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Shamly Gupta
Department of Crop
Improvement, CSK Himachal
Pradesh Agricultural University,
Palampur, Distt. Kangra,
Himachal Pradesh, India

S Lata
Professor (PBG), Department of
Crop Improvement, CSK
Himachal Pradesh Agricultural
University, Palampur, Distt.
Kangra, Himachal Pradesh,
India

Evaluation of *opaque2* introgressed lines for some grain yield and nutritional traits in maize through $L \times T$ analysis

Shamly Gupta and S Lata

Abstract

A line \times tester analysis involving thirty test-crosses generated by crossing ten *opaque2* introgressed maize inbred lines with three diverse testers and two standard checks was conducted for different yield and nutritional traits in alpha RBD design replicated twice during *kharif* 2016. The objectives of this study were to examine combining ability of inbred lines, determine the nature of gene action and enhancement of nutritional traits. Genetic differences were observed from mean squares of treatments for all traits except protein content. The GCA effect revealed that the inbred lines L_7 , L_8 and L_{10} and the tester T_1 were the best general combiners for some yield and nutritional traits. On the basis of extent of heterosis and specific combining ability effects, the hybrids $L_8 \times T_1$ and $L_{10} \times T_1$ were the best since both were either at par with standard check-1 (Vivek QPM-9) and standard check-2 (Palam Sankar makka-2) or significantly superior for yield and nutritional traits.

Keywords: *Zea mays* L., Specific combining ability, general combining ability, gene action, line \times tester

Introduction

The agriculture sector in India employs more than 90 million people and contributes 15.4 percent gross value addition to the Indian economy (MAFW 2017) ^[9] where cultivation of crops is one of the oldest occupations that probably began around 3000 BC. Maize alone is responsible for providing 15% of the protein and 20% of the calories in the human diet, and this crop covered a cultivated area of 181.44 million hectare in 2016. This is the only crop for which area and production have consistently increased (India Maize Summit 2015) ^[7]. Maize can be processed into a variety of food and industrial products including starch, sweeteners, oil, beverages, glue, industrial alcohol, and fuel ethanol. In the recent past, hybrids have replaced the open pollinated varieties on account of their higher yield potential across the world. Around 65 percent of the area under maize is now used to cultivate hybrids, including various types of specialty produce such as sweet corn, popcorn, baby corn and protein-upgraded corn called quality protein maize (QPM). Indian diets among poor people are monotonous and cereal centric. As a consequence, they are deficient in micronutrient and are not balanced in terms of daily requirement of many nutrients. The cereal grain are inherently low in iron, zinc and carotenoid concentration and leads to poor health in human beings and lower the working efficiency of the population (Cakmak 2008) ^[6]. Under such circumstances biofortified maize with enhanced lysine, tryptophan, vitamin-A, iron and zinc possesses enormous potential to alleviate micronutrient malnutrition which have been targeted for intervention due to the magnitude of their deficiencies amongst the world's poor. The development and popularization of staple crop varieties with enhanced micronutrient (Fe and Zn) content has been proposed as an effective and sustainable strategy to ameliorate malnutrition, particularly of rural families with limited access to markets and healthcare facilities (Bouis and Welch 2010) ^[5]. It is estimated that India loses 2.5 percent of the national GDP on account of micronutrient deficiency. Development of micronutrient enriched staple foods through breeding approaches, a process popularly known as 'biofortification' holds promise to sustainable and cost effective food based solutions to combat micronutrient deficiency (Pfeiffer and McClafferty 2007) ^[11]. Therefore, to meet out the demand of maize grain with the ever- increasing human population and industrial requirements, biofortified hybrids are the only solution, as they are, much high yielder and have high nutritional factor than the traditional varieties. One of the most important objectives in maize (*Zea mays* L.) breeding programs is to develop vigorous inbred lines with high combining ability for grain

Correspondence
Shamly Gupta
Department of Crop
Improvement, CSK Himachal
Pradesh Agricultural University,
Palampur, Distt. Kangra,
Himachal Pradesh, India

yield and its primary components to produce superior hybrid combinations. Thus Information on heterosis and combining ability among maize germplasm is essential in maximizing the effectiveness of hybrid development. Partitioning the genetic variance into GCA and SCA effects would help to understand the genetic control of grain yield and its components. In view of this, the study was undertaken to estimate the general combining ability (GCA) for parents and specific combining ability (SCA) effects for single cross hybrids and to identify superior quality protein maize hybrids with higher yield potential and micronutrient content.

