Line × Tester Analysis in S1 top-crosses of Maize for Grain Yield and its Related Traits

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Abstract

The line × tester model was used to evaluate 243 top-crosses with their parents (81 S1 families and the three testers) of maize for general and specific combining abilities and to estimate the genetic components. Highly significant differences were found among crosses, lines (L), testers (T), and their interaction for grain yield/plot (GY/P), ear diameter (ED), number of kernels/row (NK/R) and days to 50% silking (SILK). The contribution of L vs. T interaction was higher than lines and testers indicating high estimates of variance due to specific combining ability for NK/R and GY/P. The general mean over all testers surpassed both S1 families and S1 top-crosses for GY/P (414.29 and 77.05%), and only S1 top-crosses for SILK (3.42%). Otherwise, the testers were less than S1 families for SILK (2.84%). Moreover, the S1 top-crosses exceeded the S1 families for GY/P (190.48%). The S1 top-crosses were earlier than both testers (-3.31%) and S1 families (-5.98%). 22, 28, and 26 S1 families possessed positive and significant GCA effects for GYP, ED, and NKR, respectively, and 16 lines with negative and significant GCA effects for SILK. Lines i.e., L26 and L33 had significant positive GCA effects for GY/P, ED, and NK/R, but negative effects for SILK. The tester T2 was a good combiner for GY/P, NK/R, and SILK, but T1 for ED.14, 46, 16, and 9 S1 top-crosses possessed significant SCA effects for GY/P, NK/R, ED and SILK (earliness), respectively. The earliness of S1 top-crosses depends on the specific combining between lines and testers.

Introduction

Maize (*Zea mays* L.) is one of the major grain crops in the world providing nutrients as human food, poultry and animals feed as source of starch, oil, food sweeteners, as well as biofuel source. The global harvested area was recorded 201.983.645 Ha producing more than 116 million tons, as in Egypt possessed 145.888.1 Ha producing 750 Million tons (FAO, 2020). To meet the ever-increasing demand, maize production can be increased by selecting superior genotypes for varietal release and commercial use (Agyeman and Ewool, 2022). In Egypt, there is a big gap between production and consumption of maize 48 %

(FAO, 2021). This gap will be increase with the increasing of population in next years.

Moreover, there is a problem to expand maize cultivation to reduce the cost of poultry and animal feeding cost. Furthermore, the new reclaimed soil has many problems especially the different abiotic stresses, which face the maize cultivation.

Abiotic stresses such as drought, heat, are the major problems, which reducing the chances of expanding the crop cultivation and significant yield losses of maize i.e., maize in new reclaimed lands environments (Fischer *et al.*, 2020).

Grain yield as the most important trait of selection programs, exhibited a significant association with non-additive gene action which suggested that specific combining ability (SCA) remark a good predictor for grain yield (Kamara *et al.*, 2021 and Emam and Mohamed, 2021). The low GCA to SCA variance ratio revealed the preponderance of non-additive gene action in the inheritance of grain yield (Kaur *et al.*, 2010 and Dinesh *et al.*, 2016). Moreover, SCA could be used to predict the hybrid performance (Ibrahim *et al.*, 2021). Moreover, Abrha *et al.*, (2013) and Ganapati Mukri *et al.*, (2022) reported that both of additive and non-additive gene actions were important in controlling the behavior of genetic potential of the inbred lines of maize development for yield and related traits. Otherwise, the high GCA revealed to the additive gene effects controlled the trait i.e., grain yield in maize (Ismail *et al.*, 2020) and good predictor for grain yield in maize (Mutimaamba *et al.*, 2020).

Line × tester analysis possessed an effective method to determine GCA and SCA for lines, testers and their hybrids for most traits (Rahman, 2013).

The two most important activities in maize improvement are a- development the inbred lines with high estimates of general combining ability (GCA) and specific combining ability (SCA), and b- identification the hybrids with high yield potentials. Genomic selection (GS) is a promising genomic tool to perform selection program on the untested breeding material based on the genomic estimated breeding values estimated from the genomic prediction (GP) (Zhang *et al.*, 2022).

The major objectives of the current investigation were designed to study the performance of S1 families, testers and their crosses, as well as estimate the genetic variances, general and specific combining abilities and genetic parameter using line × tester model in 243 S1 top-crosses of maize.

Materials and Methods

This study was carried out during the summer seasons of 2020 and 2021 at Agricultural Research Farm, Faculty of Agriculture, New valley University to study the general and specific combining abilities of the grain yield and its associated traits for 81 S1 families, three testers and 243 S1 top-crosses, respectively. The S1 families were derived from two sources i.e., IY-148 and Mallawy-121, which were obtained from National Maize Research Program (NMRP), Field Crops Research Institute, Agric. Res. Centre (ARC).

Procedure and Field Experiment

In 2020 season top crosses were formed in three isolated blocks for 81 S1 families using three testers i.e., SC168, TWC370 and IY335 at Agricultural Research Farm, Faculty of Agriculture, New Valley University.

In 2021 season 243 top-crosses with their parents (81 S1 families and the three testers were evaluated at Agricultural Research Farm, Faculty of Agriculture, New valley University, in a Randomized Complete Block Design (RCBD) with three replications. Experimental plot size was one row, 4 meters long and 70 cm apart and 25 cm between hills within row (2.8 m²). Seedlings were thinned to one plant/hill before the first irrigation (two weeks after sowing). Fertilizer was applied at the rate of 120 kg nitrogen/Fed. in three doses. Normal cultural practices were applied as recommended in sandy soil as in the new valley. The data were recorded for ear diameter (ED), number of kernels/row (NK/R), grain yield/plot (GY/P) and days to 50% silking (SILK).

Statistical analysis

I- Top crosses evaluation (season 2021)

Data of top-crosses were subjected to analysis of variance of RCBD as described by Steel and Torrie (1980). When differences among top-crosses were found significant, line × tester analysis according to Kempthorne (1957) was practiced (Table 1) to estimate the general and specific combining abilities of the tested lines and testers.

Table 1. Analysis of variance for the evaluated traits involving top crosses evaluated in 2021 season

Source of variance	d.f.	MS	EMS
Replication (r)	r-1		
Crosses (C)	c-1		
Lines (L)	l-1	M_1	$\sigma^2_e + r\sigma^2_{lt} + rt\sigma^2_l$
Testers (T)	t-1	M_2	$\sigma^2_e + r\sigma^2_{lt} + rl\sigma^2_t$
Line × tester (L×T)	(l-1)(t-1)	M_3	$\sigma^2_e + r\sigma^2_{lt}$
Error	(r-1)(g-1)	M_4	σ^2_e

Where r, l, t, c, and g refer to no. of replications, lines, testers, crosses and genotypes, respectively.

I-1. Estimation of GCA and SCA effects:

The model used to estimate GCA and SCA effects of the ijkth observation was $Y_{ijk} = \mu + g_i + g_j + s_{ij} + e_{ijk}$

Where, μ = overall population mean.; g_i = GCA effects of the ith line parent.

g_j = GCA effects of the jth tester parent.; s_{ij} = SCA effects of the ijth combination.

e_{ijk} = the error associated with any observation.; and

i = 1, 2………., 81.; j = 1, 2, 3.; and k= 1, 2, 3.

I-1. a. Estimation of GCA effects for lines:

$$g_i = \frac{Y_{i..}}{tr} - \frac{Y_{...}}{ltr}$$

Where: $Y_{i..}$ = total of ith line over all testers and replications.

$Y_{...}$ = total of all lines over all testers and replications.

I-1. b. Estimation of GCA effects for testers

$$g_t = \frac{Y_{.j.}}{lr} - \frac{Y_{...}}{Ltr}$$

I-1. c. Estimation of SCA effects (Sij):

$$S_{ij} = \frac{Y_{ij.}}{r} - \frac{Y_{i..}}{tr} - \frac{Y_{.j.}}{lr} + \frac{Y_{...}}{rtl}$$

I-1. d. Estimation of standard errors (SE) for combining ability effects

SE GCA for lines = (Me/rt)1/2; SE GCA testers = (Me/rl)1/2; and

SE SCA effects = (Me/r)1/2

The significance of general and specific combining ability effects was tested as follows:

L.S.E. (least significant effect) = SE GCA × tα; L.S.E. for SCA effects = SE SCA x tα

I-2. Estimation of variance components:

From the expectation of mean squares of analysis of variance (Table 1), the variance components according to Singh and Chaudhary (1985) were estimated as follows:

$\sigma^2 l$ = (M1 - M3)/rt; $\sigma^2 t$ = (M2 - M3)/rl; and $\sigma^2 lt$ = (M3 − M4)/r

Where: $\sigma^2 l$ = variance due to lines.; $\sigma^2 t$ = variance due to testers.

$\sigma^2 lt$ = variance due to line × tester interaction.

The covariance of half-sib (H.S.) and full-sib were estimated as follows:

$$\text{Cov H.S. (line)} = \frac{Ml - Mlt}{rt}$$

$$\text{Cov H.S. (tester)} = \frac{Mt - Mlt}{rl}$$

$$\text{Cov H.S. (average)} = \frac{1}{r\,(2lt-l-t)} \left[\frac{(l-1)Ml + (t-1)Mt}{l + t - 2} - Mlt \right]$$

$$\text{Cov. F.S.} = \frac{(Ml-Me)+(Mt-Me)+Mlt-Me)}{3r} + \frac{6\,r\,\text{Cov. H.S. (average)} - (l+t)\,\text{Cov. H.S. (average)}}{3r}$$

$$\sigma^2 GCA = \text{Cov H.S. (average)} = \left[\frac{1+F}{4} \right] \sigma^2 A$$

$$\sigma^2 SCA = \frac{Mlt - Me}{r} = \left[\frac{1+F}{2} \right] \sigma^2 D$$

In the present case F= 0

- $\sigma^2A = 4 \sigma^2GCA$

- $\sigma^2D = 2\sigma^2SCA$

- The genetic (σ^2G) and phenotypic (σ^2P) variances were calculated as:

$\sigma^2G = \sigma^2A + \sigma^2D$; and $\sigma^2P = \sigma^2G + \sigma^2E/r$

- Broad sense heritability = Hbs = σ^2G / σ^2P

- Narrow sense heritability = Hns = σ^2A / σ^2P

-The combining ability ratio (CAR) was calculated to expect the gene action using the equation of Baker (1978) as following

CAR = $2\sigma^2GCA / (2\sigma^2GCA + \sigma^2SCA)$

Where: σ^2GCA and σ^2SCA are the GCA and SCA variances, respectively.

When the value of CAR<1 this means that the trait controlling by non-additive gene action.

- ($\sigma^2GCA / \sigma^2SCA$) and ($\sigma^2D / \sigma^2A$)1/2ratios were used to assess the relative weight of additive versus non-additive type of gene actions (Verma and Srivastava, 2004).

- The contributions of lines, testers and line × tester were accounted as following:

Contributions of lines = SS lines/ (SS lines + SS testers+ SS line × tester) (Total SS)

Contributions of testers = SS testers/ (SS lines + SS testers+ SS line × tester)

Contributions of SS line × tester = SS line × tester / (SS lines + SS testers+ SS line × tester)

The greater contributions of line × tester interaction than testers for any trait indicates high estimates of variance due to specific combing ability.

II- Comparing the observed means for S1 families as well as S1 top-crosses were calculated using R.L.S.D. as R.L.S.D. α = t α* Sd.

Results and Discussion

I- Analysis of variance of line × tester model in S1 top-crosses of maize

The analyses of variance for all genotypes expressed highly significant mean squares in S1 top-crosses of studied traits of maize. Consequently, the line*tester model can be used to analyze the obtained data. The partitioning of summation of square for crosses to lines (L), testers (T) and L vs. T revealed highly significant differences among each of crosses, lines, testers and their interaction for studied traits i.e., grain yield/plot, ear diameter, number of kernels/row and days to 50% silking (Table 2). The greater contributions of L vs. T interaction than both of lines and testers indicates higher estimates of variance due to specific combining ability

for traits i.e., number of kernels/row and grain yield/plot. Moreover, the high contributions of both lines and L vs. T interaction than testers indicated higher estimates of variance due to general and specific combining abilities predominant of lines and L vs. T interaction influence, respectively, for ear diameter and days to 50% silking (Table 2). The obtained results possessed different genetic make-up of genes control the studied traits whose coming from lines, testers or expressed from the interaction between them. This will be very benefit to understand and knowledge the type of gene action correlated with different traits of maize under New Valley region. The obtained results are in line with Dinesh *et al*., (2016) and Sayed *et al*., (2020).

