COMBINING ABILITY AND HETEROSIS FOR EARLINESS, GRAIN YIELD AND QUALITY CHARACTERS OF WHITE AND YELLOW MAIZE (*Zea mays* L.) ACROSS EIGHT ENVIRONMENTS

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ABSTRACT: Two separate line x tester experiments of white and yellow maize were evaluated under eight environmental conditions to study earliness, grain yield and quality characters. Seven inbred lines were crossed to each of three testers giving a total of twenty one top crosses of both white and yellow maize. The eight environments included two sowing dates, two nitrogen levels and two locations. General and specific combining ability effects were estimated using line x tester design as proposed by Kempthorne (1957).

Mean squares due to environments, genotypes and genotypes x environments showed highly significant differences for days to 50% silking, protein%, oil%, total carbohydrate% and grain yield/ha in both white and yellow maize. Variances due to top crosses and their components i.e., line effect, tester effect and line x tester effect were highly significant across eight environments indicating the existence of genetic variability in both white and yellow maize except oil and protein% for line effect and tester effect in yellow maize.

White inbred line L_3 had the best combination of general combining ability effects for protein and oil % across environments (0.89[**] and 0.10[**], respectively). Also, white lines L_1 and L_4 had positive and significant GCA effects for total carbohydrates, while white inbred line L_7 and tester T_{10} had the best desirable significant GCA effects for days to 50% tasseling and grain yield/ha. Yellow

inbred L_1 had the best combination of GCA effects for all traits across environments except protein %. White top cross (L_2 x T_{10}) had the most favorable significant SCA effects for protein and oil % and one hybrid (L_2 x T_8) for carbohydrate % over eight environments. The ratio of σ^2 GCA/σ^2 SCA was more than unity for days to 50% silking but less than unity for all quality characters and grain yield in both white and yellow maize, indicating that non additive genetic variance was predominant and played the major role in the gene expression of these traits.

Higher heritability of narrow sense T_n (%) was found (> 70%) for days to 50% silking and carbohydrate% in both white and yellow maize. While, moderate heritabilities were found for grain yield (33.21%) of white maize, protein (31.10%) and oil% (35.74%) of yellow maize. Heterosis for grain yield/ha ranged from 40.50 to 68.33% for mid parent; 10.08 to 60.99% for high parent and from -39.30 to 3.90 for standard heterosis (S.C. 10) of white maize, and varied from 42.62 to 64.75% for mid parent; 29.98 to 63.93% for high parent and from -34.81 to 0.63% for standard heterosis (S.C. 155) of yellow maize. The white hybrid (L_6 x T_8) was superior to its commercial control (S.C. 10) for grain yield and quality characters.

Key words: Maize, *Zea mays* L, line x tester, combining ability, heritability, heterosis.

INTRODUCTION

Maize (*Zea mays* L.; 2n=20) is an important cereal crop of the world. High grain yield, elevated kernel oil, kernel protein and early maturity are important traits in global bread maize breeding programmes. Improving these three traits simultaneously is difficult due to the negative association between grain yield and maturity and also grain yield and kernel oil and protein content.

High oil kernels may also have smaller endosperms, which is undesirable since this phenotype may contribute to decrease grain yield.

The protein content in maize kernels is about 9.5% and the 50 million tons of maize protein approximately produced account for 15% of the world protein production and 20% of the calories derived from food crops in the world's diet (National Research

Council, 1988). Maize oil is valued as a component of animal feed and as food. It is the best source of metabolizable energy in livestock feeding programs (Bajaj, 1994). Maize producer substantial amounts of carbohydrates, stored in the endosperm, high levels of glutamine acid and leucine-rich protein. However, nutritional quality of maize protein is poor because of deficiencies of the essential amino acids lysine, tryptophan, and methionine. The majority of maize protein (> 50%) in the grain fraction consists of zeins, which have very low amounts of these amino acids.

Research over several decades has indicated that while environmental effects can influence oil and protein accumulation. Jellum and Marion (1966) found that location and year of planting had a statistically significant effect on oil content, but the relative oil content among hybrids was similar in each test. (Jellum *et al.*, 1973) have investigated the impact of nitrogen on maize oil content, and found either no effect but (Genter *et al.,* 1956; Welch 1969; Duarte *et al,.* 2005; Miao *et al.*, 2006) observed that small effects from nitrogen treatments caused much larger

changes in grain yield and/or protein content. Several studies have looked at the effects of severe abiotic stresses on grain quality. The relative stability of the oil trait in response to environmental conditions is an advantage to researchers who interested in modification of oil content, since small differences between different varieties can be reliably measured.

The use of testers in a maize program has been well documented (Matzinger, 1953; Rawlings and Thompson, 1962; Allison and Curnow, 1966, Hallauer, 1975; Hallauer and Miranda, 1988; Russell *et al.,* 1992, Menz *et al.,* 1999 and Narro *et al.,* 2003). These authors concluded that choice of a suitable tester should be based on simplicity in its use, its ability to classify the relative merit of lines, maximize genetic gain, and enhance the expected mean yield of a population generated using selected cultivars. However, it is difficult to identify testers having all these characteristics because, initially in a breeding program, only open pollination varieties (OPV) are available.

The use of the parental variety as a tester results in some improvement of the mean

performance of the population (Rawlings and Thompson, 1962). Allison and Curnow (1966) suggested use of low-yielding varieties as testers. The use of a single-cross as a tester has been reported by Horner *et al.* (1976). The use of an inbred as tester in a recurrent selection program was suggested by Russell and Eberhart (1975) and it has been widely used by breeders (Darrah, 1985; Horner *et al.,* 1989). Genotype x environment interaction (GEI) is an important consideration in plant programs because it reduces the progress from selection in any environment (Hill, 1975). The interactions can be used to explain how the environment affects a plant. This interaction is a very important part of understanding the stability of plant performance.

The objectives of this study to estimate the general and specific combining ability and heterosis in both white and yellow maize for earliness characters, grain yield and quality characters. Investigate genotype x environment interaction across eight environments for these traits. Identify the most superior lines and top crosses that may be used in the future of maize breeding programs.

MATERIALS AND METHODS

Two separate line x tester experiments of white and yellow maize were carried out during two summer successive growing seasons. Using line x tester analysis described by Kempthorne (1957), in 2003, summer growing season, both of 7 inbred maize lines and 3 testers (two inbred lines and one open pollinated variety) either white or yellow maize were sown each in the separate experiments on two sowing dates, i.e. 11 June and 21 June at Experimental Farm, Fac. of Agric., Zagazig University (Ghazala village, Zagazig district in Sharkia governorate, Egypt).

Each inbred line was sown in 10 ridges; each ridge was 6 meters length; plant to plant and ridge to ridge distances were 25 and 70 cm, respectively. At the proper time, the seven white inbred lines were crossed with 3 different testers, i.e., Sids 7, Sids 63 and Giza 2. As well as, seven yellow maize inbred lines were crossed with 3 different testers, i.e., Composite 21 yellow, Gm. 1004 and Gm. 1021 by hand crossing to obtain seeds of 31 genotypes i.e., twenty-one top cross and seven inbred lines and

three tester genotypes in both white and yellow maize.

In the 2nd growing season 2004, the obtained seeds of white and yellow maize parental genotypes i.e., inbred lines (7) + testers (3) + top crosses (21) + commercial checks (2) were tested separately in two trials planted side by side in eight different environments, i.e., two sowing date in 1st May and 1st June under two nitrogen levels, i.e, 288 Kg N/hectare (medium-N) and 360 Kg N/hectare (high-N) and two locations at Experimental Farm, Fac. of Agric., Zagazig University (Ghazala village) and Elmalkiean village, El-Hosseinea district, Sharkia governorate in a randomized complete block design with three replications. Nitrogen rates were split and applied at 20, 35 and 50 day after planting for the first sowing date and at 15, 30 and 45 day after planting for the second sowing date. Phosphorus and potassium were applied uniformly on the basis of recommendations before planting.

The experimental plot was single ridge of 6 meters length. The plant to plant and the ridge to ridge distances were 25 and 70 cm, respectively. Trials at both sites were hand-planted with two seeds per hill and thinned at the 3-leaf stage. A plant density of 57 142 plants per hectare was kept after thinning. The recommended agricultural practices for maize production were applied at the proper time.