Materials and Methods

The experiment was carried out in the *kharif* 2016 at Experimental Farm, Department of Crop Improvement, CSK HPKV Palampur Distt. Kangra, Himachal Pradesh. The region is located at 32°6' N latitude and 76°3' E longitude and an altitude of 1290.8 amsl. The climate of the area is characterized as warm and temperate with an average annual temperature is 19.1°C. It is characterized by high rainfall with unimodal pattern of precipitation.

The Experimental Materials

In CSKHPKV, Palampur *opaque2* introgressed inbred lines have been generated through marker assisted backcross breeding followed by selfing and selection. These lines were crossed with three diverse testers (for tryptophan, iron and zinc, respectively). Thirteen inbred lines were used in this study, ten *opaque2* introgressed inbred lines (560, 561, 574, 580, 601, 607, 631, 642, 649 and 658) were used as lines and three diverse inbred lines namely (KI-29, CML-169 and BAJIM-06-10) were used as testers and two standard checks viz., Vivek QPM-9 and Palam Sankar makka-2 presented in table 1.1. These lines were crossed according to line × tester technique mating desi to generate thirty F₁ cross combinations. Field evaluation of genotypes (30 F₁ hybrids plus 13 parental inbred lines) was performed during *kharif* 2016. All recommended cultural practices and operations (planting, irrigation) were conducted.

Design and Experimental managements

The experiment was conducted in alpha Randomized Block Design with two replications. Each plot comprised of two rows of 2 m long with the spacing of 60 m between rows and 20 m between plants. One seeds was planted per hill. Other cultural practices like weeding and disease management has

been done manually throughout the entire growing season as required.

Data Collected

Morphological traits were measure based on maize descriptors developed by Biodiversity international. Days to 50 % pollen shed: Number of days from planting to when 50% of the plant in a plot shed pollen. Days to 50 % silking: Number of days from planting to when 50% of the plants in a plot produced 2-3 cm long silk. Days to 75 percent maturity: The numbers of days from sowing to the time when cobs attain 75 percent maturity. Plant height (cm): The plant height was recorded in centimeters (cm) from the base of the plant to the tassel bearing node at maturity. Cob placement height (cm): The cob placement height was measured at dry silk stage in cm from the base of the plant to the base of the uppermost cob. Cob length (cm): The length of the individual cob of selected plants was measured with a measuring tape in cm from the base to the filled grain point. Cob girth (cm): The cob girth of all the selected plants was recorded in cm by wrapping a measuring tape just below the centre of each cob. Kernel rows/ear: The numbers of kernel rows per cob were counted for all the ears of the selected plants. 100 seed weight: A random sample of 100 seeds were taken from each plot and weight was recorded in grams. Grain yield/plant: At harvest, the dehusked cob weight of all the plants was recorded. The moisture percentage was determined in the grains obtained from randomly selected cobs from each plot with the help of "Universal Moisture Meter". The grain weight was adjusted for 15 percent moisture level, and was converted into grain yield assuming shelling percentage at 80 percent.

Analysis of variance

The analysis was performed using PROC GLM of SAS software. All possible pair wise treatment comparisons were performed using LSMEANS statement of PROC GLM. Entry means adjusted for block effects as analyzed according to alpha RBD were used to perform combining ability analysis. The analysis of variance indicated significant differences among the treatments for all the traits except protein (%) at 5 and 1 percent level of significance presented in that justifying the presence of adequate variability with regard to material under study. Further analysis was done according to the line × tester analysis to partition the mean square due to crosses into lines, tester and line by tester effects.