Table 2. Analysis of variance for l studied traits using line × tester analysis

S.O.V.	D.F.	MS			
		Ear diameter, cm	No. of kernels/row	Grain yield/plot (kg)	Days to 50% silking
Replications	2	0.25 N.S.	5.34 **	0.02 *	2.89 NS
Crosses (C)	242	0.58 **	100.35 **	0.56 **	44.07 **
Lines (L)	80	0.90 **	131.86 **	0.83 **	50.04 **
Testers (T)	2	4.65 **	1235.62 **	5.01 **	254.01 **
L × T	160	0.36 **	70.41 **	0.36 **	38.46 **
Error	484	0.11	8.29	0.08	12.54
Contribution of lines (L)		0.517	0.434	0.434	0.49
Contribution of testers (T)		0.066	0.102	0.102	0.07
Contribution of (L × T)		0.417	0.464	0.464	0.43

II- Means of S1 families, testers and S1 top-crosses for studied traits

Means and standard errors of S1 families, testers and S1 top-crosses were presented in Tables 3, 4 and 5. The obtained data exhibited that the general means over all testers surpassed both of S1 families and S1 top crosses for grain yield/plot (414.29 and 77.05%), and only S1 top-crosses for days to 50% silking (3.42%). Otherwise, the average of testers was less than S1 families for days to 50% silking by (2.84%). Moreover, the S1 top-crosses exceeded the S1 families for grain yield/plot (190.48%). It is clear result that the S1 top-crosses were earlier than both of testers (-3.31%) and S1 families (-5.98%). The obtained data exhibited that the genetic make-up may be transmitted from testers to S1 top-crosses.

The mean of 81 S1 families ranged from 62.00 (L31) to 76.50 (L28) with an average of 70.90 day, and 0.04 (L55) to 0.72 (L9) with an average of 0.21 kg for, days to 50% silking and grain yield/plot, respectively (Table 3). These results possessed different genetic performance for the studied traits of the current S1 families. Thirty-five S1 families surpassed their general mean of lines in range of 0.59 to 244.88 with an average of 62.86% for grain yield/plot. Out of them, the superior fourteen S1 families exceeded the general mean of lines in range of 48.49 to 244.88 with an average of 99.74% for grain yield/plot. These S1 families in ranking were L9 (244.88); L41 (158.66); L14 (110.76); L10 (105.97); L22 and L53 (86.81); L63 (67.65); L31 (62.86); L52 (58.07); L12, L60 and L64 (53.28); and L49 and L50 (48.49%). The proposed results for S1 families reflect their

different genetic make-up as estimated in significant mean square of lines (Table 3).

Table 3. Means of 81 parents (S1-families) for all studied traits

S1 families	Days to 50% Silking			Grain yield/plot (kg)			S1 families	Days to 50% Silking			Grain yield/plot (kg)		
	Mean	±	SE	Mean	±	SE		Mean	±	SE	Mean	±	SE
1	67.50	±	0.87	0.20	±	0.01	44	73.50	±	0.87	0.08	±	0.01
2	67.50	±	0.87	0.24	±	0.01	45	71.50	±	2.02	0.07	±	0.01
3	71.50	±	2.02	0.14	±	0.01	46	67.50	±	1.44	0.13	±	0.01
4	67.00	±	0.58	0.29	±	0.01	47	70.50	±	0.87	0.13	±	0.01
5	69.00	±	0.58	0.30	±	0.01	48	74.00	±	1.16	0.16	±	0.01
6	73.50	±	1.44	0.18	±	0.01	49	72.50	±	0.29	0.31	±	0.02
7	69.00	±	0.58	0.18	±	0.01	50	70.00	±	0.01	0.31	±	0.02
8	67.00	±	0.58	0.28	±	0.01	51	73.00	±	1.16	0.24	±	0.01
9	72.50	±	0.44	0.72	±	0.04	52	69.00	±	0.58	0.33	±	0.02
10	75.00	±	0.58	0.43	±	0.02	53	72.50	±	1.44	0.39	±	0.02
11	72.50	±	0.02	0.19	±	0.01	54	72.00	±	1.73	0.18	±	0.01
12	71.50	±	1.44	0.32	±	0.02	55	67.50	±	1.44	0.04	±	0.01
13	72.50	±	1.44	0.14	±	0.01	56	73.00	±	1.16	0.05	±	0.01
14	72.50	±	0.87	0.44	±	0.02	57	73.00	±	1.16	0.06	±	0.01
15	72.00	±	0.16	0.28	±	0.01	58	70.50	±	0.29	0.22	±	0.01
16	67.50	±	0.87	0.22	±	0.01	59	70.50	±	0.29	0.17	±	0.01
17	72.00	±	0.16	0.21	±	0.01	60	72.50	±	1.44	0.32	±	0.02
18	73.00	±	0.58	0.30	±	0.01	61	76.00	±	0.01	0.21	±	0.01
19	73.50	±	0.87	0.18	±	0.01	62	68.50	±	0.29	0.30	±	0.01
20	66.50	±	0.87	0.28	±	0.01	63	72.00	±	1.73	0.35	±	0.02
21	68.50	±	1.44	0.25	±	0.01	64	71.50	±	2.02	0.32	±	0.02
22	66.50	±	0.87	0.39	±	0.02	65	72.50	±	2.60	0.14	±	0.01
23	72.00	±	1.73	0.30	±	0.01	66	70.00	±	0.01	0.24	±	0.01
24	75.50	±	0.29	0.28	±	0.01	67	72.00	±	2.31	0.16	±	0.01
25	71.50	±	0.29	0.22	±	0.01	68	75.50	±	0.29	0.17	±	0.01
26	68.00	±	0.58	0.15	±	0.01	69	75.00	±	0.58	0.17	±	0.01
27	73.50	±	0.87	0.27	±	0.01	70	76.00	±	0.58	0.15	±	0.01
28	76.50	±	0.29	0.08	±	0.01	71	73.00	±	1.16	0.10	±	0.01
29	67.00	±	0.58	0.18	±	0.01	72	72.50	±	1.44	0.08	±	0.01
30	76.00	±	0.58	0.16	±	0.01	73	68.00	±	1.16	0.11	±	0.01
31	62.00	±	0.58	0.34	±	0.02	74	72.00	±	1.73	0.11	±	0.01
32	66.50	±	0.87	0.05	±	0.01	75	72.00	±	1.73	0.07	±	0.01
33	69.00	±	0.58	0.12	±	0.01	76	69.00	±	0.58	0.12	±	0.01
34	69.00	±	0.58	0.10	±	0.01	77	74.50	±	0.87	0.12	±	0.01
35	66.50	±	0.87	0.29	±	0.01	78	73.00	±	1.73	0.07	±	0.01
36	73.50	±	0.87	0.11	±	0.01	79	66.50	±	0.87	0.23	±	0.01
37	73.00	±	1.73	0.11	±	0.01	80	71.50	±	2.02	0.10	±	0.01
38	69.00	±	0.58	0.19	±	0.01	81	66.50	±	0.87	0.11	±	0.01
39	69.50	±	0.87	0.15	±	0.01	Average	70.90	±	0.99	0.21	±	0.01
40	67.50	±	0.87	0.22	±	0.01	Max.	76.50	±	0.29	0.72	±	0.04
41	70.00	±	0.58	0.54	±	0.03	Min.	62.00	±	0.58	0.04	±	0.006
42	70.00	±	0.58	0.13	±	0.01	Rev LSD	3.05			0.02		
43	69.00	±	0.58	0.14	±	0.01							

The mean of three testers ranged from 67.50 (T3) to 71.33 (T1) with an average of 68.94 day, and 0.52 (T3) to 1.85 (T1) with an average of 1.08 kg for days to 50% silking and grain yield/plot, respectively (Table 4). It remarkable results that the SCI 168 (T1) ranked in the first order among the testers for days to 50% silking and grain yield/plot and surpassed their general mean by 3.47 and 71.30%, respectively.

The different performance of lines and testers of maize will be a powerful tool to mate series of crosses and select the superior ones for grain yield. The obtained results are in accordance with Ganapati Mukri *et al.*, (2022) who found significant wide genetic diversity and variation due to lines and testers which reflect the high genetic differences for grain yield in maize. Consequently, the remark notes must consider to the performance of those lines and testers which shared in series of crosses. Furthermore, Sayed *et al.*, (2020) found different responses for grain yield/plot and its components among 100 S1-lines and two testers of maize using Line × Tester analysis.

Table 4. Means of days 50% silking and grain yield of the testers

Testers	Days to 50% silking			Grain yield/ plot, Kg		
	Mean	±	SE	Mean	±	SE
SC1 168 (T1)	71.33	±	0.88	1.85	±	0.03
TWC 370 (T2)	68.00	±	1.16	0.87	±	0.02
IY 335 (T3)	67.50	±	0.87	0.52	±	0.03
Average	68.94	±	0.97	1.08	±	0.03
Max.	71.33		0.88	1.85		0.03
Min.	67.50		0.87	0.52		0.03
LSD	NS			0.02		

The mean of 243 S1 top-crosses ranged from 2.67 (L59T2) to 5.50 (L29T1 & L38T1) with an average of 4.61 cm; 8.33 (L56T3) to 40.67 (L33T2) with an average of 27.76; 33.00 (L56T2) to 75.00 (L64T1) with an average of 66.66 day; and 0.03 (L56T3) to 1.37 (L29T2) with an average of 0.61 kg for ear diameter, no. of kernels/row, days to 50% silking, and grain yield/plot, respectively (Table 5). These results exerted different genetic behavior of the obtained S1 top-crosses for the studied traits.