The data were recorded on ten guarded and competitive plants from each ridge for parents, top crosses and check varieties to estimate the days to 50% silking grain yield/ha and quality characters analysis. Seeds of white and yellow maize genotypes which resulted from line x tester crosses, parents and check varieties were used to study quality characters. Near Infrared Reflection Spectroscopy (NIRS) method by the maize Department of Bavarian State Research Centre for Agriculture, Freising, Germany, has been used for measuring the protein content (%), oil content (%) and total carbohydrate (%) at all environments.

Before the biometrical analysis of combining ability, genetic component and heterosis for the obtained data of earliness, quality characters and grain yield/ha were statistically analyzed using conventional two way analysis of variance according to Steel and Torrie (1980). A PC Microsoft Excel and SAS 9.1 ® Computer

program for Windows (2003) were used for the statistical analysis. The combined analyses were performed using the PC Microsoft Excel program, GLM and PROC MIXED procedures included in SAS 9.1 for comparison purposes. Genotypes and environments were considered as fixed effects while replications were considered as random effects. The linear model utilized for the combined analyses was as follows:

$$Y_{ijk} = \mu + g_i + e_j + (ge)_{ij} + r(e)_{jk} + \varepsilon_{ijk}$$

Where:

Y_{ijk} is the value of the ijk^{th} plot,

μ is mean of all genotypes over all the environments

g_i is the effect due to the ith genotype;

e_j is the effect due to the jth environment;

$(ge)_j$ is the effect due to the interaction of ith genotype with j^{th} environment;

$r(e)_{jk}$ is the effect due to the kth replicate within the jth environment;

ε_{ijk} is the error associated with the ijk^{th} individual observation.

Analysis of variance for general (GCA) and specific (SCA) combining abilities were carried out using mean values at each environment, and across environments as per Kempthorne (1957) related to method of Comstock and Robinson (1952).

t-tests were used to test the significance of the GCA and SCA effects where t = GCA/SEGCA or SCA/SESCA, respectively (Singh and Chaudhary, 1977 and Sharma, 1998).

Across environments, heritability was calculated as

$$T_n = \frac{\sigma^2 A}{\sigma^2 A + \dfrac{\sigma^2 AE}{e} + \dfrac{\sigma^2 E}{er}} \times 100$$

Where, $\sigma^2 A$ is the additive variance, $\sigma^2 AE$ is the additive x environment variance, $\sigma^2 E$ is the error variance, e is the number of environments, and r is the number of replications for a single environment.

The following formulae were employed to estimate the hybrid vigor according to both mid-parents $(\overline{M}.\overline{P}.)$, high-parent $(\overline{H}.\overline{P}.)$ and check variety (standard heterosis).

$$\% \text{Heterosis}(\overline{M}.\overline{P}.) = \frac{\overline{F_1} - \overline{M}.\overline{P}.}{\overline{F_1}} \times 100$$

$$\% \text{Heterosis} (\overline{H.P.}) = \frac{\overline{F}_1 - \overline{H.P.}}{\overline{F}_1} \times 100$$

% Heterosis of check varitey =

$$\frac{\overline{F}_1 - \text{mean of check variety}}{\overline{F}_1} \times 100$$

A test of significance for the F_1 crosses mean from the mid parent values were calculated according to Bhatt (1971) using t-test where:

The significance of heterosis over the mid-parent

$$t = (F_{1ij} - \overline{M.P.}_{ij}) / \sqrt{3/8 \text{ Mse}}$$

The significance of heterosis over the high parent

$$t = (\overline{F}_{1ij} - \overline{H.P.}_{ij}) / \sqrt{\frac{2}{cb} \text{ Mse}}$$

The t-test was used to detect significance of heterosis for check variety.

$$t = (\overline{F}_{1ij} - \text{mean of check variety}) / \sqrt{\frac{2}{cb} \text{ Mse}}$$

$\overline{F}_{1ij}$ = The mean of the ij th F_1

$\overline{M.P.}_{ij}$ = The mean of mid parent of ij th cross.

$\overline{H.P.}_{ij}$ = The mean of the high-parent of ij th cross.

b = Number of replications.

c = Number of samples.

RESULTS AND DISCUSSION

Combining Ability over Environments

Analysis of variance

The combined analyses of variance for combining ability revealed that mean squares for environments, genotypes and genotype x environment showed highly significance differences for days to 50% silking, protein%, oil%, total carbohydrate% and grain yield/ha in both white and yellow maize Table 1. The significant for environments, genotypes and genotype x environment component of interaction indicated wide differences between the environments and differential genotypic behavior across the environments. These results are in agreement with those obtained by Soliman *et al.* (1995), Shehata *et al.* (1997) and El-Zeir *et al.* (2000).

Highly significant variances were observed among genotypes components i.e., parents (lines, testers and line x tester), parents *vs.* hybrids and hybrids for all

characters except carbohydrate% for parents (line x tester), indicating the presence of adequate amount of genetic variability for applying various genetic approaches. Also, variance due to top crosses and it components i.e., line effect, tester effect and line x tester effect were highly significant across eight environments in both white and yellow maize except oil and protein for line effect and tester effect in yellow maize, indicating the prevalence of additive and non additive gene action in the gene expression of these characters. Mean squares due to commercial checks and checks *vs.* top crosses were highly significant for all these traits except protein content for checks in white maize and oil for check *vs.* top crosses in yellow maize. Combined analyses of variance for genotypes x E and their components, i.e., parents x E, parents vs. hybrids and hybrids x E were highly significant for all traits except grain yield/ha for parents x E of yellow maize. Top crosses x E and line x tester x E were significant for all characters except days to 50% tasseling of white maize. Non significant variances were observed for line effect x E and tester effect x E for all traits

except days to 50% tasseling and grain yield/ha of white maize. In contrast, significant variances were found among checks x E and checks vs. crosses x E for all characters except grain yield in both white and yellow maize and days to 50 % tasseling for yellow maize.

General combining ability effects (GCA) across environments

Combined analyses showed that lines and testers varied significantly for all characters in both white and yellow maize across environments. Mean performance for lines ranged from 68.17 (L_7) to 73.54 (L_3) for days to 50% silking of white maize (Table 2). These results indicate that white inbred line L_1 gave the highest values for total carbohydrate (70.49%) and grain yield/ha (3.66 ton). Also, white inbred L_3 had the highest value for protein % and it was later than all other lines for maturity (73.54 d). White maize tester T_8 had the highest value for oil (2.79%) and carbohydrate (71.87%) percentage, while, white tester T_{10} had the best values for days to 50% silking (59.58d), protein (10.91%) and grain yield/ha (7.70 ton).

Table 1. Combined analyses of line x tester for days to 50% silking, grain yield/ha and quality traits of the white and yellow maize across eight environments