Table 1.1: List of maize genotypes (*Zea mays*. L) evaluated under present study

Sr. No.	Hybrids	Source/Pedigree
1	560×KI-29	B76Q-22-05 × Selection from K-25
2	560×CML169	B76Q -22-05 × G26Qc22MH7-1-1-1-1-B-B
3	560×BAJIM-06-10	B76 Q -22-05 × HAREC 95 Pool-99
4	561×KI-29	B76Q -22-06 × Selection from K-25
5	561×CML169	B76Q-22-06 × G26Qc22MH7-1-1-1-1-B-B
6	561×BAJIM-06-10	B76Q -22-06 × HAREC 95 Pool-99
7	574×KI-29	B69Q-66-1 × Selection from K-25
8	574×CML169	B69Q -66-1 × G26Qc22MH7-1-1-1-1-B-B
9	574×BAJIM-06-10	B69Q -66-1 × HAREC 95 Pool-99
10	580×KI-29	B70Q -5-8 × Selection from K-25
11	580×CML169	B70Q -5-8 × G26Qc22MH7-1-1-1-1-B-B
12	580×BAJIM-06-10	B70 Q -5-8 × HAREC 95 Pool-99
13	601×KI-29	B70Q -22-2 × Selection from K-25
14	601×CML169	B70Q -22-2 × G26Qc22MH7-1-1-1-1-B-B
15	601×BAJIM-06-10	B70Q -22-2 × HAREC 95 Pool-99
16	607×KI-29	B70Q -5-2 × Selection from K-25

17	607×CML169	B70Q -5-2 × G26Qc22MH7-1-1-1-1-B-B
18	607×BAJIM-06-10	B70Q -5-2 × HAREC 95 Pool-99
19	631×KI-29	D25Q -3 × Selection from K-25
20	631×CML169	D25Q -3 × G26Qc22MH7-1-1-1-1-B-B
21	631×BAJIM-06-10	D25Q -3 × HAREC 95 Pool-99
22	642×KI-29	D39 Q -2 × Selection from K-25
23	642×CML169	D39Q -2 × G26Qc22MH7-1-1-1-1-B-B
24	642×BAJIM-06-10	D39Q -2 × HAREC 95 Pool-99
25	649×KI-29	D30Q -2 × Selection from K-25
26	649×CML169	D30Q -2 × G26Qc22MH7-1-1-1-1-B-B
27	649×BAJIM-06-10	D30Q -2 × HAREC 95 Pool-99
28	658×KI-29	D31Q -73-2 × Selection from K-25
29	658×CML169	D31Q -73-2 × G26Qc22MH7-1-1-1-1-B-B
30	658×BAJIM-06-10	D31Q -73-2 × HAREC 95 Pool-99
31	560	B76Q -22-05
31	561	B76Q -22-06
33	574	B69Q -66-1
34	580	B70Q -5-8
35	601	B70Q -22-2
36	607	B70Q -5-2
37	631	D25Q -3
38	642	D39Q -2
39	649	D30Q -2
40	658	D31Q -73-2
41	KI-29	Selection from K-25
42	CML169	G26Qc22MH7-1-1-1-1-B-B
43	BAJIM-06-10	HAREC 95 Pool-99
44	Vivek QPM-9	VQL 1 × VQL 2
45	Palam Sankar makka-2	BAJIM-08-26 × BAJIM-08-27

Results and Discussion
Analysis of Variance

The analysis of variance indicated significant differences among the treatments for all the traits except protein (%) at 5 and 1 percent level of significance presented in table 1.2 that justifying the presence of adequate variability with regard to material under study. This indicates that the crosses were sufficiently different from each other for these traits and

hence, selection is possible to identify the most desirable crosses. Results are in congruence with the findings of Lal and Singh (2014) revealed significant differences among the genotypes for days to 50 percent pollen shed, 50 percent silking, 75 percent maturity, plant height, cob placement height, grain yield/plant (g), cob girth (cm) and tryptophan in contrary to protein(%).

Table 1.2: Analysis of variance for alpha randomized block design for yield, its component and nutritional traits in maize

Source of variation →	Replication	Blocks within replication	Treatments	Error
Traits df→	1	16	44	28
Mean sum of square				
Days to 50 percent pollen shed	8.10	1.02	16.49**	0.82
Days to 50 percent silking	8.71	0.79	16.64**	0.88
Days to 75 percent maturity	8.71	1.85*	10.84**	0.85
Plant height (cm)	105.67	64.25*	617.59**	28.30
Cob placement (cm)	30.13	38.49*	234.93**	13.84
100 seed weight (g)	16.10	3.88	18.96**	3.01
Grain yield (g)	7.92	33.63	1840.35**	23.73
Cob length (cm) (cm)	0.42	0.85	4.56**	0.87
Cob girth (cm) (cm)	0.89	1.80	6.69**	1.22
Kernel rows/cob	0.43	0.74	3.63**	1.01
Protein (%)	0.40	0.11	0.43	0.24
Tryptophan content (%)	0.0018	0.0002	0.0175**	0.0006
Iron (mg/kg)	0.47	4.49	16.02**	4.39
Zinc (mg/kg)	0.72	2.57	18.35**	3.06

