2000) reported that the additive types of gene action were more affected by environment than non-additive ones.

The study suggest that four testcrosses (L-2 x Gm 1021, L-7 x Gm 1021, L-10 x Gm 1021 and L-4 x Gm 638) should be tested further for

commercial use. In addition, the four inbreds included in these crosses (L-2, L-4, L-7 and L-10) had good GCA effects for yield, earliness and late wilt resistance, and three more inbreds (L-6, L-13 and L-14) have good GCA effects for late wilt resistance, shortness and lower ear placement (Table 3).These inbreds should be intermated to born a new synthetic variety of yellow maize, which can be used as a base population for the extraction of more favourable yellow lines for the development of high yielding, earlier and disease resistant single cross hybrids of yellow maize.

Table 5. Estimates of general (σ^2 GCA) and specific (σ^2 SCA) combining ability variances and their interaction with locations for grain yield and other traits.

Estimates	Grain yield	Days to mid silking	Plant height	Ear position	L. W. resistance %
σ^2gca	11.967	0.344	160.896	3.469	0.536
σ^2sca	7.878	0.144	34.056	0.289	0.656
σ^2gca x Loc.	4.396	0.022	3.404	0.147	9.228
σ^2sca x Loc	1.600	0.133	4.267	1.067	18.267

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استخدام كشافات ذات قاعدة وراثية ضيقة لتقييم القدرة على التآلف لسلالات جديدة من الذرة الشامية الصفراء

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في موسم ١٩٩٨ تم التهجين القمي لعدد ١٤ سلاله صفراء الحبوب من الذرة الشامية مستنبطة في الجيل الانعزالي الثالث من المجتمع الأصفر جيزة ٤٥ (حلقة التحسين الثالث) مع ثلاث سلالات صفراء كشافة صفراء الحبوب هي جيزة ٦٣٨ , جميزة ١٠٠٢ , جميزة ١٠٢١ تم تقييم الـ٤٢ هجينا قميا الناتجة في تجارب مكررة تم تنفيذها في محطات البحوث الزراعية بسخا والجميزة وسدس خلال موسم ١٩٩٩. وقيمت الهجن القمية الناتجة لصفات محصول الحبوب ، المقاومة لمرض الذبول المتأخر ، ميعاد ظهور النورة المؤنثة ، ارتفاع النبات ، موقع الكوز. وحللت البيانات بطريقة كمبثورن ١٩٥٧. ويمكن تلخيص أهم النتائج كما يلي:-

وجد أن التباين بين السلالات الكشافة كان اكبر من التباين بين السلالات المختبرة كما كان تباين السلالات الكشافة اكثر تأثراً بالظروف البيئية من السلالات المختبرة. وقد رتبت السلالات الكشافة السلالات المختبرة بصورة مختلفة. كانت السلالات الأبوية أرقام ٢، ٤، ٧، ١٠ احسن السلالات بالنسبة للمحصول حيث أظهرت تقديرات موجبة ومعنوية للقدرة العامة على التآلف لصفة محصول الحبوب وكذلك كانت القدرة العامة على التآلف للسلالات أرقام ٢، ٤، ٦، ١٣، ١٤ موجبة ومعنوية لصفة المقاومة لمرض الذبول المتأخر. بينما بالنسبة لصفة التزهير فان السلالات الأبوية أرقام ٤، ٥، ٧، ٩، ١٢ أظهرت تأثيرات سالبة ومعنوية اى مرغوبة (اتجاه التبكير) للقدرة العامة على التآلف. لذلك توصي الدراسة باستخدام السلالات الأبوية أرقام ٢، ٤، ٦، ٧، ١٠، ١٣، ١٤ في برنامج التربية للهجن عالية المحصول مع المقاومة العالية لمرض الذبول المتأخر وكذلك استعمالها في تكوين مجتمع وراثي جديد يخدم برنامج عزل السلالات. هذا وقد أعطت السلالة الكشافة جميزة ١٠٢١ اعلى محصول بالنسبة لهجنها الاختبارية إذا ما قورنت بالسلالة الكشافة جيزة ٦٣٨ أو جميزة ١٠٠٢ وقد أظهرت النتائج أن السلالة الكشافة جميزة ١٠٢١ عند تهجينها مع السلالات أرقام ١٠، ٢، ٧ أعطت ثلاث هجن فردية فاقت معنويا الهجين التجاري الأصفر ١٦١ (٣٠,٦ اردب/فدان) بمقدار ٧,٠٣ ، ٥,٦١ ، ٥,١٤ اردب/فدان على التوالي. بالإضافة لذلك فان الهجين الاختباري السالف الذكر (سلالة ١٠ X جميزة ١٠٢١) تفوق معنويا على الهجين الفردي التجاري الأبيض جيزة ١٠ (٣٣,٢٤ اردب/فدان) بمقدار ٤,٣٩ اردب/فدان. ومن الجدير بالذكر أن الهجين (سلالة ١٠ X جميزة ١٠٢١) أظهر تأثيرا موجبا ومعنويا للقدرة الخاصة على التآلف لصفة محصول الحبوب. اعطى عدد ٩ هجن قمية من جملة الـ٤٢ هجين المختبرة قدرة خاصة على التآلف عالية ومعنوية لصفة

المحصول العالي. كما اظهر ٤ هجن قيمة تقديرات موجبة ومعنوية للقدرة الخاصة على التآلف بالنسـبة لصفـة المقاومة لمرض الذبول المتأخر في حين انه اظهر هجين واحد تفوقا معنويا في القدرة الخاصة على التآلف لصفـة التبكير.

اظهر التباين الراجع للفعل الوراثي المضيف دورا اكثر أهمية بالمقارنة بالتباين الراجع للفعـل الوراثـي الغير مضيف في وراثة جميع الصفات تحت الدراسة عدا صفة المقاومة لمرض الذبول المتأخر ومــع ذلـك كـان التفاعل بين التأثير الغير مضيف والبيئة أعلى من التفاعل بين التأثير المضيف والبيئة لجميع الصفات المدروســة عدا صفة محصول الحبوب.