Source of variation	df	White maize					Yellow maize				
		Days to 50% silking	Grain yield (ton/ha.)	Protein %	Oil %	Carbohydrate %	Days to 50% silking	Grain yield (ton/ha.)	Protein %	Oil %	Carbohydrate %
Environments	7	2328.65**	19.90**	1.761**	0.148**	3.887**	1872.34**	46.80**	15.267**	1.377**	26.037**
Replicates (Env.)	16	1.54	0.91*	0.144	0.004	0.130**	7.17**	1.98**	0.031	0.020	0.028
Genotypes	32	264.89**	197.53**	24.141**	0.389**	31.043**	227.64**	149.34**	6.769**	0.526**	9.081**
Parents	9	365.99**	61.40**	15.240**	0.769**	21.980**	167.08**	19.20**	5.602**	0.964**	9.228**
Parents (Lines)	6	99.07**	7.924**	10.010**	0.803**	12.525**	199.58**	5.231**	6.838**	1.387**	12.657**
Parents (Testers)	2	706.17**	105.613**	5.739**	1.048**	4.772**	140.29**	56.731**	4.601**	0.040**	3.550**
Parents (L vs. T)	1	1287.14**	293.83**	65.624**	0.006	113.126**	25.71**	27.9783**	0.191**	0.271**	0.008
P. vs. H	1	3493.64**	5338.89**	442.668**	1.338**	610.261**	3472.35**	4405.13**	87.052**	4.058**	96.538**
Hybrids	22	76.77**	19.52**	8.757**	0.191**	8.422**	104.92**	9.14**	3.597**	0.186**	5.053**
Top crosses	20	65.33**	19.19**	8.760**	0.183**	8.562**	100.93**	8.73**	2.791**	0.200**	4.436**
Line effect	6	86.80**	14.61**	16.077**	0.325**	15.051**	296.93**	11.95*	4.049	0.270	8.905**
Tester effect	2	375.84**	125.44**	28.574**	0.040	30.116**	65.77**	20.44*	0.855	0.315	3.023
Line x Tester effect	12	2.84**	3.78**	1.799**	0.136**	1.726**	8.79**	5.17**	2.484**	0.146**	2.437**
Checks	1	114.08**	7.67**	0.078	0.471**	2.048**	27.00**	0.40	15.715**	0.070*	17.011**
Checks vs. Crosses	1	268.29**	37.94**	17.392**	0.061**	11.987**	262.73**	26.07**	7.594**	0.021	5.439**
Genotypes x E	224	2.92**	1.21**	1.098**	0.083**	1.159**	3.32**	1.22**	1.410**	0.200**	1.171**
Parents x E	63	3.12**	0.89**	1.341**	0.113**	1.407**	4.20**	0.41	1.333**	0.201**	1.299**
Parents (Lines) x E	42	2.22	0.553	1.575**	0.111**	1.434**	2.21	0.464	1.161**	0.195**	1.036**
Parents (Testers) x E	14	4.21**	1.309**	0.684**	0.107**	1.645**	8.75**	0.335	1.613**	0.217**	1.726**
Parents (L vs. T) x E	7	6.30**	2.091**	1.252**	0.136**	0.771**	7.04**	0.221	1.801**	0.202**	2.023**
(P. vs. H) x E	7	7.43**	10.20**	1.516**	0.111**	4.734**	7.21**	18.18**	1.585**	0.226**	1.095**
Hybrids x E	154	2.63**	0.93**	0.980**	0.069**	0.895**	2.79**	0.79**	1.434**	0.198**	1.122**
Top crosses x E	140	2.46**	0.98**	1.009**	0.067**	0.825**	2.89**	0.83**	1.500**	0.209**	1.125**
Line effect x E	42	3.08**	1.44**	0.987	0.065	0.882	2.78	0.92	2.095	0.204	1.667
Tester effect x E	14	5.97**	1.74**	0.599	0.072	0.803	2.85	0.96	1.018	0.260	0.622
Line x Tester effect x E	84	1.56	0.63*	1.088**	0.067**	0.799**	2.95**	0.76**	1.282**	0.202**	0.938**
Checks x E	7	2.94*	0.15	0.224**	0.041**	0.525**	1.52	0.67	0.468**	0.104**	0.916**
Checks vs. Crosses x E	7	5.73**	0.22	1.153**	0.149**	2.678**	1.92	0.16	1.090**	0.084**	1.269**
Error	512	1.24	0.49	0.081	0.004	0.066	1.84	0.40	0.072	0.014	0.083

*,** Significant at P= 0.05 and P=0.01, respectively

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White inbred line L_3 had the best combination of general combining ability (GCA) effects for protein and oil % across environments (0.89^{**} and 0.10^{**}, respectively) (Table 2). White lines L_1 and L_4 had positive and significant GCA effects for total carbohydrates. While white inbred line L_7 and tester T_{10} had the best desirable significant GCA effects for days to 50% tasseling (0.46^* and -1.66^{**}, respectively) and grain yield/ha (0.26^* and 0.23^*, respectively), indicating that these parents contributed to reduce the days of the flowering and increase of the yield in crosses. For protein% and carbohydrate%, tester T_8 and T_9 had positive and significant GCA effects, indicating that these parents contributed to increase the percentage of the protein and carbohydrate in crosses.

Yellow inbred lines L_3, L_6 and L_2 gave the highest values for protein, oil and grain yield/ha, respectively (Table 3). On the other hand, inbred L_4 was the lowest and highest mean performance for days to silking and total carbohydrate% across environments for yellow maize,

respectively. Yellow tester T_9 showed the highest values for protein (11.06%) and oil (2.90%), while, tester T_{10} (broad genetic base) had the best values for days to 50% silking (64.33d), carbohydrate % (71.84%) and grain yield/ha (5.92 ton) (Table 3).

Yellow inbred L_1 had the best combination of GCA effects for all traits across environments except protein %. The yellow tester T_{10} showed the most favorable GCA effects for carbohydrate and grain yield. It had positive and significant GCA effects for these traits across eight environments.

Specific combining ability effects (SCA) across environments

Specific combining ability (SCA) is a genetic property of great interest in breeding programs aiming at hybrid cultivars. It enables assessment of the genotype combinations most promising for hybridization. Combined analyses showed that top crosses and check varieties for white and yellow maize varied significantly from character to character and from cross to cross for all studied traits. Mean performance of check varieties showed that commercial

Table 2. Mean performance and general combining ability effects (GCA) for days to silking, grain yield/ha and quality characters of white maize kernels of line x tester analysis across eight environments

Genotypes	Days to 50% silking		Grain yield (ton / ha.)		Protein %		Oil %		Carbohydrate%	
	$\overline{X}$	GCA	$\overline{X}$	GCA	$\overline{X}$	GCA	$\overline{X}$	GCA	$\overline{X}$	GCA
Lines										
L_1	68.54	-0.71**	3.66	0.01	10.73	-0.59**	2.65	-0.08**	70.49	0.48**
L_2	69.50	-1.13**	2.98	-0.42**	11.15	0.20	2.45	-0.02	70.41	-0.15
L_3	73.54	2.01**	3.22	-0.12	12.76	0.89**	2.79	0.10**	68.45	-0.90**
L_4	71.04	-0.70**	1.84	-0.55**	11.81	-0.21	2.85	0.03	69.44	0.41**
L_5	72.13	0.15	3.09	0.01	11.28	-0.34**	2.80	-0.01	69.91	0.15
L_6	72.13	0.83**	2.66	0.81**	11.37	0.06	2.41	-0.08**	70.39	0.04
L_7	68.17	-0.46*	2.63	0.26*	11.78	-0.01	2.51	0.05	69.90	-0.03
Mean	70.72		2.87		11.55		2.64		69.86	
S.E.$_{gi}$		0.13		0.082		0.033		0.01		0.03
S.E.$_{(gi-gj)}$		0.19		0.131		0.11		0.03		0.10
Testers										
T_8 (Sids 7)	67.42	0.41**	4.26	0.73**	9.93	-0.44**	2.79	0.00	71.87	0.46**
T_9 (Sids 63)	70.00	1.25**	3.89	-0.95**	10.40	0.37**	2.41	-0.02	71.14	-0.37**
T_{10} (Giza 2)	59.58	-1.66**	7.70	0.23**	10.91	0.07	2.75	0.02	71.06	-0.10
Mean	65.67		5.28		10.41		2.65		71.35	
S.E.$_{gi}$		0.09		0.054		0.021		0.01		0.02
S.E.$_{(gi-gj)}$		0.15		0.083		0.05		0.02		0.06
L.S.D $_{0.05}$	1.78		1.12		0.46		0.10		0.41	

*,** Significant at P= 0.05 and P=0.01, respectively.