Table 5. Means and standard error (SE) for studied traits for all S1 top-crosses

S1 families	Testers	Ear diameter (cm)			No. kernels/row			Grain yield/plot (Kg)			Days to 50% silking		
		Mean	±	SE	Mean	±	SE	Mean	±	SE	Mean	±	SE
1	T1	3.50	±	0.10	16.01	±	0.77	0.06	±	0.01	69.00	±	0.01
	T2	4.00	±	0.39	28.50	±	1.44	0.41	±	0.02	65.00	±	2.31
	T3	4.00	±	0.19	22.50	±	1.06	0.24	±	0.01	70.50	±	2.60
2	T1	3.83	±	0.10	16.34	±	0.96	0.08	±	0.01	72.00	±	1.73
	T2	4.33	±	0.39	23.33	±	1.15	0.26	±	0.01	64.00	±	1.73
	T3	4.33	±	0.58	22.00	±	1.15	0.48	±	0.03	67.00	±	0.01
3	T1	4.83	±	0.48	21.50	±	0.87	0.24	±	0.02	67.00	±	0.01
	T2	4.50	±	0.10	26.84	±	0.68	0.41	±	0.03	63.50	±	1.44
	T3	4.33	±	0.01	24.33	±	0.39	0.24	±	0.01	69.50	±	0.29
4	T1	5.17	±	0.10	30.00	±	0.19	0.88	±	0.05	63.50	±	1.44
	T2	4.67	±	0.01	34.00	±	0.00	0.76	±	0.06	68.00	±	4.04
	T3	4.67	±	0.01	22.00	±	1.54	0.28	±	0.02	72.50	±	1.44
5	T1	4.33	±	0.19	26.84	±	1.25	1.07	±	0.07	65.00	±	2.31
	T2	4.83	±	0.10	29.00	±	2.89	0.93	±	0.02	63.50	±	1.44
	T3	5.00	±	0.01	30.33	±	0.96	0.90	±	0.03	64.00	±	1.73
6	T1	5.33	±	0.19	36.50	±	1.44	1.22	±	0.06	63.50	±	1.44
	T2	4.83	±	0.10	35.17	±	1.63	0.81	±	0.04	66.00	±	0.01
	T3	4.50	±	0.29	25.17	±	1.44	0.46	±	0.02	66.50	±	0.29
7	T1	3.67	±	0.19	15.50	±	3.18	0.18	±	0.01	71.50	±	3.18
	T2	4.33	±	0.19	27.33	±	0.96	0.40	±	0.01	67.00	±	0.01
	T3	4.33	±	0.19	32.67	±	2.31	0.29	±	0.02	66.00	±	2.89
8	T1	4.83	±	0.10	32.33	±	1.35	0.93	±	0.03	67.50	±	0.87
	T2	4.67	±	0.19	29.67	±	1.73	0.68	±	0.02	65.00	±	2.31
	T3	4.67	±	0.19	29.50	±	2.02	0.59	±	0.02	66.50	±	0.29
9	T1	4.50	±	0.48	24.50	±	2.60	0.24	±	0.01	66.00	±	2.89
	T2	4.33	±	0.19	34.00	±	1.15	0.85	±	0.02	69.00	±	1.73
	T3	4.83	±	0.29	31.17	±	1.06	0.71	±	0.06	65.5	±	2.60
10	T1	3.83	±	0.10	19.17	±	1.25	0.20	±	0.01	73.00	±	2.31
	T2	4.50	±	0.48	32.50	±	1.06	0.70	±	0.05	62.50	±	3.75
	T3	4.83	±	0.48	36.34	±	2.12	0.82	±	0.02	70.50	±	2.60
11	T1	5.33	±	0.19	34.17	±	2.02	1.32	±	0.04	66.50	±	0.29
	T2	4.33	±	0.19	22.67	±	0.58	0.24	±	0.02	71.50	±	0.87
	T3	4.67	±	0.39	25.50	±	3.18	0.22	±	0.02	71.50	±	0.87
12	T1	4.67	±	0.01	19.67	±	0.96	0.29	±	0.01	67.50	±	0.29
	T2	4.83	±	0.29	25.67	±	2.12	0.71	±	0.04	68.00	±	4.04
	T3	4.50	±	0.29	27.17	±	2.98	0.48	±	0.04	67.50	±	0.87
13	T1	5.17	±	0.10	30.33	±	1.35	0.83	±	0.06	67.50	±	0.87
	T2	5.00	±	0.01	27.17	±	3.18	0.55	±	0.03	68.00	±	1.15
	T3	4.00	±	0.19	22.67	±	1.35	0.11	±	0.01	68.00	±	0.58
14	T1	5.33	±	0.01	33.83	±	2.60	1.07	±	0.03	61.00	±	2.89
	T2	4.83	±	0.10	28.17	±	0.87	1.06	±	0.04	61.00	±	0.01
	T3	4.33	±	0.19	17.33	±	1.15	0.40	±	0.01	68.50	±	1.44
15	T1	4.67	±	0.19	26.17	±	2.98	0.59	±	0.04	66.00	±	0.01
	T2	4.00	±	0.39	25.83	±	2.21	0.65	±	0.02	70.50	±	2.60
	T3	4.50	±	0.10	27.17	±	0.10	0.54	±	0.03	64.00	±	1.73
16	T1	3.67	±	0.19	22.67	±	0.00	0.31	±	0.02	69.00	±	1.15
	T2	5.00	±	0.01	30.17	±	1.06	0.66	±	0.02	66.00	±	0.01
	T3	4.33	±	0.01	24.83	±	1.06	0.40	±	0.01	66.50	±	0.29
17	T1	5.00	±	0.19	31.00	±	1.15	1.02	±	0.03	66.00	±	0.01
	T2	5.00	±	0.01	35.83	±	0.48	1.30	±	0.03	63.50	±	1.44
	T3	4.50	±	0.10	24.83	±	1.44	0.79	±	0.03	63.50	±	1.44
18	T1	4.83	±	0.10	27.83	±	0.48	1.17	±	0.02	66.00	±	0.01
	T2	4.67	±	0.01	31.50	±	0.68	1.11	±	0.01	68.00	±	1.15
	T3	3.67	±	0.77	24.67	±	0.00	0.43	±	0.05	71.50	±	3.18
19	T1	5.33	±	0.01	30.33	±	0.19	0.67	±	0.06	66.00	±	0.01
	T2	4.17	±	0.29	19.50	±	5.48	0.90	±	0.05	68.00	±	1.15

S1 families	Testers	Ear diameter (cm)			No. kernels/row			Grain yield/plot (Kg)			Days to 50% silking		
		Mean	±	SE	Mean	±	SE	Mean	±	SE	Mean	±	SE
	T3	4.67	±	0.01	29.83	±	2.02	0.39	±	0.02	64.00	±	1.73
	T1	4.67	±	0.19	29.83	±	2.02	0.90	±	0.05	73.00	±	4.04
20	T2	5.00	±	0.19	30.67	±	0.77	1.10	±	0.06	66.00	±	0.01
	T3	4.83	±	0.10	33.33	±	1.73	0.81	±	0.05	67.50	±	0.87
	T1	5.33	±	0.19	24.17	±	1.83	0.60	±	0.05	66.00	±	0.01
21	T2	4.83	±	0.10	31.83	±	0.87	0.82	±	0.03	67.50	±	0.87
	T3	4.50	±	0.10	25.17	±	3.18	0.56	±	0.05	67.50	±	0.87
	T1	5.17	±	0.10	26.00	±	0.58	0.63	±	0.03	66.00	±	0.01
22	T2	3.50	±	0.10	09.50	±	0.10	0.29	±	0.03	69.50	±	0.29
	T3	4.50	±	0.10	23.50	±	0.68	0.50	±	0.02	65.50	±	2.60
	T1	4.33	±	0.19	28.00	±	0.58	0.45	±	0.01	68.00	±	1.15
23	T2	4.50	±	0.29	33.17	±	0.68	0.47	±	0.05	70.50	±	2.60
	T3	4.33	±	0.19	21.17	±	2.60	0.26	±	0.02	68.50	±	0.29
	T1	5.00	±	0.19	26.67	±	0.77	0.61	±	0.01	66.00	±	0.01
24	T2	4.50	±	0.29	22.67	±	0.77	0.52	±	0.03	66.00	±	0.01
	T3	4.83	±	0.29	18.17	±	0.29	0.35	±	0.01	68.00	±	0.58
	T1	4.33	±	0.19	33.33	±	1.35	0.85	±	0.05	64.00	±	1.73
25	T2	4.33	±	0.39	26.83	±	4.72	1.13	±	0.03	69.00	±	4.62
	T3	4.50	±	0.48	21.67	±	5.77	0.85	±	0.02	71.50	±	3.18
	T1	5.00	±	0.01	38.83	±	1.44	1.17	±	0.05	61.00	±	0.01
26	T2	4.83	±	0.10	37.67	±	0.39	1.09	±	0.06	61.00	±	0.01
	T3	5.17	±	0.10	32.00	±	0.39	0.88	±	0.04	64.50	±	0.87
	T1	4.67	±	0.19	23.00	±	0.19	0.32	±	0.03	70.50	±	2.60
27	T2	5.00	±	0.19	33.33	±	0.00	1.02	±	0.05	63.50	±	1.44
	T3	4.67	±	0.01	22.83	±	1.06	0.38	±	0.01	68.00	±	0.58
	T1	4.00	±	0.19	24.84	±	2.41	0.59	±	0.06	70.00	±	5.20
28	T2	4.33	±	0.19	33.17	±	1.83	0.68	±	0.03	68.00	±	4.04
	T3	4.17	±	0.29	20.33	±	1.35	0.19	±	0.02	68.00	±	4.04
	T1	5.50	±	0.29	34.17	±	2.22	1.18	±	0.05	65.50	±	2.60
29	T2	5.17	±	0.10	39.33	±	2.89	1.37	±	0.05	61.00	±	0.01
	T3	5.00	±	0.01	32.83	±	0.87	0.66	±	0.02	66.50	±	0.29
	T1	5.33	±	0.01	35.83	±	0.87	1.17	±	0.06	63.50	±	1.44
30	T2	5.17	±	0.10	34.67	±	0.77	0.91	±	0.05	64.00	±	1.73
	T3	4.67	±	0.01	27.83	±	2.21	0.69	±	0.01	66.50	±	0.29
	T1	4.83	±	0.10	26.83	±	0.48	0.91	±	0.02	61.00	±	0.01
31	T2	5.00	±	0.01	34.50	±	0.87	0.81	±	0.01	66.00	±	0.01
	T3	4.33	±	0.01	21.17	±	0.10	0.30	±	0.04	66.50	±	0.29
	T1	4.67	±	0.01	25.83	±	0.29	0.48	±	0.02	67.00	±	0.58
32	T2	5.00	±	0.01	33.33	±	1.15	0.85	±	0.02	61.00	±	0.01
	T3	4.33	±	0.19	22.50	±	1.44	0.43	±	0.05	66.50	±	0.29
	T1	5.00	±	0.01	31.83	±	1.06	0.85	±	0.02	63.50	±	1.44
33	T2	5.00	±	0.01	40.67	±	1.73	1.15	±	0.08	61.00	±	2.89
	T3	5.00	±	0.01	31.67	±	0.00	0.84	±	0.01	61.00	±	0.01
	T1	5.00	±	0.01	28.50	±	0.87	0.90	±	0.02	61.50	±	2.60
34	T2	5.33	±	0.01	34.83	±	1.44	1.14	±	0.01	58.00	±	1.15
	T3	4.33	±	0.19	28.33	±	1.73	0.51	±	0.02	66.00	±	0.01
	T1	5.17	±	0.10	33.83	±	1.44	0.89	±	0.06	63.50	±	1.44
35	T2	4.83	±	0.29	37.33	±	0.58	1.32	±	0.03	63.50	±	1.44
	T3	4.83	±	0.10	21.50	±	2.02	0.30	±	0.03	66.50	±	0.29
	T1	5.17	±	0.10	31.83	±	1.06	0.88	±	0.03	63.50	±	1.44
36	T2	5.17	±	0.10	31.83	±	0.10	0.67	±	0.02	66.00	±	0.01
	T3	4.50	±	0.29	26.17	±	1.06	0.57	±	0.06	71.00	±	2.31