*Significant at $P \leq 0.05$, **Significant at $P \leq 0.01$

Combining Ability Analysis

The analysis of variance for combining ability revealed significant differences among crosses for all the traits presented in table 1.3. Further partitioning of the sum of square of crosses into lines (females), testers (males) and line \times tester (female \times male) indicated that mean sum of squares due to lines were not significant for all the traits except kernel rows/cob, protein (%), tryptophan and iron over line \times tester mean sum of square but all the lines were significant for over all error mean sum of square. Variances due to the testers were significantly different when tested against mean sum of square due to line \times tester interaction except cob length (cm), kernel rows/cob and protein (%). Mean sum of squares due to line \times tester interactions were significant for all the traits

when tested against variances due to error. This indicated the presence of considerable genetic variability among the parents (lines and testers) used in the present study. The significant difference for all the traits except few traits were also reported by Melkamu (2013) [10]. Analysis of variance for line \times tester also showed highly significant differences for most of the grain yield and nutritional traits. The results of analysis of combining abilities indicated the importance of both additive and non-additive gene actions in controlling *viz.*, such as days to 50 percent pollen shed and silking, 75 percent maturity, grain yield, 100 seed weight, plant and cob placement heights, and kernel rows per ear. Therefore, both additive and non-additive variances are important in exploiting the genetic potential of the inbred lines in hybrid development program.

Table 1.3: Analysis for variance for combining ability

Source of variation \rightarrow Traits df \rightarrow	Replication 2	Crosses 29	Lines 9	Testers 2	Line \times Tester 18	Error 36
Days to 50 percent pollen shed	4.82	14.19*	10.37*	92.62@*	7.39*	0.89
Days to 50 percent silking	6.67	13.62*	8.96*	96.72@*	6.72*	0.81
Days to 75 percent maturity	7.35	9.35*	6.01*	62.52@*	5.11*	1.18
Plant height(cm)	113.76	792.16*	476.76*	7129.15@*	245.75*	39.59
Cob placement(cm)	115.29	460.46*	397.05*	2897.96@*	221.33*	22.92
100 seed weight (g)	7.33	15.91*	19.99*	49.91@*	10.08*	3.78
Grain yield(g)	13.26	717.62*	510.73*	248.90@*	873.15*	33.75
Cob length (cm)	2.35	2.71*	2.09*	2.46*	3.06*	1.05
Cob girth (cm)	0.28	3.87*	3.95*	9.29@*	3.23*	1.16
Kernel rows/cob	0.76	2.22*	4.08@*	2.46*	1.26*	0.76
Protein (%)	0.13	0.62*	1.17@*	0.24	0.39*	0.18
Tryptophan (%)	0.002	0.014*	0.004@*	0.16@*	0.002*	0.0004
Iron (mg/kg)	0.01	14.38*	20.00@*	26.71@*	10.19*	4.97
Zinc (mg/kg)	0.12	19.41*	17.91*	53.68@*	16.34*	3.44

* Significant at 5% level of significance when tested against MSS due to error, @* Significant at 5% level of significance when tested against MSS error and lines \times tester interactions

Estimates of general combining ability effects

In the present study, parents were classified as good, average and poor combiners based on the GCA estimates for yield component and nutritional traits. Parents with the desirable GCA effects significantly differing from zero were considered as good combiners, while those with non-significant estimates were called as average combiners. Poor combiners had significant but undesirable GCA effects. The estimates of GCA effects for all the traits showing significant mean sum of square due to lines and testers are presented in Table 1.4. Estimates of GCA effects for 100 seed weight and grain yield/plant showed that line L₁₀ exhibited the maximum GCA effect whereas L₄ exhibited the lowest GCA effect, indicating the existence of best and poorest general combiners, respectively. Therefore, line L₁₀ could be utilized in maize grain improvement programs as it has higher tendency to inherit their trait of interest to their cross combinations. Tester, T₁ was the best general combiner while T₂ was poor general combiner for 100 seed weight and grain yield/plant. Among lines, L₈ and L₁₀ were found to be most desirable general combiner as it revealed significant negative GCA effects for 75 percent maturity which indicates the tendency of earliness and the reverse is true for those with positive GCA effects and same is the case with testers T₁. For plant height and cob placement height, L₁, L₁₀ and tester T₂