Table 3. Mean performance and general combining ability effects (GCA) for days to silking, grain yield/ha and quality characters of yellow maize kernels of line x tester analysis across eight environments

Genotypes	Days to 50% silking $\overline{X}$	GCA	Grain yield (ton / ha.) $\overline{X}$	GCA	Protein % $\overline{X}$	GCA	Oil % $\overline{X}$	GCA	Carbohydrate % $\overline{X}$	GCA
Lines										
L_1	67.67	-0.73**	3.08	0.22*	10.21	-0.46**	3.05	0.001	71.98	0.65**
L_2	65.33	-0.98**	4.09	0.69**	10.91	0.06	3.05	0.12*	71.01	0.03
L_3	63.25	-1.81**	3.78	-0.11	11.70	0.30	2.62	-0.03	70.14	-0.49**
L_4	63.04	-2.25**	3.24	0.17	10.15	-0.07	2.93	0.04	72.08	0.09
L_5	71.25	3.47**	2.80	-0.37**	10.76	0.01	3.12	-0.07	71.67	0.03
L_6	66.38	0.80**	3.11	-0.54**	10.45	0.15	3.16	-0.04	71.93	-0.04
L_7	67.96	1.50**	3.73	-0.05	10.93	0.02	2.57	-0.02	70.89	-0.27
Mean	66.41		3.41		10.73		2.93		71.39	
S.E.$_{gi}$		0.16		0.075		0.03		0.01		0.03
S.E.$_{(gi-gj)}$		0.18		0.105		0.16		0.05		0.14
Testers										
T_8 (Gm. 1021)	68.50	-0.52**	3.34	0.08	10.75	0.08	2.83	0.01	71.19	-0.15**
T_9 (Gm. 1004)	68.54	0.69**	3.19	-0.38**	11.06	-0.01	2.90	0.04	71.16	0.05
T_{10} (Composite 21)	64.33	-0.17	5.92	0.30**	10.19	-0.07	2.83	-0.05	71.84	0.11*
Mean	67.13		4.15		10.67		2.85		71.40	
S.E.$_{gi}$		0.10		0.049		0.02		0.01		0.02
S.E.$_{(gi-gj)}$		0.11		0.062		0.06		0.03		0.05
L.S.D $_{0.05}$	2.17		1.02		0.43		0.19		0.46	

*,** Significant at P= 0.05 and P=0.01, respectively.

check S.C.129 was earlier (60.83 d) than all top crosses across environments for days to 50% silking in white maize (Table 4).

Mean performance for white top crosses ranged from 8.41 (L_1 x T_8) to 10.42% (L_3 x T_{10}) for protein, from 2.58 (L_1 x T_8) to 2.93% (L_3 x T_8) for oil and from 70.80 (L_3 x T_9) to 73.31 (L_1 x T_8) for carbohydrate % Table 4. These results indicating that top cross (L_1 x T_8) gave the lowest values for protein and oil % with the highest value for total carbohydrate and grain yield. On the other hand, white top cross (L_3 x T_9) had the highest mean performance for protein and oil% with lowest value for total carbohydrate and grain yield/ha. So, efforts to increase kernel oil content through breeding have had considerable success, but high oil lines usually have significant reduced yield (Lambert 2001). Kernel oil also has negative correlation with starch content (Song and Chen 2004; Clark *et al.* 2006). Several studies have demonstrated that the high oil trait is typically associated with an increase in embryo size and evaluated oil concentration in the embryo (Lambert *et al.* 1997; Lambert 2001; Dudley; Lambert 2004 and Dale et al. 2009).

Similar results were observed for yellow maize, where commercial check S.C.155 was earlier than all top crosses for days to 50% silking (59.08d) across environments. Yellow top cross (L_1 x T_8) had the lowest values for protein and oil% with the highest values for total carbohydrate% and grain yield (Table 5).

White top cross (L_2 x T_{10}) had the most favorable significant SCA effects for protein and oil % (0.491^{**} and 0.10^*, respectively) (Table 4). Two top crosses (L_2 x T_{10}) and (L_3 x T_8) had positive and significant SCA effects for oil % and one hybrid (L_2 x T_8) for carbohydrate % over eight environments. It is of great interest to note that SCA effects for grain yield/ha had positive and highly significant for five hybrids (L_1 x T_8), (L_1 x T_{10}), (L_3 x T_8), (L_4 x T_9) and (L_5 x T_9), showing that these crosses are important for the breeding programs in white maize.

Three top crosses (L_3 × T_9), (L_6 × T_8) and (L_7 × T_9) had negative and significant SCA effects for days to 50% silking, indicating that these hybrids could be employed in breeding program for improving earliness in yellow maize (Table 5). Yellow hybrid (L_2 x T_8) out 21 top crosses gave positive and

Table 4. Mean performance and combined analyses of specific combining ability effects (SCA) for days to 50% silking, grain yield/ha and quality characters of line x tester analysis for white maize across eight environments

Genotypes	Days to 50% silking		Grain yield (ton/ha.)		Protein %		Oil %		Carbohydrate %	
	Mean	SCA	Mean	SCA	Mean	SCA	Mean	SCA	Mean	SCA
Top crosses										
L_1 x T_8	64.92	0.365	10.20	0.305*	8.41	-0.196	2.58	-0.072	73.31	0.203
L_1 x T_9	65.08	-0.302	7.53	-0.683**	9.33	-0.088	2.66	0.027	72.39	0.113
L_1 x T_{10}	62.42	-0.063	9.77	0.378**	9.41	0.285	2.71	0.045	72.23	-0.316*
L_2 x T_8	64.29	0.157	9.28	-0.187	8.99	-0.407*	2.61	-0.094*	72.77	0.290*
L_2 x T_9	64.75	-0.218	8.01	0.224	10.13	-0.084	2.68	-0.007	71.82	0.172
L_2 x T_{10}	62.13	0.062	8.93	-0.037	10.41	0.491**	2.82	0.100*	71.46	-0.462*
L_3 x T_8	67.00	-0.274	10.15	0.375**	10.16	0.073	2.93	0.101*	71.62	-0.117
L_3 x T_9	68.58	0.476*	7.81	-0.275*	11.01	0.109	2.81	-0.005	70.80	-0.099
L_3 x T_{10}	65.00	-0.202	9.17	-0.099	10.42	-0.182	2.75	-0.096*	71.39	0.217
L_4 x T_8	64.83	0.268	9.20	-0.140	9.04	0.057	2.74	-0.024	73.07	0.024
L_4 x T_9	65.42	0.018	8.07	0.415**	9.82	0.015	2.75	0.008	71.97	-0.246
L_4 x T_{10}	62.21	-0.286	8.56	-0.275*	9.43	-0.072	2.79	0.015	72.70	0.222
L_5 x T_8	65.04	-0.371	9.33	-0.572**	9.15	0.289	2.74	0.024	72.50	-0.287*
L_5 x T_9	66.50	0.254	8.66	0.438**	9.45	-0.219	2.66	-0.042	72.18	0.223
L_5 x T_{10}	63.46	0.117	9.53	0.134	9.30	-0.070	2.75	0.019	72.29	0.063
L_6 x T_8	65.71	-0.385	10.92	0.219	9.30	0.044	2.66	0.010	72.57	-0.105
L_6 x T_9	67.00	0.073	8.90	-0.117	10.24	0.167	2.70	0.073	71.78	-0.069
L_6 x T_{10}	64.33	0.312	10.09	-0.101	9.56	-0.211	2.58	-0.083*	72.29	0.174
L_7 x T_8	65.04	0.240	10.15	-0.0004	9.32	0.141	2.83	0.054	72.60	-0.008
L_7 x T_9	65.33	-0.302	8.47	-0.0002	10.10	0.101	2.71	-0.054	71.68	-0.094
L_7 x T_{10}	62.79	0.062	9.65	0.001	9.46	-0.241	2.79	-0.001	72.15	0.102
Mean	64.85		9.16		9.64		2.73		72.17	
S.E.$_{sij}$		0.23		0.142		0.056		0.01		0.05
S.E.$_{(sij - sji)}$		0.193		0.122		0.161		0.040		0.138
Checks										
S.C.10	63.92		10.49		8.97		2.66		72.90	
S.C.129	60.83		9.69		9.05		2.86		72.49	
Mean	62.38		10.09		9.01		2.76		72.69	
L.S.D $_{0.05}$	1.78		1.12		0.46		0.10		0.41	

*,** Significant at P= 0.05 and P=0.01, respectively

Table 5. Mean performance and combined analyses of specific combining ability effects (SCA) for days to 50% silking, grain yield/ha and quality characters of line x tester analysis for yellow maize across eight environments