S1 families	Testers	Ear diameter (cm)			No. kernels/row			Grain yield/plot (Kg)			Days to 50% silking		
		Mean	±	SE	Mean	±	SE	Mean	±	SE	Mean	±	SE
37	T1	4.83	±	0.10	29.67	±	1.73	0.76	±	0.04	67.50	±	0.87
	T2	5.00	±	0.19	33.50	±	0.48	0.79	±	0.02	66.00	±	0.01
	T3	4.83	±	0.29	29.67	±	2.12	0.50	±	0.02	67.50	±	0.29
38	T1	5.50	±	0.10	26.33	±	0.96	0.56	±	0.01	66.00	±	0.01
	T2	5.00	±	0.01	30.83	±	0.48	0.73	±	0.03	67.00	±	0.58
	T3	4.33	±	0.58	24.00	±	3.46	0.80	±	0.03	66.50	±	0.29
39	T1	4.50	±	0.10	25.67	±	2.12	0.99	±	0.05	64.00	±	1.73
	T2	4.67	±	0.01	30.33	±	0.39	0.61	±	0.05	66.50	±	0.29
	T3	4.33	±	0.01	25.00	±	0.00	0.32	±	0.01	72.00	±	2.89
40	T1	4.83	±	0.10	35.17	±	2.21	1.17	±	0.05	61.00	±	0.01
	T2	4.67	±	0.01	34.33	±	0.58	0.81	±	0.03	63.50	±	1.44
	T3	4.83	±	0.10	31.33	±	1.73	0.60	±	0.05	66.00	±	0.01
41	T1	4.50	±	0.10	20.17	±	0.68	0.34	±	0.03	66.50	±	0.29
	T2	4.33	±	0.19	26.00	±	1.92	0.33	±	0.01	61.00	±	0.01
	T3	4.00	±	0.19	22.17	±	1.06	0.14	±	0.01	66.50	±	0.29
42	T1	5.17	±	0.10	29.67	±	0.96	0.90	±	0.03	63.50	±	1.44
	T2	5.17	±	0.10	28.50	±	1.06	0.79	±	0.06	67.50	±	0.87
	T3	4.67	±	0.19	24.33	±	1.73	0.61	±	0.05	66.50	±	0.29
43	T1	4.00	±	0.19	22.50	±	0.87	0.37	±	0.02	66.00	±	0.01
	T2	4.50	±	0.10	23.17	±	1.44	0.39	±	0.01	67.50	±	0.87
	T3	4.00	±	0.39	25.17	±	1.64	0.39	±	0.04	67.00	±	0.58
44	T1	5.17	±	0.10	27.67	±	2.31	0.58	±	0.05	66.50	±	0.29
	T2	4.67	±	0.19	26.50	±	1.83	0.46	±	0.04	66.00	±	0.01
	T3	4.17	±	0.29	21.50	±	1.25	0.30	±	0.02	68.00	±	0.58
45	T1	4.67	±	0.01	26.67	±	1.92	0.74	±	0.05	70.50	±	2.60
	T2	4.83	±	0.10	25.00	±	1.92	0.88	±	0.02	70.50	±	2.60
	T3	5.00	±	0.01	29.83	±	0.10	0.69	±	0.03	66.50	±	0.29
46	T1	5.00	±	0.01	29.83	±	1.25	0.86	±	0.04	63.50	±	1.44
	T2	4.83	±	0.29	25.83	±	2.98	0.83	±	0.03	63.50	±	1.44
	T3	4.50	±	0.29	28.00	±	1.54	0.57	±	0.04	68.50	±	0.29
47	T1	5.00	±	0.19	32.67	±	0.19	0.80	±	0.02	63.50	±	1.44
	T2	4.83	±	0.10	34.17	±	0.87	0.65	±	0.06	64.00	±	1.73
	T3	4.83	±	0.29	29.33	±	0.77	0.78	±	0.05	63.50	±	1.44
48	T1	4.17	±	0.29	20.83	±	1.44	0.37	±	0.02	71.00	±	2.31
	T2	4.50	±	0.10	28.17	±	1.83	0.54	±	0.02	67.50	±	0.29
	T3	4.33	±	0.01	23.50	±	1.06	0.22	±	0.01	71.00	±	2.31
49	T1	4.67	±	0.01	30.83	±	0.48	0.53	±	0.02	66.50	±	0.29
	T2	4.50	±	0.29	38.50	±	2.41	0.77	±	0.03	64.00	±	1.73
	T3	4.33	±	0.01	28.50	±	2.98	0.38	±	0.01	69.00	±	0.01
50	T1	5.00	±	0.19	35.84	±	1.83	0.71	±	0.05	66.50	±	0.29
	T2	5.00	±	0.01	30.50	±	1.83	0.55	±	0.06	66.00	±	0.01
	T3	3.67	±	0.01	19.00	±	0.19	0.06	±	0.01	72.00	±	1.73
51	T1	4.67	±	0.19	29.50	±	1.25	0.52	±	0.04	64.00	±	1.73
	T2	4.83	±	0.10	36.67	±	2.89	1.12	±	0.05	63.50	±	1.44
	T3	4.83	±	0.10	31.67	±	0.77	0.51	±	0.02	67.00	±	0.01
52	T1	5.00	±	0.19	28.67	±	0.19	0.57	±	0.01	72.00	±	2.89
	T2	5.33	±	0.01	38.17	±	1.44	1.13	±	0.03	66.50	±	0.29
	T3	5.17	±	0.29	31.17	±	1.06	0.67	±	0.02	68.00	±	0.58
53	T1	5.33	±	0.01	25.00	±	0.58	0.57	±	0.03	66.00	±	0.01
	T2	5.17	±	0.29	24.33	±	1.73	0.74	±	0.02	72.00	±	1.73
	T3	4.83	±	0.10	29.00	±	1.35	0.76	±	0.05	63.50	±	1.44
54	T1	5.00	±	0.19	24.50	±	1.06	0.35	±	0.01	67.50	±	0.29
	T2	4.50	±	0.29	29.17	±	1.64	0.49	±	0.04	69.00	±	0.58
	T3	4.17	±	0.10	19.50	±	1.25	0.22	±	0.01	64.00	±	1.73
55	T1	4.33	±	0.19	18.83	±	0.29	0.23	±	0.01	66.00	±	0.01
	T2	4.33	±	0.39	21.50	±	1.25	0.31	±	0.02	69.00	±	0.01

S1 families	Testers	Ear diameter (cm)			No. kernels/row			Grain yield/plot (Kg)			Days to 50% silking		
		Mean	±	SE	Mean	±	SE	Mean	±	SE	Mean	±	SE
	T3	3.33	±	0.01	23.50	±	0.58	0.40	±	0.05	68.50	±	0.87
56	T1	4.33	±	0.19	20.17	±	0.87	0.21	±	0.02	72.00	±	2.89
	T2	4.33	±	0.01	25.33	±	0.00	0.39	±	0.02	33.00	±	9.05
	T3	4.00	±	0.01	08.33	±	1.35	0.03	±	0.01	72.00	±	1.73
57	T1	5.33	±	0.01	31.67	±	0.00	0.54	±	0.03	68.50	±	0.87
	T2	3.83	±	0.29	18.83	±	1.83	0.31	±	0.02	71.00	±	2.31
	T3	4.33	±	0.01	24.83	±	2.02	0.31	±	0.02	71.50	±	2.02
58	T1	5.17	±	0.10	28.00	±	1.15	0.92	±	0.02	66.50	±	0.29
	T2	5.00	±	0.01	31.67	±	1.15	0.90	±	0.05	63.50	±	0.44
	T3	4.50	±	0.10	21.00	±	0.00	0.49	±	0.05	64.00	±	1.73
59	T1	4.83	±	0.10	27.50	±	0.29	0.44	±	0.03	64.50	±	2.02
	T2	2.67	±	0.01	26.59	±	0.53	0.48	±	0.05	71.00	±	2.31
	T3	4.00	±	0.01	25.50	±	1.63	0.43	±	0.04	68.00	±	0.58
60	T1	5.00	±	0.01	33.67	±	1.73	0.94	±	0.02	65.00	±	2.31
	T2	5.00	±	0.01	39.00	±	1.15	0.83	±	0.03	64.00	±	1.73
	T3	4.67	±	0.01	27.33	±	0.77	0.38	±	0.05	67.00	±	0.01
61	T1	4.17	±	0.48	26.50	±	1.06	0.43	±	0.02	67.00	±	0.58
	T2	4.17	±	0.10	25.00	±	0.96	0.36	±	0.03	68.00	±	0.01
	T3	3.67	±	0.01	10.67	±	0.00	0.07	±	0.01	73.50	±	2.02
62	T1	4.67	±	0.19	20.17	±	0.29	0.32	±	0.02	69.00	±	0.01
	T2	4.33	±	0.19	33.67	±	0.77	1.14	±	0.05	67.50	±	0.87
	T3	4.33	±	0.01	35.67	±	2.89	0.60	±	0.03	67.50	±	0.87
63	T1	4.50	±	0.29	25.84	±	1.83	0.26	±	0.02	73.00	±	2.31
	T2	3.83	±	0.29	23.50	±	1.25	0.24	±	0.02	73.50	±	2.02
	T3	3.83	±	0.29	24.00	±	1.15	0.30	±	0.02	72.00	±	1.73
64	T1	4.00	±	0.01	14.00	±	2.31	0.07	±	0.01	75.00	±	0.01
	T2	4.17	±	0.10	21.83	±	1.63	0.29	±	0.05	65.50	±	2.60
	T3	4.50	±	0.29	31.83	±	2.02	0.38	±	0.05	68.50	±	0.87
65	T1	4.00	±	0.19	19.33	±	0.77	0.24	±	0.01	72.00	±	1.73
	T2	4.83	±	0.10	30.50	±	1.06	0.66	±	0.05	66.00	±	0.58
	T3	4.50	±	0.10	23.83	±	2.02	0.40	±	0.03	69.00	±	0.58
66	T1	4.00	±	0.19	21.00	±	1.54	0.26	±	0.02	69.50	±	0.29
	T2	4.50	±	0.10	36.33	±	0.00	0.39	±	0.03	68.00	±	4.04
	T3	3.67	±	0.01	18.33	±	0.00	0.19	±	0.01	75.00	±	0.01
67	T1	4.83	±	0.10	29.00	±	3.85	0.41	±	0.03	65.50	±	2.60
	T2	4.50	±	0.10	28.50	±	0.29	0.46	±	0.01	69.50	±	0.29
	T3	4.33	±	0.01	21.33	±	0.00	0.20	±	0.02	73.00	±	2.31
68	T1	4.83	±	0.10	25.67	±	3.85	0.54	±	0.03	67.50	±	0.87
	T2	4.67	±	0.01	24.50	±	0.29	0.37	±	0.02	71.00	±	2.31
	T3	4.67	±	0.19	31.83	±	0.87	0.39	±	0.02	67.00	±	0.01
69	T1	4.83	±	0.29	23.83	±	2.21	0.40	±	0.02	67.50	±	0.87
	T2	5.00	±	0.01	37.50	±	2.02	0.89	±	0.03	66.00	±	0.01
	T3	4.83	±	0.29	32.50	±	2.41	0.78	±	0.06	64.00	±	1.73
70	T1	5.17	±	0.29	25.83	±	0.87	0.89	±	0.04	66.50	±	0.29
	T2	5.17	±	0.10	39.33	±	0.96	1.11	±	0.06	61.00	±	0.01
	T3	4.67	±	0.19	28.00	±	1.15	0.62	±	0.05	64.00	±	1.73
71	T1	4.50	±	0.29	38.17	±	1.44	0.91	±	0.03	67.00	±	0.58
	T2	4.67	±	0.01	35.00	±	1.35	0.65	±	0.03	67.00	±	0.01
	T3	4.17	±	0.10	21.00	±	0.58	0.13	±	0.01	68.00	±	0.58
72	T1	4.67	±	0.01	32.50	±	3.37	0.58	±	0.05	64.50	±	2.02
	T2	4.83	±	0.10	36.83	±	0.68	1.06	±	0.03	61.00	±	0.01
	T3	4.67	±	0.01	30.67	±	1.54	0.96	±	0.03	65.50	±	2.60
73	T1	4.67	±	0.19	34.00	±	1.15	0.77	±	0.05	61.00	±	0.01
	T2	4.33	±	0.19	31.05	±	3.05	0.98	±	0.05	61.00	±	0.01

S1 families	Testers	Ear diameter (cm)			No. kernels/row			Grain yield/plot (Kg)			Days to 50% silking		
		Mean	±	SE	Mean	±	SE	Mean	±	SE	Mean	±	SE
	T3	4.67	±	0.19	30.83	±	0.48	0.63	±	0.05	70.50	±	2.60
	T1	4.83	±	0.10	32.33	±	0.77	1.02	±	0.02	63.50	±	1.44
74	T2	4.83	±	0.10	32.83	±	2.79	1.29	±	0.02	59.00	±	1.15
	T3	4.83	±	0.10	30.17	±	2.79	0.80	±	0.05	64.00	±	1.73
	T1	5.33	±	0.01	30.83	±	1.06	0.73	±	0.02	64.00	±	1.73
75	T2	4.50	±	0.10	27.17	±	2.60	0.42	±	0.01	68.00	±	0.58
	T3	4.33	±	0.19	25.34	±	1.54	0.42	±	0.06	71.00	±	2.31
	T1	4.33	±	0.19	34.33	±	1.15	0.70	±	0.04	68.00	±	1.15
76	T2	4.33	±	0.19	29.50	±	2.41	0.71	±	0.04	71.50	±	3.18
	T3	4.67	±	0.01	28.00	±	2.70	0.45	±	0.05	70.50	±	2.60
	T1	4.67	±	0.01	35.00	±	2.12	1.02	±	0.03	63.00	±	1.15
77	T2	4.83	±	0.10	28.50	±	2.21	0.55	±	0.01	68.50	±	0.87
	T3	4.17	±	0.29	16.00	±	2.50	0.17	±	0.03	68.00	±	0.58
	T1	4.67	±	0.01	21.33	±	0.58	0.46	±	0.02	64.00	±	1.73
78	T2	4.67	±	0.01	29.67	±	2.50	0.72	±	0.03	70.50	±	2.60
	T3	5.17	±	0.10	30.00	±	1.54	0.64	±	0.05	63.50	±	1.44
	T1	4.50	±	0.10	21.00	±	0.96	0.23	±	0.01	68.50	±	0.87
79	T2	4.17	±	0.10	33.33	±	0.39	0.77	±	0.05	63.50	±	1.44
	T3	4.33	±	0.01	26.50	±	1.83	0.28	±	0.01	72.00	±	1.73
	T1	4.50	±	0.10	28.00	±	0.00	0.52	±	0.03	66.50	±	0.29
80	T2	4.33	±	0.19	35.83	±	1.06	0.59	±	0.03	64.50	±	2.02
	T3	4.67	±	0.01	32.67	±	1.15	0.54	±	0.02	65.00	±	2.31
	T1	4.50	±	0.29	22.50	±	1.25	0.21	±	0.02	67.50	±	0.87
81	T2	4.33	±	0.01	22.17	±	1.25	0.26	±	0.02	68.50	±	0.87
	T3	3.67	±	0.19	21.00	±	0.96	0.15	±	0.02	68.00	±	1.15
Average		04.61	±	0.14	27.76	±	1.36	0.61	±	0.03	66.67	±	1.29
Max.		5.50	±	0.17	40.67	±	1.00	1.37	±	0.03	75.00	±	.006
Min.		2.67	±	0.01	8.33	±	0.78	0.03	±	0.02	33.00	±	0.99
Rev. LSD		0.52									5.89		