exhibited good and poor general combining ability revealed significant negative GCA effect this indicates that L₁ and T₂ has a tendency to reduce whereas L₁₀ has a tendency to increase plant height in the hybrid progenies. No significant positive GCA effect were observed for cob length and cob girth therefore, all the lines studied were average combiners for these two traits. With respect to kernel rows/ear, L₆ showed positive and significant GCA effects, as it is the most important yield component that directly contributes to increased grain yield, whereas L₄ showed significant negative GCA effect. Hence, inbred lines with high GCA effects for this trait can be suitable parents for hybrid development as well as for inclusion in future breeding programs. For protein and tryptophan content, L₁ and L₃ showed significant GCA effect, respectively. Tester T₂ showed significant GCA effect for tryptophan as it was considered as the best check for tryptophan (%). However, for iron and zinc L₈ showed significant GCA effect. But in case of testers T₁ and T₃ showed positive significant GCA for iron and zinc and also regarded as best checks for these two quality traits. Therefore, the testers T₁ (KI-29), T₂ (CML-169) and T₃ (BAJIM-06-10) could be used in biofortification breeding programme after further testing. These results were in agreement with Ahmed *et al.* (2017) [11] and Shushay *et al.* (2013) [12].

Table 1.4: Estimates of general combining ability of lines and testers for yield, its components and nutritional traits

Entry	Days to 50 percent pollen shed	Days to 50 percent silking	Days to 75 percent maturity	Plant height(cm)	Cob placement height(cm)
Lines					
L ₁	1.22**	0.97*	1.42**	-6.85*	-7.76**
L ₂	0.05	0.47	-0.08	-2.84	8.17**
L ₃	0.38	0.47	-0.25	-0.50	0.22
L ₄	0.72	0.62	0.58	6.43*	3.68
L ₅	-0.45	-0.20	-0.75	-6.87*	2.01
L ₆	2.22**	1.97**	1.08*	-0.62	-1.54
L ₇	-0.12	-0.37	-0.08	3.26	-6.99**
L ₈	-1.95**	-2.03**	-1.42**	-3.00	5.39*
L ₉	0.05	-0.03	0.92*	10.17**	-15.10**
L ₁₀	-2.12**	-1.87**	-1.42**	21.16**	11.94**
SE(gi) ±	0.38	0.37	0.44	2.57	1.95
SE(gi-gj) ±	0.54	0.52	0.63	3.63	2.76
CD(5%)	1.11	1.06	1.28	7.45	5.67
CD(1%)	1.49	1.43	1.73	10.03	7.63
Testers					
T ₁	-2.48**	-2.53**	-2.02**	21.21**	13.66**
T ₂	1.17**	1.12**	1.28**	-14.98**	-9.07**
T ₃	1.32**	1.42**	0.73**	-6.23**	-4.59**
SE(gj) ±	0.21	0.20	0.24	1.40	1.07
SE(gi-gj)±	0.54	0.28	0.34	1.99	1.51
CD(5%)	0.61	0.58	0.70	4.08	3.10
CD(1%)	0.82	0.78	0.95	5.49	4.18

Entry	100 seed weight(g)	Grain yield/plant(g)	Cob length (cm)	Cob girth (cm)	Kernel rows/ cob	Protein (%)	Tryptophan (%)	Iron (mg/kg)	Zinc (mg/kg)
Lines									
L ₁	-2.08*	-0.95	-0.14	-0.01	1.01	0.62**	0.00	0.68	0.29
L ₂	1.33	2.72	0.78	0.92	0.48	0.17	0.01	0.31	0.78
L ₃	-1.73*	-10.57**	0.81	-1.48**	-0.86	-0.20	0.03**	0.52	0.97
L ₄	- 2.68**	-14.58**	-0.59	-0.08	-1.04**	0.18	0.02*	1.43	-0.74
L ₅	0.13	-4.83	-0.39	-0.34	-0.69	-0.50	-0.03**	0.47	0.34
L ₆	0.57	-2.09	0.28	0.93	0.98*	0.05	-0.01**	-0.23	0.77
L ₇	-0.41	-2.36	-0.99	-0.43	-0.71	0.30	0.04	-0.32	-0.63
L ₈	0.29	6.65**	0.41	0.68	-0.49	0.33	0.01	2.07*	3.13**
L ₉	1.12	10.03**	-0.32	-0.87	0.55	-0.90	-0.05**	-4.76**	-3.39**
L ₁₀	3.45**	15.98**	0.15	0.69	0.76*	-0.03	-0.02*	-0.2	-1.53**
SE(gi) ±	0.79	2.37	0.42	0.44	0.36	0.18	0.01	0.91	0.76
SE(gi-gj) ±	1.12	3.35	0.59	0.62	0.50	0.25	0.01	1.29	1.07
CD(5%)	2.30	6.88	1.21	1.28	1.03	0.50	0.02	2.64	2.19
CD(1%)	3.09	9.26	1.64	1.72	1.39	0.68	0.03	3.55	2.95
Testers									
T ₁	1.67**	3.95**	-0.03	0.76	-0.14	-0.05	-0.05**	1.26*	-1.77
T ₂	-1.47**	-2.85*	-0.33	-0.54	-0.26	-0.07	0.10**	-0.24	0.30
T ₃	-0.20	-1.09	0.37	-0.22	0.40	0.13	-0.06**	-1.02	1.47**