Genotypes	Days to 50% silking		Grain yield (ton/ha.)		Protein %		Oil %		Carbohydrate %	
	Mean	SCA	Mean	SCA	Mean	SCA	Mean	SCA	Mean	SCA
Top crosses										
L_1 x T_8	60.83	-0.202	9.10	0.114	9.19	-0.449**	2.69	-0.071	72.91	0.296*
L_1 x T_9	62.08	-0.167	8.84	0.307*	9.68	0.127	2.81	0.024	72.73	-0.079
L_1 x T_{10}	61.75	0.369	8.80	-0.420**	9.82	0.322	2.75	0.047	72.65	-0.217
L_2 x T_8	60.71	-0.077	9.62	0.160	10.66	0.500**	2.84	-0.041	71.47	-0.532**
L_2 x T_9	61.88	-0.125	9.12	0.125	9.65	-0.428*	2.89	-0.022	72.76	0.559**
L_2 x T_{10}	61.33	0.202	9.40	-0.285*	9.95	-0.072	2.88	0.063	72.23	-0.028
L_3 x T_8	60.33	0.381	8.90	0.246	10.70	0.292	2.80	0.063	71.23	-0.247
L_3 x T_9	60.33	-0.833**	8.38	0.179	10.19	-0.122	2.69	-0.073	71.74	0.059
L_3 x T_{10}	60.75	0.452	8.46	-0.425**	10.09	-0.170	2.69	0.010	71.93	0.188
L_4 x T_8	59.29	-0.216	9.11	0.173	9.80	-0.233	2.83	0.039	72.09	0.033
L_4 x T_9	60.67	-0.056	8.71	0.223	10.19	0.248	2.74	-0.091	72.02	-0.228
L_4 x T_{10}	60.13	0.272	8.77	-0.396**	9.87	-0.015	2.79	0.051	72.51	0.195
L_5 x T_8	65.54	0.312	8.16	-0.239	9.94	-0.166	2.69	0.004	72.33	0.339*
L_5 x T_9	65.96	-0.486	7.93	-0.016	10.10	0.080	2.73	0.013	71.97	-0.217
L_5 x T_{10}	65.75	0.175	8.88	0.255	10.05	0.086	2.61	-0.018	72.13	-0.122
L_6 x T_8	62.33	-0.230	8.28	0.049	10.33	0.079	2.79	0.071	71.85	-0.086
L_6 x T_9	64.79	1.014**	7.09	-0.681**	9.98	-0.185	2.79	0.037	72.25	0.127
L_6 x T_{10}	62.13	-0.784**	9.09	0.632**	10.21	0.106	2.56	-0.108	72.15	-0.041
L_7 x T_8	63.29	0.034	8.22	-0.502**	10.09	-0.024	2.68	-0.066	71.89	0.197
L_7 x T_9	65.13	0.653*	8.12	-0.137	10.31	0.280	2.88	0.112	71.67	-0.221
L_7 x T_{10}	62.92	-0.687**	9.59	0.639**	9.72	-0.257	2.64	-0.046	71.97	0.024
Mean	62.28		8.69		10.02		2.75		72.12	
S.E.$_{sij}$		0.28		0.130		0.05		0.02		0.06
S.E.$_{(sij - sji)}$		0.265		0.134		0.175		0.069		0.149
Checks										
S.C.155	59.08		9.56		9.04		2.77		73.07	
T.W.C. 352	60.58		9.37		10.18		2.69		71.88	
Mean	59.83		9.46		9.61		2.73		72.47	
L.S.D $_{0.05}$	2.17		1.02		0.43		0.19		0.46	

*,** Significant at P= 0.05 and P=0.01, respectively.

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significant SCA effects (0.500^{**}) for protein%. Moreover, three yellow top crosses (L_1 x T_8), (L_2 x T_9) and (L_5 x T_8) had desirable significant SCA effects for carbohydrate %. Also, three hybrids (L_1 x T_9), (L_6 x T_{10}) and (L_7 x T_{10}) had positive and significant SCA effects for grain yield/ha of yellow maize across environments (Table 5).

These results are of great importance for corn breeder to improve hybrid maize for early maturity, chemical composition of kernel characters and grain yield.

Genetic Component and Proportional Contribution of Lines, Tester and Line x Tester to the Total Variability

Table 6, revealed that variances due to line (σ^2_{line}) were highly significant for days to 50% silking, protein, carbohydrate % of white maize and for days to 50% silking and total carbohydrate % of yellow maize. Significant differences were observed for σ^2 line x E for all traits except oil% of both white and yellow maize. Variances due to tester and tester x E were highly significant for protein and grain yield/ha for white maize. Meanwhile, σ^2GCA, σ^2GCA x E and σ^2SCA were non-significant for all these characters. In contrast

σ^2SCA x E showed significant for all traits in both white and yellow maize across environments.

The ratio of σ^2 GCA/σ^2 SCA was more than unity for days to 50% silking in both white and yellow maize, indicating that GCA variances were more important than SCA ones in the inheritance of this character. In other words, this means that additive genetic variances were predominant and played the major role in the gene expression of this trait. The importance of additive gene action in inheritance of this character could be improved through phenotypic selection. Similar results were observed by Matzinger *et al.* (1959), El-Zier (1999), Soliman and Sadek (1999).

The ratio of σ^2GCA/σ^2SCA was less than unity for all quality characters and grain yield in both white and yellow maize, indicating that non additive genetic variance was predominant and played the major role in the gene expression of these traits (Table 6). The average degree of dominance $(D/A)^{0.5}$ was more than unity for all characters except days to 50% silking in both white and yellow maize, showing the importance of non additive gene action in the genetics of these characters.

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Table 6. Genetic components of line x tester analysis for days to 50% silking, grain yield/ha and quality characters for white and yellow maize genotypes across eight environments

Genetic components	White maize					Yellow maize				
	Days to 50% silking	Grain yield (ton/ ha.)	Protein %	Oil %	Carbohydrate %	Days to 50% silking	Grain yield (ton/ ha.)	Protein %	Oil %	Carbohydrate %
σ^2 Line	1.17**	0.15	0.1983**	0.0026	0.1851**	4.00**	0.09	0.022	0.0017	0.090**
σ^2 Line x E	0.17**	0.09**	-0.0113**	-0.0002	0.0092*	-0.02	0.02*	0.090**	0.0002	0.081**
σ^2 Tester	2.22**	0.72**	0.1594**	-0.0006	0.1690	0.34**	0.09	-0.010	0.0010	0.003
σ^2 Tester x E	0.21**	0.05**	-0.0233**	0.0002	0.0002**	-0.005	0.01	-0.013**	0.0028*	-0.015**
σ^2 GCA	0.20	0.05	0.0227	0.0002	0.0223	0.30	0.01	0.001	0.0002	0.007
σ^2 GCA x E	0.02	0.01	-0.0021	-0.000002	0.0007	-0.002	0.002	0.006	0.0002	0.005
σ^2 SCA	0.07	0.14	0.0715	0.0055	0.0691	0.29	0.20	0.101	0.0055	0.098
σ^2 SCA x E	0.11*	0.05**	0.3355**	0.0209**	0.2444**	0.37**	0.12**	0.403**	0.0627**	0.285**
σ^2 GCA/ σ^2 SCA	3.05	0.37	0.3167	0.0278	0.3218	1.04	0.06	0.010	0.0320	0.066
σ^2 A	0.41	0.10	0.0453	0.0003	0.0445	0.60	0.02	0.002	0.0004	0.013
σ^2 A x E	0.05	0.02	-0.0041	-0.000003	0.0013	-0.003	0.004	0.011	0.0003	0.010
σ^2 D	0.07	0.14	0.0715	0.0055	0.0691	0.29	0.20	0.101	0.0055	0.098
σ^2 D x E	0.11	0.05	0.3355	0.0209	0.2444	0.37	0.12	0.403	0.0627	0.285
$(D/A)^{0.05}$	0.40	1.17	1.2565	4.2420	1.2464	0.69	2.92	7.097	3.9551	2.745
Contribution of lines	39.86	22.83	55.06	53.21	52.73	88.26	41.07	43.53	40.46	60.22
Contribution of testers	57.53	65.35	32.62	2.17	35.17	6.52	23.42	3.06	15.73	6.81
Contribution of (L x T)	2.61	11.82	12.32	44.63	12.09	5.22	35.51	53.41	43.81	32.97
T_n (%)	87.63	33.21	94.03	63.20	93.84	88.69	57.29	31.10	35.74	73.49
C.V. (%)	1.69	9.26	2.83	2.42	0.36	2.14	8.82	2.63	4.25	0.40

Higher heritability for narrow sense T_n (%) was found (> 60%) for, days to silking (87.63%), protein (94.03%), oil (63.20%) and carbohydrate (93.84%) percentage for white maize across environments. Also, higher heritability observed for days to silking (88.69%) and carbohydrate (73.49%) percentage for yellow maize. While, lower heritabilities were found for grain yield (33.21%) for white maize, protein (31.10%) and oil (35.74%) percentage for yellow maize (Table 6).