Superior thirty-four S1 top-crosses surpassed their general mean of 243 S1 top-crosses by more than 50% comparing to its value with range of 50.82 to 124.59 with an average of 82.59% for grain yield/plot. Those superior S1 top-crosses were divided into three groups as a- sixteen S1 top-crosses were derived from T1 and exceeded the general mean in range of 50.52 to 116.39 with an average of 78.07%; b- seventeen S1 top-crosses were derived from T2 and surpassed the general mean in range of 60.66 to 124.59 with an average of 88.33%; and c- one cross was derived from T3 and exceeded the general mean by 57.38% for grain yield/plot. It is clear result that the average (88.33%) of S1 top-crosses derived from the T2 was in the first order followed by S1 top-crosses (78.07%) derived from T1. T3 came in the last order. The S1 top-crosses related to T1 in ranking were L11T1 (116.39); L6T1 (100.00); L29T1 (93.44); L18T1 (91.80); L26T1 (91.80); L30T1 (91.80); L40T1 (91.80); L5T1 (75.41); L14T1 (75.41); L17T1 (67.21); L74T1 (67.21); L77T1 (67.21); L39T1 (62.30); L60T1 (54.10); L8T1 (52.46) and L58T1 (50.82%). Furthermore, the S1 top-crosses produced from T2 in ranking were L29T2 (124.59); L35T2 (116.39); L17T2 (113.11); L74T2 (111.48); L33T2 (88.52); L34T2 (86.89); L62T2 (86.89); L25T2 (85.25); L52T2 (85.25); L51T2 (83.61); L18T2 (81.97); L70T2 (81.97); L20T2 (80.33); L14T2 (73.77); L72T2 (73.77); L27T2 (67.21) and L73T2 (60.66%). The unique S1 top cross expressed from T3 in this group was L72T3 (57.38%) Same rank could be found over all the S1 top-crosses for grain yield/plot, T2, T1 and T3 exerted 0.72, 0.64 and 0.46

which surpassed the general mean of S1 top-crosses by 18.79, 5.01 and -23.80%, respectively (Table 6). These results indicated that the T2 could be used as tester to mate the maize under New Valley climate conditions.

The mean of S1 top-crosses were in different response according to the involved S1 families, which ranged from 0.21 (L56) to 1.07 (L29) with an average of 0.61 over the three testers for grain yield/plot. The best ten S1 families for grain yield/plot in ranking, which enhanced their S1 top-crosses over the three testers were L29 (75.41); L26 (72.13); L17 (70.49); L74 (70.49); L5 (59.02); L33 (55.74); L20 (54.10); L25 (54.10); L30 (50.82) and L18 (47.54%) (review numbers from tables5 and 7) comparing to the general mean of S1 top-crosses.

Moreover, the exerted results for S1 top-crosses expressed their different genetic make-up and explained the significant mean square of line*tester (L*T interaction) as estimated in Table 2. The current results are in line with Al-Hosary and Elgammaal (2013); Dinesh *et al*., (2016); Monsif *et al*., (2018); Sayed *et al*., (2020); Fayyad and Hammadi (2021) and Ganapati Mukri *et al*., (2022), who observed significant genetic diversity due to lines, testers and their crosses.

The S1 top-crosses for No. of kernels/row revealed that the T2, T1 and T3 possessed 30.14, 27.41 and 25.72 which exceeded the general mean of S1 top-crosses by 8.57, -1.26 and -7.34%, respectively (Table 6). These results indicated that the T2 can be used as tester for No. of kernels/row in maize mating. Moreover, the S1 top-crosses were varied from 17.94 to 36.17 with an average of 27.76 depending on the S1 families and over the three testers for each line. In this context, the average of S1 top-crosses according to the best ten S1 families for No. of kernels/row in ranking, over the three testers were L26 (30.30); L29 (27.67); L33 (25.07); L40 (21.07); L60 (20.06); L72 (20.06); L30 (18.08); L52 (17.69); L49 (17.47) and L51 (17.47%) (review numbers from tables 6 and 7) comparing to the general mean of S1 top-crosses. It is remarkable data that the S1 families i.e., L26, L29, L30 and L33 shared both of grain yield/plot and no. of kernels/row (Tables 6 and7)

Table 6. Average of S1 top-crosses depending on involved testers performance and its increasing percentage over the general mean.

Tester	Ear diameter, cm		Number of kernels/row		Grain yield/plot, kg		Days to 50% silking	
	Mean	Incr.%	Mean	Incr.%	Mean	Incr.%	Mean	Incr.%
T1	4.73	2.61	27.41	-1.26	0.64	5.01	66.56	-0.16
T2	4.63	0.37	30.14	8.57	0.72	18.79	65.70	-1.46
T3	4.46	-3.28	25.72	-7.34	0.46	-23.80	67.73	1.60
Average	4.61		27.76		0.61		66.66	

Incr.%: Increase percentage over the general mean of S1 top-crosses.

Table 7. Average of S1 top-crosses depending on involved S1 families performance and its increasing percentage over the general mean

S1 line	Ear diameter, cm		Number of kernels/row		Grain yield/plot, kg		Days to 50% silking	
	Mean	Incr.%	Mean	Incr.%	Mean	Incr.%	Mean	Incr.%
1	3.83	-16.76	22.34	-19.53	0.24	-61.06	68.17	2.25
2	4.16	-9.60	20.56	-25.94	0.27	-55.02	67.67	1.50
3	4.55	-1.13	24.22	-12.73	0.30	-51.18	66.67	0.00

S1 line	Ear diameter, cm		Number of kernels/row		Grain yield/plot, kg		Days to 50% silking	
	Mean	Incr.%	Mean	Incr.%	Mean	Incr.%	Mean	Incr.%
4	4.84	5.02	28.67	3.28	0.64	5.32	68.00	2.00
5	4.72	2.49	28.72	3.48	0.97	59.07	64.17	-3.75
6	4.89	6.11	32.28	16.29	0.83	36.58	65.33	-2.00
7	4.11	-10.76	25.17	-9.33	0.29	-52.28	68.17	2.25
8	4.72	2.56	30.50	9.88	0.73	20.67	66.33	-0.50
9	4.55	-1.13	29.89	7.68	0.60	-1.27	66.83	0.25
10	4.39	-4.75	29.34	5.69	0.57	-5.65	68.67	3.00
11	4.78	3.72	27.45	-1.12	0.59	-2.36	69.83	4.75
12	4.67	1.33	24.17	-12.92	0.49	-18.82	67.67	1.50
13	4.72	2.56	26.72	-3.72	0.50	-18.27	67.83	1.75
14	4.83	4.88	26.44	-4.73	0.84	38.78	63.50	-4.75
15	4.39	-4.68	26.39	-4.93	0.59	-2.36	66.83	0.25
16	4.33	-5.91	25.89	-6.73	0.46	-24.85	67.17	0.75
17	4.83	4.95	30.55	10.07	1.04	70.59	64.33	-3.50
18	4.39	-4.68	28.00	0.87	0.90	48.65	68.50	2.75
19	4.72	2.56	26.55	-4.34	0.65	7.51	66.00	-1.00
20	4.83	4.95	31.28	12.68	0.94	54.13	68.83	3.25
21	4.89	6.11	27.06	-2.52	0.66	8.61	67.00	0.50
22	4.39	-4.68	19.67	-29.15	0.47	-22.11	67.00	0.50
23	4.39	-4.75	27.45	-1.12	0.39	-35.27	69.00	3.50
24	4.78	3.72	22.50	-18.93	0.49	-18.82	66.67	0.00
25	4.39	-4.75	27.28	-1.73	0.94	55.23	68.17	2.25
26	5.00	8.57	36.17	30.30	1.05	72.24	62.17	-6.75
27	4.78	3.79	26.39	-4.94	0.57	-5.65	67.33	1.00
28	4.17	-9.53	26.11	-5.92	0.49	-19.92	68.67	3.00
29	5.22	13.42	35.44	27.69	1.07	76.08	64.33	-3.50
30	5.06	9.80	32.78	18.08	0.92	51.94	64.67	-3.00
31	4.72	2.49	27.50	-0.93	0.67	10.80	64.50	-3.25
32	4.67	1.33	27.22	-1.94	0.59	-3.46	64.83	-2.75
33	5.00	8.57	34.72	25.10	0.95	55.78	61.83	-7.25
34	4.89	6.11	30.55	10.07	0.85	39.87	61.83	-7.25
35	4.94	7.34	30.89	11.27	0.84	37.68	64.50	-3.25
36	4.95	7.41	29.94	7.88	0.71	16.29	66.83	0.25
37	4.89	6.11	30.95	11.49	0.68	12.45	67.00	0.50
38	4.94	7.34	27.05	-2.54	0.70	14.64	66.50	-0.25
39	4.50	-2.29	27.00	-2.73	0.64	5.32	67.50	1.25
40	4.78	3.72	33.61	21.09	0.86	41.52	63.50	-4.75
41	4.28	-7.14	22.78	-17.93	0.27	-55.57	64.67	-3.00
42	5.00	8.64	27.50	-0.93	0.77	26.16	65.83	-1.25
43	4.17	-9.53	23.61	-14.93	0.38	-36.92	66.83	0.25
44	4.67	1.40	25.22	-9.13	0.45	-26.50	66.83	0.25
45	4.83	4.95	27.17	-2.13	0.77	26.71	69.17	3.75
46	4.78	3.72	27.89	0.47	0.75	23.97	65.17	-2.25
47	4.89	6.11	32.06	15.49	0.74	22.32	63.67	-4.50
48	4.33	-5.91	24.17	-12.94	0.38	-38.02	69.83	4.75
49	4.50	-2.29	33.00	17.00	0.56	-7.85	66.50	-0.25
50	4.56	-1.06	28.45	2.48	0.44	-27.60	68.17	2.25
51	4.78	3.72	32.61	17.49	0.72	17.93	64.83	-2.75
52	5.17	12.19	32.67	17.70	0.79	30.00	68.83	3.25
53	5.11	10.96	26.11	-5.93	0.69	13.54	67.17	0.75
54	4.56	-1.06	24.39	-12.13	0.35	-41.86	66.83	0.25
55	4.00	-13.22	21.28	-23.35	0.31	-48.44	67.83	1.75
56	4.22	-8.37	17.94	-35.36	0.21	-65.44	59.00	-11.50
57	4.50	-2.36	25.11	-9.54	0.39	-36.37	70.33	5.50

S1 line	Ear diameter, cm		Number of kernels/row		Grain yield/plot, kg		Days to 50% silking	
	Mean	Incr.%	Mean	Incr.%	Mean	Incr.%	Mean	Incr.%
58	4.89	6.18	26.89	-3.12	0.77	26.71	64.67	-3.00
59	3.83	-16.76	26.53	-4.42	0.45	-25.95	67.83	1.75
60	4.89	6.18	33.33	20.09	0.72	17.93	65.33	-2.00
61	4.00	-13.07	20.72	-25.34	0.29	-52.83	69.50	4.25
62	4.44	-3.52	29.84	7.49	0.69	13.00	68.00	2.00
63	4.05	-11.99	24.45	-11.93	0.27	-56.12	72.83	9.25
64	4.22	-8.30	22.55	-18.75	0.25	-59.41	69.67	4.50
65	4.44	-3.52	24.55	-11.54	0.43	-28.69	69.00	3.50
66	4.06	-11.91	25.22	-9.14	0.28	-53.92	70.83	6.25
67	4.55	-1.13	26.28	-5.33	0.36	-41.31	69.33	4.00
68	4.72	2.56	27.33	-1.53	0.43	-28.69	68.50	2.75
69	4.89	6.11	31.28	12.68	0.69	13.54	65.83	-1.25
70	5.00	8.64	31.05	11.87	0.87	43.71	63.83	-4.25
71	4.45	-3.45	31.39	13.09	0.56	-7.30	67.33	1.00
72	4.72	2.56	33.33	20.09	0.87	42.62	63.67	-4.50
73	4.56	-1.06	31.96	15.14	0.79	30.55	64.17	-3.75
74	4.83	4.88	31.78	14.48	1.04	70.59	62.17	-6.75
75	4.72	2.49	27.78	0.08	0.52	-13.88	67.67	1.50
76	4.44	-3.52	30.61	10.28	0.62	2.02	70.00	5.00
77	4.56	-1.06	26.50	-4.53	0.58	-4.56	66.50	-0.25
78	4.84	5.02	27.00	-2.73	0.61	-0.17	66.00	-1.00
79	4.33	-5.91	26.94	-2.93	0.43	-29.79	68.00	2.00
80	4.50	-2.29	32.17	15.89	0.55	-9.49	65.33	-2.00
81	4.17	-9.53	21.89	-21.14	0.21	-65.99	68.00	2.00
Average	4.61		27.76		0.61		66.66	
Max.	5.22		36.17		1.07		72.83	
Min.	3.83		17.94		0.21		59.00	

Incr.%: Increase percentage over the general mean of S1 top-crosses.