Proportional contribution of lines played an important role in the total variance for protein (55.06%), oil (53.21%) percentage and carbohydrate (52.73%) for white maize, days to 50% silking (88.26%) and carbohydrate (60.22%) for yellow maize, indicating that maternal influence was greater than parental effect for these traits across environments (Table 6). Percentage contribution of testers were greater than lines to total variance for days to silking (57.53%) and grain yield (65.35%), indicating that parental influence was greater than maternal effect for these traits in white maize. Little difference was found between contribution of

lines and lines x tester interaction for oil (53.21 and 44.63%) of white maize, protein (43.53 and 53.41%), oil (40.46 and 43.81%) and grain yield (41.07 and 35.51%) for yellow maize (Table 6).

Inheritance of the high kernel oil trait is a function of both maternal and paternal genetics (Curtis *et al.* 1956; Letchworth and Lambert 1998). Reciprocal crosses demonstrated that the oil percentage of a kernel is approximately midway between a high oil and low oil parent. This effect is not observed for kernel protein or starch contents, which are determined primarily by the genetics of the maternal parent (Letchworth and Lambert 1998). This pattern of inheritance suggests that oil accumulation in the kernel is controlled in large part by expression of genes in the embryo and endosperm.

Heterosis

The results of heterosis revealed that all white and yellow top crosses gave negative and significant heterosis of mid and high parent for days to 50% silking across environments. Meanwhile, non negative and significant heterosis was found for all top

crosses with white commercial check S.C. 129 and yellow check S.C. 155 for this trait (Table 7). Negative and significant heterosis was found for most white and yellow top crosses of mid parent and high parent for protein % in kernel and ranged from -22.84 to -5.16% and from -27.60 to -7.20% for white maize, from -14.05 to -1.06% and from -16.99 to 0.18% for yellow maize, respectively.

Heterosis for oil % ranged from -5.48^{**} to 10.90^{**} for white maize relative to mid parents, from -8.19^{**} to 10.94^{**} for high parent, from -3.43^{**} to 9.04^{**} for S.C. 10, from -11.12^{**} to 2.28^{**} for S.C. 129. Top cross (L_3 x T_8) had positive and significant heterosis of mid parent (4.84^{**}), high parent (4.86^{**}) and standard heterosis for white check S.C.10 (9.04^{**}) and S.C.129 (2.28^{**}) for this trait. For yellow maize, heterosis for oil% ranged from -16.98^{**} to 10.12^{**} for mid parent, from -23.41^{**} to 13.54^{**} for high parent, from -8.01^{**} to 15.39^{**} for S.C. 155, and from -11.21^{**} to 17.72^{**} for T.W.C. 352 (Table 8).

For total carbohydrate, most white and yellow top crosses had positive and significant heterosis values of mid parents and high parents across environments. One

top cross (L_1 x T_8) gave positive and significant heterosis value (0.56^{**}) for standard heterosis (S.C.10).

Grain yield/ha showed positive and significant heterosis of mid parents and high parents for all top crosses in both white and yellow maize. It ranged from 40.50 to 68.33% for mid parent, from 10.08 to 60.99% for high parent, from -39.30 to 3.90 for S.C. 10 for white maize. But for yellow maize it ranged from 42.62 to 64.75% for mid parent, from 29.98 to 63.93% for high parent, from -34.81 to 0.63% for S.C. 155 (Table 9).

Heterosis between these genotypes may be due, to a larger extent, to combinations of favorable alleles dominant for different functions (a possible explanation for overdominance) rather than simply the covering of recessive unfavorable alleles with dominant favorable alleles from the other parent.

White top cross (L_6 x T_8) gave the highest values for ear length (20.57cm), number of kernels/row (46.89), 100 kernel weight (32.97g), protein (9.30%), oil (2.66%), total carbohydrate (72.57%), grain yield/plant (207.07g), shelling (81.86%) and grain yield/ha (10.92 ton).

Table 7. Heterosis over mid-parent (M.P.), high-parent (H.P.) and check varieties for days to 50% silking and grain yield (ton/ha) of line x tester analysis for maize genotypes across eight environments

| | White maize | | | | | | | | Yellow maize | | | | | | | |
| | Days to 50% silking | | | | Grain yield (ton/ha) | | | | Days to 50% silking | | | | Grain yield (ton/ha) | | | |
Genotypes	M.P	H.P	S.C.10	S.C.129	M.P	H.P	S.C.10	S.C.129	M.P	H.P	S.C.155	T.W.C 352	M.P	H.P	S.C.155	T.W.C 352
$L_1 \times T_8$	-4.72**	-5.58**	1.54**	6.29**	61.18**	58.26**	-2.82	5.02**	-11.92**	-12.60**	2.88**	0.41	64.75**	63.31**	-4.98**	-2.98
$L_1 \times T_9$	-6.43**	-7.55**	1.79**	6.53**	49.84**	48.31**	-39.30**	-28.68**	-9.70**	-10.40**	4.83**	2.42**	64.56**	63.93**	-8.12**	-6.05**
$L_1 \times T_{10}$	-2.64**	-9.81**	-2.40**	2.54**	41.88**	21.24**	-7.37**	0.82	-6.88**	-4.18**	4.32**	1.89**	48.84**	32.66**	-8.64**	-6.56**
$L_2 \times T_8$	-6.48**	-4.86**	0.58	5.38**	61.03**	54.13**	-12.99**	-4.38	-10.23**	-12.83**	2.68**	0.21	61.36**	57.45**	0.63	2.53
$L_2 \times T_9$	-7.72**	-8.11**	1.29**	6.05**	57.11**	51.41**	-30.95**	-20.97**	-8.18**	-10.77**	4.51**	2.09**	60.11**	55.16**	-4.74**	-2.73
$L_2 \times T_{10}$	-3.89**	-11.87**	-2.88**	2.08**	40.24**	13.83**	-17.48**	-8.52**	-5.71**	-4.89**	3.67**	1.22*	46.72**	36.98**	-1.67	0.27
$L_3 \times T_8$	-5.19**	-9.76**	4.60**	9.20**	63.17**	58.03**	-3.39	4.49*	-9.19**	-13.54**	2.07**	-0.41	59.99**	57.49**	-7.35**	-5.30**
$L_3 \times T_9$	-4.65**	-7.23**	6.80**	11.30**	54.51**	50.18**	-34.27**	-24.03**	-9.22**	-13.60**	2.07**	-0.41	58.39**	54.83**	-14.06**	-11.88**
$L_3 \times T_{10}$	-2.40*	-13.14**	1.67**	6.41**	40.50**	16.07**	-14.42**	-5.70*	-5.01**	-5.90**	2.74**	0.27	42.62**	29.98**	-12.97**	-10.81**
$L_4 \times T_8$	-6.78**	-9.58**	1.41**	6.17**	66.87**	53.69**	-14.07**	-5.38**	-10.93**	-15.53**	0.35	-2.18**	63.91**	63.36**	-4.84**	-2.83
$L_4 \times T_9$	-7.80**	-8.60**	2.29**	7.01**	64.50**	51.75**	-30.04**	-20.12**	-8.45**	-12.98**	2.61**	0.14	63.09**	62.79**	-9.74**	-7.64**
$L_4 \times T_{10}$	-4.99**	-14.20**	-2.75**	2.21**	44.31**	10.08**	-22.59**	-13.25**	-5.93**	-7.00**	1.73**	-0.76	47.78**	32.49**	-8.91**	-6.83**
$L_5 \times T_8$	-7.27**	-10.89**	1.73**	6.47**	60.59**	54.35**	-12.45**	-3.88*	-6.61**	-8.71**	9.85**	7.57**	62.39**	59.08**	-17.09**	-14.85**
$L_5 \times T_9$	-6.86**	-8.46**	3.88**	8.52**	59.64**	55.02**	-21.21**	-11.97**	-5.97**	-8.02**	10.42**	8.15**	62.24**	59.79**	-20.54**	-18.23**
$L_5 \times T_{10}$	-3.78**	-13.66**	-0.72	4.14**	43.40**	19.26**	-10.07**	-1.68	-3.11**	-8.37**	10.14**	7.86**	50.91**	33.32**	-7.58**	-5.52**
$L_6 \times T_8$	-6.18**	-9.77**	2.73**	7.42**	68.33**	60.99**	3.90**	11.23**	-8.19**	-9.89**	5.21**	2.81**	61.01**	59.65**	-15.47**	-13.26**
$L_6 \times T_9$	-6.06**	-7.65**	4.60**	9.20**	63.20**	56.24**	-17.91**	-8.93**	-4.12**	-5.79**	8.81**	6.50**	55.55**	55.03**	-34.81**	-32.23**
$L_6 \times T_{10}$	-2.36*	-12.11**	0.65	5.44**	48.72**	23.75**	-3.95**	3.98*	-5.20**	-6.84**	4.90**	2.48**	50.27**	34.81**	-5.17**	-3.16
$L_7 \times T_8$	-4.23**	-4.80**	1.73**	6.47**	66.05**	58.05**	-3.34	4.54*	-7.80**	-8.23**	6.65**	4.28**	56.98**	62.79**	-16.30**	-14.08**
$L_7 \times T_9$	-5.74**	-7.14**	2.17**	6.89**	61.46**	54.03**	-23.88**	-14.44**	-4.80**	-5.25**	9.28**	6.97**	57.42**	60.76**	-17.62**	-15.37**
$L_7 \times T_{10}$	-1.73	-8.56**	-1.79**	3.12**	46.47**	20.24**	-8.73**	-0.44	-5.13**	-8.01**	6.09**	3.71**	49.65**	38.21**	0.31	2.22

*,** Significant at P= 0.05 and P=0.01, respectively

Table 8. Heterosis over mid-parent (M.P.), high-parent (H.P.) and check varieties for quality characters of line x tester analysis for white maize genotypes across eight environments

Genotypes	Protein %				Oil %				Carbohydrate %			
	M.P	H.P	S.C.10	S.C.129	M.P	H.P	S.C.10	S.C.129	M.P	H.P	S.C.10	S.C.129
L_1 x T_8	-22.84**	-27.60**	-6.64**	-7.60**	-5.48**	-8.19**	-3.43**	-11.12**	2.91**	1.97**	0.56**	1.13**
L_1 x T_9	-13.18**	-14.98**	3.90**	3.04**	4.98**	0.74	-0.17	-7.62**	2.18**	1.73**	-0.70**	-0.13
L_1 x T_{10}	-15.01**	-15.95**	4.67**	3.81**	0.42	-1.45**	1.65**	-5.66**	2.02**	1.63**	-0.93**	-0.35**
L_2 x T_8	-17.28**	-24.08**	0.22	-0.67	-0.22	-6.66**	-1.97**	-9.55**	2.24**	1.24**	-0.18	0.39**
L_2 x T_9	-6.40**	-10.13**	11.43**	10.64**	9.51**	8.71**	0.74	-6.64**	1.46**	0.95**	-1.50**	-0.92**
L_2 x T_{10}	-6.02**	-7.20**	13.80**	13.02**	7.90**	2.61**	5.60**	-1.42*	1.01**	0.56**	-2.02**	-1.44**
L_3 x T_8	-11.68**	-25.58**	11.69**	10.90**	4.84**	4.86**	9.04**	2.28**	2.03**	-0.35**	-1.79**	-1.21**
L_3 x T_9	-5.16**	-15.87**	18.52**	17.79**	7.47**	0.69	5.09**	-1.97**	1.43**	-0.47**	-2.96**	-2.37**
L_3 x T_{10}	-13.56**	-22.42**	13.92**	13.14**	-0.79	-1.50*	3.00**	-4.22**	2.29**	0.46**	-2.12**	-1.54**
L_4 x T_8	-20.23**	-30.62**	0.81	-0.08	-3.01**	-4.20**	2.66**	-4.57**	3.30**	1.64**	0.23*	0.80**
L_4 x T_9	-13.13**	-20.33**	8.62**	7.80**	4.52**	-3.56**	3.26**	-3.93**	2.33**	1.15**	-1.29**	-0.72**
L_4 x T_{10}	-20.46**	-25.25**	4.89**	4.04**	-0.31	-2.17**	4.56**	-2.54**	3.37**	2.26**	-0.27**	0.30**
L_5 x T_8	-15.99**	-23.38**	1.92*	1.04	-1.98**	-2.28**	2.80**	-4.43**	2.22**	0.88**	-0.55**	0.02
L_5 x T_9	-14.68**	-19.37**	5.11**	4.26**	2.04**	-5.41**	-0.17	-7.62**	2.29**	1.45**	-0.99**	-0.42**
L_5 x T_{10}	-19.28**	-21.29**	3.58**	2.71**	-0.90	-1.90**	3.16**	-4.04**	2.50**	1.70**	-0.84**	-0.27**
L_6 x T_8	-14.49**	-22.21**	3.57**	2.71**	2.16	-4.95**	-0.34	-7.80**	1.99**	0.97**	-0.45**	0.11
L_6 x T_9	-6.28**	-11.02**	12.40**	11.61**	10.90**	10.94**	1.43**	-5.91**	1.41**	0.89**	-1.56**	-0.99**
L_6 x T_{10}	-16.46**	-18.86**	6.22**	5.37**	-0.02	-6.61**	-3.34**	-11.03**	2.16**	1.70**	-0.85**	-0.28**
L_7 x T_8	-16.41**	-26.29**	3.79**	2.93**	6.52**	1.56**	5.89**	-1.11	2.37**	1.01**	-0.41**	0.16
L_7 x T_9	-9.78**	-16.60**	11.18**	10.38**	9.26**	7.43**	1.59**	-5.73**	1.63**	0.76**	-1.69**	-1.12**
L_7 x T_{10}	-19.92**	-24.49**	5.16**	4.31**	5.88**	1.53*	4.55**	-2.55**	2.31**	1.51**	-1.04**	-0.47**

*,** Significant at P= 0.05 and P=0.01, respectively

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Table 9. Heterosis over mid-parent (M.P.), high-parent (H.P.) and check varieties for quality characters of line x tester analysis for yellow maize genotypes across eight environments