Furthermore, the current S1 top-crosses for ear diameter presented that the T1, T2 and T3 exerted 4.73, 4.63 and 4.46 which surpassed the general mean of S1 top-crosses by 2.61, 0.37 and -3.28%, respectively, indicating that the T1 can be used as tester for ear diameter in maize (Table 6). Moreover, the S1 top-crosses were ranged from 3.83 to 5.22 with an average of 4.61 cm depending on the S1 families and over the three testers for each line. In this view, the average of S1 top-crosses correlating to the best ten S1 families for ear diameter over the three testers were L29 (13.42); L52 (12.19); L53 (10.96); L30 (9.80); L42 (8.64); L26 (8.57); L33 (8.57); L70 (8.64); L36 (7.41) and L35 (7.34%) comparing to the general mean of S1 top-crosses. It is clear that the S1 families i.e., L26, L29, L30 and L33 included with grain yield/plot, no. of kernels/row and ear diameter, as well as the L52 shared both of no. of kernels/row and ear diameter (Table 7).

Days to 50% silking for the S1 top-crosses resembled to T3, T1 and T2 accounted 67.73, 66.56 and 65.70, which were varied from the general mean of S1 top-crosses by 1.60, -0.16 and -1.46%, respectively, referring that T3 may a good tester for silking appearing (Table 6). The values of S1 top-crosses were varied from 59.00 to 72.83 with an average of 66.66 day depending on each S1 line over the three testers. Meanwhile, the average of S1 top-crosses for earliness from the best ten S1 families of days to 50% silking over the three testers were L56 (-11.50); L33 (-7.25); L34 (-7.25); L26 (-6.75); L74 (-6.75); L14 (-4.75); L40 (-4.75); L47

(-4.50); L72 (-4.50) and L70 (-4.25%) comparing to the general mean of S1 top-crosses. It is clearly observations that the S1 families i.e., L26 and L33 connected the four traits i.e., grain yield/plot, no. of kernels/row, ear diameter and days to 50% silking. L40 and L74 represented in two traits i.e., no. of kernels/row and days to 50% silking. L34, L70 and L72 correlated with ear diameter and no. of kernels/row, respectively (Table 7).

The mentioned results for S1 top-crosses possessed different genetic make-up and explained the significant mean square of line*tester analysis for current S1 top-crosses, their parents i.e., lines and testers as well as their interaction for studied traits. The presented results are accordance with Dinesh *et al.*, (2016), Monsif *et al.*, (2018), Sayed *et al.*, (2020) and Ganapati Mukri *et al.*, (2022), who found significant genetic differences due to lines, testers and their crosses for grain yield and its attributes. Moreover, Fayyad and Hammadi (2021) mated superior inbred lines of maize to produce superior individual crosses for grain yield and its components. Barzgari *et al.*, (2022) found significant differences for line, tester and line* tester analysis for grain yield and its attributes using line × tester analysis.

III- General combining ability (GCA)

Data of general combining ability of testers and S1 families for studied traits are presented in Table 8. The values of GCA effects ranged from -0.403** (L81) to 0.460** (L29) for grain yield/plot. The estimates of GCA effects revealed that out of current 81 S1 families of line × tester crosses, twenty-two S1 families possessed positive and significant or highly significant GCA effects. The best ten S1 families for GCA in ranking were L29 (0.460**), L26 (0.441**), L74 (0.428**), L17 (0.427**), L5 (0.356**), L33 (0.340**), L25 (0.334**), L20 (0.330**), L30 (0.318) and L18 (0.296**). Concerning the testers, T2 was the best combiner, which possessed positive and highly significant GCA effect of 0.114**, followed by T1 (0.030*). Otherwise, T3 was the poorest with undesirable GCA effect of -0.144** for grain yield/plot.

The estimates of GCA effects varied from -9.812** (L56) to 8.409** (L26) for number of kernels/row. The GCA effects exerted that out of current 81 S1 families, twenty-eight S1 families recorded positive and significant or highly significant GCA effects. The best ten S1 families of GCA in rank were L26 (8.409**), L29 (7.687**), L33 (6.965**), L40 (5.854**), L72 (5.577**), L60 (5.576**), L30 (5.020**), L52 (4.910**), L51 (4.854) and L6 (4.521**). It is obvious that the L26, L29, L30 and L33 shared their great GCA in both grain yield/plot and number of kernels/row. Concerning the testers, T2 was the great combiner, which gave positive and highly significant GCA effect of 2.382**. It is remarkable notes that the T2 recorded good combiner for grain yield/plot and number of kernels/row. T3 had inversely undesirable GCA effect of -2.035** for number of kernels/row.

The estimates of GCA effects extended from -0.772** (L1 & L59) to 0.617** (L29) for ear diameter. The GCA effects of 81 S1 families, exhibited twenty-six S1 families with positive and significant or highly significant GCA effects. The

top ten S1 families of GCA in order were L29 (0.617**), L52 (0.561**), L53 (0.505**), L30 (0.450**), L26 (0.394**), L33 (0.394**), L42 (0.394**), L70 (0.394**), L35 (0.339**) and both of L36 and L38 (0.339**). It is clearly findings that the L26, L29, L30 and L33 participated their significant positive GCA for each of grain yield/plot, number of kernels/row and ear dimeter. Moreover, Line 52 shared as good combiners for both number of kernels/row and ear dimeter. Concerning the testers, T1 was the great combiner, which presented positive and highly significant GCA effect of 0.125**. T3 conversely had GCA effect of -0.147** for ear diameter.

The GCA effects respected from -7.665** (L56) to 6.169** (L63) for days to 50% silking. The obtained GCA effects of 81 S1 families, possessed sixteen S1 families with positive significant or highly significant GCA effects. Desirable combiners for earliness, the earlier ten S1 families of GCA in ranking were L56 (-7.665**), L33 (-4.831**), L34 (-4.831**), L26 (-4.498**), L74 (-4.498**), L14 (-3.165**), L40 (-3.165**), L47 (-2.998**), L72 (-2.998**) and L70 (-2.831**) whereas had negative and highly significant GCA effects for 50% silking. Clearly findings that the lines L26 and L33 had significant positive GCA effects for grain yield/plot, number of kernels/row and ear dimeter, but negative effects to days to 50% silking. Moreover, L34 was included the powerful GCA for days to 50% silking. L40 and L72 inherited their positive GCA for number of kernels/row and negative effect for days to 50% silking. T2 is recorded to be desirable combiner for earliness with negative and highly significant GCA of -0.967** for days to 50% silking.

In general view for testers, T2 was good and significant combiner in positive trend for grain yield/plot and number of kernels/row and vice versa in negative effect of desirable earliness for days to 50% silking. Furthermore, T1 was optimum combiner for ear dimeter in current line × tester analysis.

IV- Specific combining ability (SCA)

The estimates of specific combining ability (SCA) of S1 top-crosses for studied traits are presented in Table 8. The values of SCA effects ranged from -0.464** (L11T2) to 0.697** (L11T1) for grain yield/plot. The estimates of SCA effects expressed that out of 243 S1 top-crosses produced from line × tester crosses, fourteen S1 top-crosses possessed positive and significant or highly significant SCA effects. The best ten S1 top-crosses for SCA in ranking were L11T1 (0.697**), L77T1 (0.405**), L10T3 (0.390**), L35T2 (0.370**), L6T1 (0.357**), L2T3 (0.350**), L62T2 (0.337**), L27T2 (0.329**), L39T1 (0.318**) and L71T1 (0.317**). It is clearly results that T1 involved in half of these top top-crosses, followed by T2, indicating to their good specific combiners with shared S1 families to inherit their genetic make-up into the current crosses. This finding is in accordance with the GCA effects of T1 and T2, but not for S1 families, because the best ten S1 families for GCA did not involve in the top ten crosses for grain yield/plot.

The values of SCA effects varied from -12.548** (L22T2) to 11.312** (L64T3) for number of kernels/row. The estimates of SCA effects exhibited that

out of 243 S1 top-crosses, forty-six S1 top-crosses had positive and significant or highly significant SCA effects. The top ten S1 top-crosses for SCA in ordering were L64T3 (11.312**), L7T3 (9.536**), L10T3 (9.036**), L77T1 (8.847**), L66T2 (8.729**), L62T3 (7.869**), L50T1 (7.737**), L14T1 (7.736**), L71T1 (7.126**) and L11T1 (7.071**). It is remarkable results that T1 combined in half of these best top-crosses, followed by T3, revealing to their great specific combiners with involved S1 families to inherit their genetic performance into the correlated crosses for number of kernels/row. The last result was inversely to the poor GCA for T1. Moreover, the best ten S1 families for GCA did not participate in the top ten S1 top-crosses for number of kernels/row. Consequently, the obtained best crosses depending on the specific combining between lines and testers for number of kernels/row. The S1 top crosses i.e. L10T3, L11T1, L77T1 and L71T1 were participated in the best S1 top-crosses for both grain yield/plot and number of kernels/row.

The obtained data of SCA effects ordered from -0.791** (L16T1) to 0.875** (L59T1) for ear diameter. The values of SCA effects exerted that out of 243 S1 top-crosses, sixteen S1 top-crosses presented positive and significant or highly significant SCA effects. The great ten S1 top-crosses for SCA in laying were L59T1 (0.875**), L57T1 (0.709**), L22T1 (0.653**), L16T2 (0.645**), L10T3 (0.591**), L75T1 (0.486**), L78T3 (0.480**), L38T1 (0.431**), and each of L5T3, L9T3 and L64T3 (0.425**). It is monitored results that each of T1 and T3 shared in half of these best top-crosses, expressing to their good specific combiners with involved S1 families to inherit their genetic effects into the matched crosses for ear diameter. These results were in line with GCA effects of T1, but inversely for T3. Only L38 out of the best ten S1 families for GCA participate in one top S1 top-cross (L38T1) for ear diameter. Accordingly, the best crosses depend on the specific combining between lines and testers for ear diameter. Only, the S1 top cross of L10T3 was participated in the top S1 top-crosses for grain yield/plot, number of kernels/row and ear diameter.

The SCA effects varied from -25.033** (L56T2) to 13.103** (L56T1) for days to 50% silking. Among 243 S1 top-crosses, nine S1 top-crosses possessed negative and significant or highly significant SCA effects. The earlier nine S1 top-crosses for SCA in arranging were L56T2 (-25.033**), L10T2 (-5.200**), L53T3 (-4.737**), L4T1 (-4.397**), L25T1 (-4.064**), L14T3 (-3.930*), L54T3 (-3.903**), L15T3 (-3.903**), L45T3 (-3.737**) and L67T1 (-3.730**). The results exhibited that T3 (5) and T1 (3) were involved in an eighty percent of the earlier ten top-crosses, revealing to their good specific combiners with involved S1 families to inherit their genetic make-up for earliness into the respected crosses for days to 50% silking. This result was inversely to the GCA effect for testers, were T2 was the unique tester for significant earliness with GCA effect of -0.967**. Meanwhile, L14 and L56 out of the earliest ten S1 families for GCA effects were involved in L14T3 and L56T2 crosses for days to 5% silking, respectively. Therefore, the earliness S1 top-crosses depending on the specific combining between lines and testers.

Similar results of GCA and SCA effects as additive and non-additive gene effects which played an important role in the inheritance for different traits of maize were reported by Chen *et al.*, (2015), Dinesh *et al.*, (2016), Monsif *et al.*, (2018), Ilyas et al., (2019), El-Hefny et al., (2020), Mukhlif *et al.*, (2020), Sayed *et al.*, (2020), Abdulazeez *et al.*, (2021), ALdulaimy and Hammadi (2021), Ibrahim *et al.*, (2021), Kamara *et al.*, (2021), Barzgari *et al.*, (2022), Belay (2022), Ganapati Mukri *et al.*, (2022), Sheikh Abdulla *et al.*, (2022), and Zhang *et al.*, (2022).