Genotypes	Protein %				Oil %				Carbohydrate %			
	M.P	H.P	S.C.155	T.W.C. 352	M.P	H.P	S.C.155	T.W.C. 352	M.P	H.P	S.C.155	T.W.C. 352
L₁ x T₈	-14.05**	-16.99**	1.65*	-10.80**	-9.39**	-13.55**	-2.97**	-0.14	1.81**	1.27**	-0.21**	1.42**
L₁ x T₉	-9.86**	-14.25**	6.64**	-5.19**	-5.77**	-8.44**	1.65	4.36**	1.59**	1.03**	-0.46**	1.18**
L₁ x T₁₀	-3.91**	-3.83**	7.96**	-3.70**	-6.95**	-10.93**	-0.60	2.17	1.02**	0.92**	-0.57**	1.07**
L₂ x T₈	-1.52	-3.47**	15.27**	4.54**	-3.61	-7.48**	2.39**	5.08**	0.52*	0.65**	-2.23**	-0.57**
L₂ x T₉	-13.78**	-14.57**	6.37	-5.49**	-3.07	-5.61**	4.09**	6.74**	2.30**	2.19**	-0.42**	1.21**
L₂ x T₁₀	-6.01**	-2.44**	9.19**	-2.30**	-1.92	-5.64**	4.06**	6.71**	1.12**	0.54	-1.16**	0.49**
L₃ x T₈	-4.96**	-0.50	15.51**	4.81**	2.54	-1.19	0.98	3.71**	0.80**	0.06	-2.57**	-0.90**
L₃ x T₉	-11.63**	-14.79**	11.36**	0.13	-2.62	-7.84**	-2.88**	-0.05	1.51**	0.80**	-1.85**	-0.19
L₃ x T₁₀	-8.49**	-15.96**	10.45**	-0.89**	-1.43	-5.38**	-2.96**	-0.13	1.30**	0.11	-1.59**	0.07
L₄ x T₈	-6.66**	-9.74**	7.75**	-3.94**	-1.55	-3.29**	2.33*	5.02**	0.62*	0.01	-1.36**	0.29**
L₄ x T₉	-4.05**	-8.52**	11.32**	0.09	-6.54*	-7.00**	-1.19	1.60	0.56*	-0.08	-1.45**	0.20**
L₄ x T₁₀	-3.03**	-3.27**	8.45**	-3.14**	-3.15	-4.84**	0.86	3.59**	0.75**	0.58**	-0.77**	0.87**
L₅ x T₈	-8.16**	-8.12**	9.11**	-2.40**	-10.49**	-15.88**	-2.86**	-0.02	1.25**	0.92**	-1.01**	0.63**
L₅ x T₉	-7.97**	-9.46**	10.55**	-0.78	-10.18**	-14.15**	-1.33	1.46	0.78**	0.43**	-1.52**	0.14
L₅ x T₁₀	-4.21**	-7.01**	10.10**	-1.28**	-13.79**	-19.24**	-5.84**	-2.93**	0.52*	0.40**	-1.30**	0.35**
L₆ x T₈	-2.62	-4.08**	12.50**	1.42*	-7.17**	-13.14**	0.97	3.70**	0.39**	-0.12	-1.70**	-0.04
L₆ x T₉	-7.78**	-10.83**	9.43**	-2.04**	-8.57**	-13.24**	0.88	3.61**	0.98**	0.45**	-1.12**	0.53**
L₆ x T₁₀	-1.06	0.18	11.52**	0.31	-16.98**	-23.41**	-8.01**	-5.04**	0.36	0.30**	-1.27**	0.38**
L₇ x T₈	-7.42**	-8.33**	10.46**	-0.88	-0.79	-5.70**	-3.43**	-0.58	1.18**	0.97**	-1.64**	0.02
L₇ x T₉	-6.65**	-7.25**	12.35**	1.25	5.25*	-0.57	4.06**	6.71**	0.90**	0.71**	-1.95**	-0.29**
L₇ x T₁₀	-8.70**	-12.50**	7.01**	-4.77**	-2.16	-7.22**	-4.76**	-1.87	0.84**	0.18	-1.52**	0.14

*,** Significant at P= 0.05 and P=0.01, respectively

This hybrid (L6 x T8) was superior to its commercial control (S.C. 10) for these characters, can be commercially exploited especially in maize to improve nutritional qualities along with yield to suit the farmers.

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القدرة علي الائتلاف وقوة الهجين للتبكير في النضج ومحصول وجودة حبوب
الذرة الشامية البيضاء والصفراء تحت ثماني بيئات

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أجريت هذه الدراسة في تجربتين منعزلتين بنظام السلالة x الكشاف لتقيـيم سـلالات
وهجن الذرة الشامية البيضاء والصفراء تحت بيئات مختلفة خلال الموسم الصيفي لأعـوام
٢٠٠٣ و ٢٠٠٤ ، وذلك بعمل التهجين بين سبعة سلالات مرباه داخليا وثلاثـة كشـافات
للحصول علي واحد وعشرون هجين قمي في كل من الذرة البيضاء والصفراء ، وتم التقييم
في تصميم القطاعات الكاملة العشوائية في ثلاثة مكررات في ثماني بيئات (ميعادين للزراعة
ومستويين للتسميد النيتروجيني ومنطقتين) وذلك لدراسة صفات التبكير في النضج وجـودة
ومحصول الحبوب وتم تحليل البيانات بطريقة السلالة في الكشاف الخاصة بكمبثرون لعــام
١٩٥٧ لتقدير القدرة علي التآلف وتفاعلاتها مع البيئة، كما تم تقدير قوة الهجين طبقاً لـــ
Bhatt (1971) .

وتشير أهم نتائج الدراسة إلى ما يلي :

١ – كان التباين الراجع إلي البيئات والتراكيب الوراثية والتفاعل بين التراكيب الوراثية في
البيئة عالي المعنوية لصفات التبكير في النضج، نسبة البروتين الخام، نسبة الزيـت،
نسبة الكربوهيدرات ومحصول الحبوب في كل من الذرة البيضاء والصفراء.

٢ – أظهر التباين الراجع إلي الهجن القمية ومكوناتها (تأثير السـلالة، تـأثير الكشـاف
وتأثير التفاعل بين السلالة في الكشاف) اختلافات عالية المعنويـة لجميـع الصـفات
المدروسة في الذرة البيضاء والصفراء ماعدا نسبة البروتين والزيت لتأثير السـلالة
والكشاف في الذرة الصفراء.

٣- أظهرت السلالة L_3 أفضل قدرة عامة علي الائتلاف لصفات البروتين والزيت وأعطت السلالات البيضاء L_1 و L_4 أعلي قدرة عامة علي الائتلاف لصفة نسبة الكربوهيدرات في حين تفوقت السلالة L_4 والكشاف T_{10} حيث أعطت قيما مرتفعة ومرغوبة في قدرتها الائتلافية العامة لصفات التبكير في النضج والمحصول في الذرة البيضاء.

٤- أعطت سلالة الذرة الصفراء L_1 أفضل التقديرات للقدرة العامة علي الائتلاف لجميـع الصفات ما عدا نسبة البروتين في الحبوب.

٥- أعطى الهجين القمى L_2 X T_{10} أفضل قدرة خاصة علــي التــآلف لصفـات نسـبة البروتين الخام والزيت والهجين القمى L_2 X T_8 لصفة نسـبة الكربوهيـدرات فـي الذرة البيضاء.

٦- أوضحت الدراسة أن نسبة التباين الراجع إلي القدرة العامة والخاصة علي التآلف كان أكبر من الوحدة لصفة التبكير في النضج في الذرة البيضاء والصفراء مما يشير إلـي أهمية الفعل الجيني المضيف في وراثة هذه الصفة، في حين كانت هذه النسبة أقل من الوحدة لصفات جودة ومحصول الحبوب في الذرة البيضاء والصفراء مما يشير إلـي أهمية الفعل الجيني غير المضيف.

٧- كانت كفاءة التوريث بالمعنى الضيق مرتفعه وأكثر من ٧٠٪ لميعاد طـرد ٥٠٪ مـن النورات المؤنثة فى كل من الذرة الشامية البيضاء والصفراء، بينما كانـت متوسـطة لصفه محصول الحبوب (٣٣،٢٪) للذرة الشامية البيضاء و لنسبة البروتين (٣١،١٪) والزيت (٣٥،٧٪) فى الذرة الصفراء.

٨- تراوحت قيم قوة الهجين لمحصول الحبوب فى الذرة البيضـاء بـين ٤٠،٥٪ إلـى ٦٨،٣٪بالنسبة لمتوسط الأبوين ومن ١٠،٨ إلى ٦٠،٩٪ بالنسبة للأب الأعلى، ومن -٣٩،٣٪ إلى ٣،٩٪ مقارنة بالهجين الفردى ١٠، فى حين أظهرت الـذرة الشـامية الصفراء قوة هجين لمحصول الحبوب تراوحت من ٤٢،٦٪ إلــى ٦٤،٧٪ لمتوسط الأبوين ومن ٢٩،٩٪ إلى ٦٣،٩٪ للأب الأعلى ومن -٣٤،٨ إلــى ٠،٦٣٪ مقارنـة بالهجين الفردي ١٥٥. وتفوق الهجين القمـي الأبـيض L_6 X T_8 علـي الهجـين التجاري (فردي ١٠) لمعظم الصفات المدروسة.