Table 8. General (GCA) and Specific (SCA) combining abilities of parents and crosses for studied traits

Lines & Testers	Ear diameter (cm)				Number of kernels/row			
	GCA	SCA			GCA	SCA		
		T1	T2	T3		T1	T2	T3
1	-0.772**	-0.458*	0.145	0.313	-5.421**	-5.982**	3.782*	2.201
2	-0.439**	-0.458*	0.145	0.313	-7.201**	-3.873*	0.394	3.479*
3	-0.05	0.153	-0.078	-0.075	-3.534**	-2.375	0.23	2.146
4	0.228*	0.209	-0.189	-0.02	0.91	1.681	2.951	-4.632**
5	0.117	-0.514**	0.089	0.425*	0.966	-1.54	-2.105	3.646*
6	0.283*	0.32	-0.078	-0.242	4.521**	4.569**	0.506	-5.075**
7	-0.495**	-0.569**	0.2	0.369	-2.59**	-9.32**	-0.216	9.536**
8	0.117	-0.014	-0.078	0.091	2.743**	2.181	-3.216	1.035
9	-0.05	-0.18	-0.244	0.425*	2.131*	-5.041**	1.729	3.312*
10	-0.217	-0.68**	0.089	0.591**	1.577	-9.82**	0.785	9.036**
11	0.172	0.431*	-0.466*	0.036	-0.312	7.071**	-7.161**	0.09
12	0.061	-0.125	0.145	-0.02	-3.59**	-4.153*	-0.882	5.035**
13	0.117	0.32	0.256	-0.575**	-1.035	3.959*	-1.937	-2.022
14	0.228*	0.375	-0.022	-0.353	-1.313	7.736**	-0.66	-7.076**
15	-0.217	0.153	-0.411*	0.258	-1.368	0.125	-2.938	2.813
16	-0.272*	-0.791**	0.645**	0.147	-1.869	-2.874	1.894	0.98
17	0.228*	0.042	0.145	-0.187	2.798**	0.792	2.896	-3.688*
18	-0.217	0.32	0.256	-0.575**	0.243	0.181	1.118	-1.298
19	0.117	0.486*	-0.578**	0.091	-1.202	4.126*	-9.437**	5.312**
20	0.228*	-0.291	0.145	0.147	3.519**	-1.097	-2.993	4.091*
21	0.283*	0.32	-0.078	-0.242	-0.702	-2.541	2.394	0.147
22	-0.217	0.653**	-0.911**	0.258	-8.091**	6.681**	-12.548**	5.867**
23	-0.217	-0.18	0.089	0.091	-0.313	0.903	3.34*	-4.243*
24	0.172	0.097	-0.3	0.202	-5.258**	4.515**	-2.217	-2.298
25	-0.217	-0.18	-0.078	0.258	-0.479	6.403**	-2.827	-3.576*
26	0.394**	-0.125	-0.189	0.313	8.409**	3.013	-0.882	-2.131
27	0.172	-0.236	0.2	0.036	-1.368	-3.042	4.562**	-1.521
28	-0.439**	-0.291	0.145	0.147	-1.645	-0.929	4.673**	-3.743*
29	0.617**	0.153	-0.078	-0.075	7.687**	-0.932	1.507	-0.576
30	0.45**	0.153	0.089	-0.242	5.02**	3.403*	-0.495	-2.909
31	0.117	-0.014	0.256	-0.242	-0.257	-0.319	4.618**	-4.298**
32	0.061	-0.125	0.311	-0.187	-0.535	-1.042	3.729*	-2.687
33	0.394**	-0.125	-0.022	0.147	6.965**	-2.542	3.562*	-1.021
34	0.283*	-0.014	0.422*	-0.409*	2.798**	-1.708	1.896	-0.188
35	0.339**	0.097	-0.133	0.036	3.132**	3.292*	4.062*	-7.354**
36	0.339**	0.097	0.2	-0.298	2.187*	2.237	-0.493	-1.744
37	0.283*	-0.18	0.089	0.091	3.188**	-0.929	0.173	0.757
38	0.339**	0.431*	0.034	-0.464*	-0.701	-0.375	1.395	-1.021
39	-0.106	-0.125	0.145	-0.02	-0.757	-0.986	0.951	0.035
40	0.172	-0.069	-0.133	0.202	5.854**	1.903	-1.66	-0.244
41	-0.328**	0.097	0.034	-0.131	-4.979**	-2.264	0.842	1.422
42	0.394**	0.042	0.145	-0.187	-0.258	2.515	-1.383	-1.131
43	-0.439**	-0.291	0.311	-0.02	-4.146**	-0.763	-2.826	3.589*
44	0.061	0.375	-0.022	-0.353	-2.535**	2.792	-1.105	-1.687
45	0.228*	-0.291	-0.022	0.313	-0.591	-0.152	-4.55**	4.702**
46	0.172	0.097	0.034	-0.131	0.131	2.292	-4.437**	2.145

47	0.283*	-0.014	-0.078	0.091	4.299**	0.958	-0.271	-0.687
48	-0.272*	-0.291	0.145	0.147	-3.59**	-2.986	1.618	1.368
49	-0.106	0.042	-0.022	-0.02	4.854**	-1.43	3.505*	-2.076
50	-0.05	0.32	0.422*	-0.742**	0.688	7.737**	-0.327	-7.41**
51	0.172	-0.236	0.034	0.202	4.854**	-2.764	1.673	1.091
52	0.561**	-0.291	0.145	0.147	4.91**	-3.653*	3.118	0.535
53	0.505**	0.097	0.034	-0.131	-1.646	-0.763	-4.161*	4.924**
54	-0.05	0.32	-0.078	-0.242	-3.369**	0.459	2.394	-2.853
55	-0.606**	0.209	0.311	-0.52**	-6.48**	-2.097	-2.161	4.258*
56	-0.383**	-0.014	0.089	-0.075	-9.812**	2.571	5.006**	-7.577**
57	-0.106	0.709**	-0.689**	-0.02	-2.646**	6.903**	-8.66**	1.757
58	0.283*	0.153	0.089	-0.242	-0.868	1.458	2.395	-3.854*
59	-0.772**	0.875**	-1.189**	0.313	-1.228	1.318	-2.326	1.008
60	0.283*	-0.014	0.089	-0.075	5.576**	0.681	3.284*	-3.965*
61	-0.606**	0.042	0.145	-0.187	-7.035**	6.123**	1.897	-8.021**
62	-0.161	0.097	-0.133	0.036	2.076*	-9.319**	1.45	7.869**
63	-0.55**	0.32	-0.244	-0.075	-3.312**	1.737	-3.327*	1.59
64	-0.383**	-0.347	-0.078	0.425*	-5.202**	-8.208**	-3.104	11.312**
65	-0.161	-0.569**	0.367	0.202	-3.202**	-4.874**	3.563*	1.312
66	-0.55**	-0.18	0.422*	-0.242	-2.535**	-3.876*	8.729**	-4.853**
67	-0.05	0.153	-0.078	-0.075	-1.479	3.07	-0.16	-2.909
68	0.117	-0.014	-0.078	0.091	-0.424	-1.319	-5.215**	6.534**
69	0.283*	-0.18	0.089	0.091	3.52**	-7.097**	3.84*	3.256
70	0.394**	0.042	0.145	-0.187	3.299**	-4.875**	5.895**	-1.021
71	-0.161	-0.069	0.2	-0.131	3.632**	7.126**	1.228	-8.354**
72	0.117	-0.18	0.089	0.091	5.577**	-0.485	1.117	-0.632
73	-0.05	-0.014	-0.244	0.258	4.203**	2.387	-3.296*	0.908
74	0.228*	-0.125	-0.022	0.147	4.021**	0.903	-1.327	0.424
75	0.117	0.486*	-0.244	-0.242	0.021	3.402*	-2.994	-0.408
76	-0.161	-0.236	-0.133	0.369	2.853**	4.069*	-3.494*	-0.575
77	-0.05	-0.014	0.256	-0.242	-1.257	8.847**	-0.382	-8.465**
78	0.228*	-0.291	-0.189	0.48*	-0.758	-5.32**	0.285	5.036**
79	-0.272*	0.042	-0.189	0.147	-0.813	-5.597**	4.007*	1.591
80	-0.106	-0.125	-0.189	0.313	4.41**	-3.82*	1.284	2.536
81	-0.439**	0.209	0.145	-0.353	-5.869**	0.958	-2.103	1.146
T1	0.125**				-0.347			
T2	0.022				2.382**			
T3	-0.147**				-2.035**			

LSE for GCA (Lines)		
0.05	0.22	1.88
0.01	0.29	2.47
LSE for GCA (Testers)		
0.05	0.04	0.36
0.01	0.06	0.47
LSE for SCA (Effects)		
0.05	0.38	3.26
0.01	0.5	4.27
S.E. (GCA for Line)	0.11	0.96
S.E. (GCA for Tester)	0.02	0.18
S.E. (SCA Effects)	0.19	1.66
S.E. (gi-gj) Line	0.16	1.36
S.E. (gi-gj) Tester	0.03	0.26
S.E. (Sij-Sij)	0.27	2.35

*, ** means there is a significant effect at 5% and 1% levels of probability, respectively.

Table 8. continued.

S1 families & Testers	Days to 50% silking				Grain yield/plot (Kg)			
	GCA	SCA			GCA	SCA		
		T1	T2	T3		T1	T2	T3
1	1.502	0.936	-2.2	1.263	-0.374**	-0.207	0.061	0.145
2	1.002	4.436*	-2.7	-1.737	-0.337**	-0.222	-0.128	0.35*
3	0.002	0.436	-2.2	1.763	-0.311**	-0.086	-0.002	0.088
4	1.335	-4.397*	0.967	3.43	0.03	0.21	0.005	-0.215
5	-2.498*	0.936	0.3	-1.237	0.356**	0.071	-0.148	0.077
6	-1.331	-1.73	1.634	0.097	0.222**	0.357**	-0.134	-0.223
7	1.502	3.436	-0.2	-3.237	-0.316**	-0.141	-0.003	0.144
8	-0.331	1.27	-0.366	-0.903	0.123	0.164	-0.167	0.003
9	0.169	-0.73	3.134	-2.403	-0.009	-0.392**	0.136	0.255
10	2.002	4.436*	-5.200**	0.763	-0.035	-0.402**	0.012	0.39**
11	3.169**	-3.23	2.634	0.597	-0.014	0.697**	-0.464**	-0.234
12	1.002	-0.064	1.3	-1.237	-0.113	-0.231	0.097	0.134
13	1.169	-0.23	1.134	-0.903	-0.112	0.302*	-0.065	-0.238
14	-3.165**	-2.397	-1.533	**-3.930***	0.237**	0.199	0.105	-0.303*
15	0.169	-0.73	4.634*	-3.903*	-0.014	-0.029	-0.058	0.088
16	0.502	1.936	-0.2	-1.737	-0.152	-0.181	0.094	0.087
17	-2.331*	1.77	0.134	-1.903	0.427**	-0.047	0.151	-0.104
18	1.835	-2.397	0.467	1.93	0.296**	0.234	0.091	-0.325*
19	-0.665	0.103	2.967	-3.07	0.046	-0.011	0.129	-0.118
20	2.169*	4.27*	-1.866	-2.403	0.33**	-0.069	0.051	0.017
21	0.335	-0.897	1.467	-0.57	0.052	-0.086	0.046	0.04
22	0.335	-0.897	3.467	-2.57	-0.134	0.127	-0.298*	0.171
23	2.335*	-0.897	2.467	-1.57	-0.213**	0.022	-0.036	0.014
24	0.002	-0.564	0.3	0.263	-0.115	0.086	-0.086	-0.001
25	1.502	-4.064*	1.8	2.263	0.334**	-0.125	0.072	0.053
26	-4.498**	-1.064	-0.2	1.263	0.441**	0.092	-0.071	-0.021
27	0.669	3.27	-2.866	-0.403	-0.034	-0.283*	0.329*	-0.046
28	2.002	1.436	0.3	-1.737	-0.121	0.075	0.077	-0.151
29	-2.331*	1.27	-2.366	1.097	0.46**	0.078	0.188	-0.265
30	-1.998	-1.064	0.3	0.763	0.318**	0.217	-0.128	-0.089
31	-2.165*	-3.397	2.467	0.93	0.067	0.2	0.026	-0.227
32	-1.831	2.27	-2.866	0.597	-0.019	-0.134	0.149	-0.014
33	-4.831**	1.77	0.134	-1.903	0.34**	-0.124	0.084	0.04
34	-4.831**	-0.23	-2.866	3.097	0.244**	0.023	0.174	-0.197
35	-2.165*	-0.897	-0.033	0.93	0.229**	0.019	0.37**	-0.389**
36	0.169	-3.23	0.134	3.097	0.098	0.143	-0.15	0.007
37	0.335	0.603	-0.033	-0.57	0.075	0.049	-0.01	-0.039
38	-0.165	-0.397	1.467	-1.07	0.089	-0.167	-0.079	0.246
39	0.835	-3.397	-0.033	3.43	0.036	0.318*	-0.143	-0.175
40	-3.165**	-2.397	0.967	1.43	0.25**	0.282*	-0.167	-0.115
41	-1.998	1.936	-2.7	0.763	-0.334**	0.04	-0.055	0.015
42	-0.831	-2.23	2.634	-0.403	0.157*	0.102	-0.092	-0.009
43	0.169	-0.73	1.634	-0.903	-0.225**	-0.045	-0.106	0.151
44	0.169	-0.23	0.134	0.097	-0.163*	0.102	-0.1	-0.002
45	2.502*	1.436	2.3	-3.737*	0.162*	-0.061	-0.006	0.067
46	-1.498	-1.564	-0.7	2.263	0.148	0.076	-0.039	-0.037
47	-2.998**	-0.064	1.3	-1.237	0.134	0.028	-0.207	0.179
48	3.169**	1.27	-1.366	0.097	-0.232**	-0.033	0.049	-0.016
49	-0.165	0.103	-1.533	1.43	-0.05	-0.064	0.095	-0.031
50	1.502	-1.564	-1.2	2.763	-0.168*	0.238	0	-0.238
51	-1.831	-0.73	-0.366	1.097	0.111	-0.225	0.291*	-0.066
52	2.169*	3.27	-1.366	-1.903	0.184*	-0.251	0.228	0.023
53	0.502	-1.064	5.800**	-4.737*	0.079	-0.151	-0.064	0.215
54	0.169	0.77	3.134	-3.903*	-0.256**	-0.037	0.02	0.017
55	1.169	-1.73	2.134	-0.403	-0.295**	-0.115	-0.113	0.227
56	-7.665**	13.103**	-25.033**	11.93**	-0.397**	-0.036	0.069	-0.034
57	3.669**	-1.73	1.634	0.097	-0.218**	0.121	-0.19	0.069
58	-1.998	1.936	-0.2	-1.737	0.164*	0.122	0.016	-0.138

59	1.169	-3.23	4.134*	-0.903	-0.159*	-0.04	-0.087	0.127
60	-1.331	-0.23	-0.366	0.597	0.11	0.191	0	-0.191
61	2.835**	-2.397	-0.533	2.93	-0.321**	0.108	-0.037	-0.071
62	1.335	1.103	0.467	-1.57	0.08	-0.396**	0.337*	0.059
63	6.169**	0.27	1.634	-1.903	-0.341**	-0.032	-0.145	0.177
64	3.002**	5.436**	-3.2	-2.237	-0.364**	-0.207	-0.071	0.278*
65	2.335*	3.103	-2.033	-1.07	-0.174*	-0.22	0.109	0.111
66	4.169**	-1.23	-1.866	3.097	-0.325**	-0.049	-0.002	0.051
67	2.669*	-3.73*	1.134	2.597	-0.248**	0.023	-0.012	-0.011
68	1.835	-0.897	3.467	-2.57	-0.173*	0.075	-0.179	0.104
69	-0.831	1.77	1.134	-2.903	0.083	-0.321*	0.089	0.233
70	-2.831**	2.77	-1.866	-0.903	0.266**	-0.011	0.118	-0.107
71	0.669	-0.23	0.634	-0.403	-0.046	0.317*	-0.028	-0.289*
72	-2.998**	0.936	-1.7	0.763	0.259**	-0.317*	0.076	0.241
73	-2.498*	-3.064	-2.2	5.263**	0.187*	-0.051	0.069	-0.017
74	-4.498**	1.436	-2.2	0.763	0.428**	-0.047	0.139	-0.092
75	1.002	-3.564	1.3	2.263	-0.084	0.176	-0.218	0.041
76	3.335**	-1.897	2.467	-0.57	0.015	0.05	-0.022	-0.027
77	-0.165	-3.397	2.967	0.43	-0.027	0.405**	-0.142	-0.264
78	-0.665	-1.897	5.467**	-3.57	0.001	-0.178	0.002	0.176
79	1.335	0.603	-3.533	2.93	-0.181*	-0.225	0.226	-0.001
80	-1.331	1.27	0.134	-1.403	-0.059	-0.06	-0.072	0.132
81	1.335	-0.397	1.467	-1.07	-0.403**	-0.029	-0.062	0.091
T1	-0.103				0.03*			
T2	-0.967**				0.114**			
T3	1.07**				-0.144**			

LSE for GCA (Lines)		
0.05	2.1	0.15
0.01	2.75	0.2

LSE for GCA (Testers)		
0.05	0.4	0.03
0.01	0.53	0.04

LSE for SCA (Effects)		
0.05	3.63	0.27
0.01	4.76	0.35

S.E. (GCA for Line)	1.07	0.08
S.E. (GCA for Tester)	0.21	0.02
S.E. (SCA Effects)	1.85	0.14
S.E. (gi-gj) Line	1.51	0.11
S.E. (gi-gj) Tester	0.29	0.02
S.E. (Sij-Sij)	2.62	0.19

*,** means a there is significant effect at 5% and 1% levels of probability, respectively.

V- Genetic components and heritability

The analysis of variance for crosses as well as the calculated genetic parameters i.e., covariance half-sib (Cov. H.S.) for lines, testers and average, covariance full-sib (Cov. F.S.), variances of general (σ^2GCA) and specific (σ^2SCA) combining abilities, variances of additive (σ^2A) and dominance (σ^2D), combining ability ratio (CAR), ratio of σ^2GCA/ σ^2SCA and (σ^2D / σ^2A)1/2, and both broad (Hbs) and narrow (Hns) sense heritability were presented in Table 9. It remarkable results that the specific combining ability variance (σ^2SCA) was more important than the general combining ability (σ^2GCA) for studied traits of maize crosses, revealing the preponderance of dominance variance in controlling these traits. These finds are in line with the variances of additive (σ^2A) and dominance

(σ^2D), where the dominance gene action was more important in inheritance of these traits. Moreover, the estimates of combining ability ratio (CAR) were much lower than 0ne (CAR<1), indicating the preponderance of dominance variance in controlling these traits. In accordance results, the ratios of σ^2GCA/ σ^2SCA and (σ^2D / σ^2A)1/2 expressed this situation of inheritance monitor of dominance, were the first one was very less (0.0016-0.0096) and the last one recorded very high value than unity (5.184-12.545) for the studied traits. Finally, the narrow sense heritability (Hns) exhibited very low values ranging from 0.43 (days to 50% silking) to 3.18 (grain yield/plot), and it coupled the same trend of non-additive and resembled that the dominance was the most likely to inherit the studied trait in the current crosses of maize. In the same context, the broad sense heritability (Hbs) possessed high values which ranged from 67.54 (days to 50% silking) to 97.35% (grain yield/plot), giving enough genetic variance for future improvement depending on non-additive behavior due to the less additive one for all studied in the current crosses of maize. Fellahi et al., (2013) found that the non-additive gene effects were dominant in the genetic control and inheritance of the studied traits, due to coupled reasons i.e. a- the dominant genetic variance was higher than the additive one, b-σ^2GCA/ σ^2SCA ratio was lower than unity, and c- (σ^2D / σ^2A)1/2 ratio, which is an indicator of dominancy degree, was higher than unity. Dinesh *et al*., (2016); Talukder *et al*., (2016) and Kaur, *et al*., (2010) found low GCA variance to SCA variance ratio revealed a preponderance of non-additive gene action, indicating the non-additive gene action in the inheritance of grain yield and its related traits in maize. Moreover, Abrha *et al*., (2013) and Ganapati Mukri *et al*., (2022) reported that both of additive and non-additive gene actions were important in controlling the behavior of genetic potential of the inbred lines of maize development for yield and related traits. In addition, Mutimaamba *et al.*, (2020) found desirable and good predictor of SCA effects for grain yield. Consequently, priority should be to select specific crosses with desirable SCA in maize especially under stress conditions.

Table 9. Genetic Parameters for all studied traits of 81 s1 families and three testers

		Ear diameter (cm)	Number of kernels/row	Days to 50% silking	Grain yield/plot (kg)
Replications	2	0.2525	5.3427	2.8899	0.0115
Lines (L)	80	0.9046	131.8578	50.0406	0.4677
Testers (T)	2	4.65	1235.62	254.0123	4.2113
L x T	160	0.3668	70.41	38.4592	0.1281
Error	484	0.1122	8.26	12.5387	0.0035
Cov H.S. (line)		0.0597	6.8275	1.2868	0.0377
Cov H.S. (tester)		0.0176	4.7951	0.887	0.0168
Cov H.S. (average)		0.0005	0.0733	0.0137	0.0004
Cov. F.S.		0.6167	156.4746	33.7767	0.5303
$\sigma^2 GCA$		0.0005	0.0733	0.0137	0.0004
$\sigma^2 SCA$		0.0849	20.7167	8.6402	0.0415
σ^2_A		0.0021	0.2931	0.0549	0.0014
σ^2_D		0.0849	20.7167	8.6402	0.0415
CAR		0.0116	0.0070	0.0032	0.0189
$\sigma^2 GCA / \sigma^2 SCA$		0.0059	0.0035	0.0016	0.0096
$(\sigma^2_D / \sigma^2_A)^{1/2}$		6.358	8.407	12.545	5.445
H_{bs}		69.94	88.41	67.54	97.35
H_{ns}		1.69	1.23	0.43	3.18

Cov H.S: covariance half-sib; Cov. F.S.: covariance full-sib; $\sigma^2 GCA$ & $\sigma^2 SCA$: variances of general and specific combining abilities, respectively.; $\sigma^2 A$ & $\sigma^2 SCA$: additive and dominance variances, respectively.; and CAR: combining ability ratio. Hbs &Hns: broad and narrow sense heritability, respectively.

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تحليل السلالة × الكشاف لهجن قميه من الذرة الشامية لمحصول الحبوب وبعض الصفات المرتبطة

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الملخص

تم استخدام تحليل السلالة × الكشاف لتقييم 234 هجين قمي وآبائهم (81 سلالة S1 و 3 كشاف) لتقدير القدرة العامة والخاصة على الائتلاف وكذلك المكونات الوراثية. وأظهرت النتائج وجود اختلافات معنوية بين كل من الهجن والسلالات والكشافات والتفاعل بينهما بالنسبة للصفات المدروسة (محصول الحبوب وقطر الكوز وعدد حبوب الصف وظهور 50% حريرة).

كانت اسهامات تفاعل السلالة × الكشاف أكبر من أي منهما على حدة مما ادى الى تقديرات عالية للتباين بسبب القدرة الخاصة على الائتلاف لصفتي محصول الحبوب للقطعة التجريبية وعدد حبوب فى الصف. أظهر المتوسط العام تفوق الكشافات عن السلالات والهجن القميه في محصول الحبوب وأقل منها في ظهور 50% حريرة. وتفوقت الهجن القميه عن السلالات في محصول الحبوب ومبكرة عن الكشافات والسلالات.

وجد عدد 22، 28، 26 سلالة تملك قدرة ائتلافية عامة موجبة ومعنوية لصفات محصول الحبوب وقطر الكوز وعدد حبوب بالصف على التوالي. وهناك 16 سلالة كانت سالبة ومعنوية القدرة العامة على الائتلاف. وأظهرت السلالتان L33 , L26 قدرة عامة موجبة معنوية لصفات محصول الحبوب وقطر الكوز وعدد حبوب/الصف وسالبة لظهور 50% حريرة.

يفضل الكشاف T2 لصفات محصول الحبوب/حوض وعدد حبوب/الصف وظهور 50% حريرة بينما الكشاف T1 لقطر الكوز.

وجد عدد 14، 46، 16، 9 من الهجن القميه لها قدرة ائتلافية خاصة معنوية ومرغوبة لصفات محصول الحبوب وعدد حبوب الصف وقطر الكوز وظهور 50% حريرة على التوالي. أعتمد التبكير في الهجن القميه على القدرة الائتلافية الخاصة بين السلالة والكشاف.

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