SE(gj) ±	0.43	1.29	0.23	0.24	0.19	0.09	0.004	0.49	0.41
SE(gi-gj) ±	0.62	1.84	0.32	0.34	0.28	0.14	0.006	0.71	0.59
CD(5%)	1.26	3.77	0.67	0.69	0.57	0.28	0.01	1.45	1.20
CD(1%)	1.69	5.07	0.89	0.94	0.76	0.37	0.02		1.62

*Significant at $P \leq 0.05$, **Significant at $P \leq 0.01$

Estimation of specific combining ability

The results of desirable SCA effects presented in the table 1.5 exhibited significant SCA effects for days to 75 percent maturity [(L₁ × T₂), (L₄ × T₁), (L₅ × T₃), (L₆ × T₂) and (L₈ × T₃)], plant height [(L₇ × T₂) and (L₉ × T₁)], cob placement height [(L₃ × T₂), (L₄ × T₃), (L₅ × T₃), (L₈ × T₂), (L₉ × T₁) and (L₁₀ × T₂)], 100 seed weight (L₇ × T₁), grain yield/plant [(L₁ × T₂), (L₂ × T₂), (L₂ × T₃), (L₄ × T₁), (L₅ × T₂), (L₇ × T₁), (L₇ × T₃), (L₈ × T₁), (L₉ × T₃) and (L₁₀ × T₁)], cob length (L₈ × T₁), cob girth (L₄ × T₁), kernel rows/cob (L₇ × T₃), protein (L₁ × T₁), tryptophan (L₈ × T₂) and zinc [(L₃ × T₃), (L₆ × T₁) and (L₉ × T₃)] had at least one of the parents as good or average or poor

general combiner. In most of the cases, good general combiners did not necessarily result in a good cross combination (L₉ × T₁) and same was true for poor combiners. Further, for grain yield/plant, cross (L₂ × T₃) although revealed significant SCA effects but both the parents of this hybrid were average general combiners. This implies that it is not necessary that the good cross combinations will have their parents showing high GCA effects only. Parents with average or poor GCA effects can give rise to good cross combinations as a consequence of complementation.

Table 1.5: Estimates of specific combining ability of crosses for yield, its components and nutritional traits

Traits→	Days to 50 percent pollen shed	Days to 50 percent silking	Days to 75 percent maturity	Plant height (cm)	Cob placement height (cm)
Crosses					
L ₁ × T ₁	0.98	1.03	0.18	-6.14	-4.49
L ₁ × T ₂	-2.67**	-2.62**	-2.12*	11.39*	10.69**
L ₁ × T ₃	1.68*	1.58*	1.93*	-5.25	-6.20
L ₂ × T ₁	1.15	0.53	0.18	1.64	0.83
L ₂ × T ₂	-1.00	-0.62	-0.62	-0.87	-4.15
L ₂ × T ₃	-0.15	0.08	0.43	-0.77	3.32
L ₃ × T ₁	-1.18	-0.97	1.65*	-4.44	-7.92*
L ₃ × T ₂	-1.33	-1.12	0.05	-5.81	2.80
L ₃ × T ₃	2.52**	2.08**	1.60*	10.25*	5.12
L ₄ × T ₁	-1.52*	-1.63	-1.98*	8.18	8.13*
L ₄ × T ₂	-0.17	-0.28	1.72*	-3.24	-0.95
L ₄ × T ₃	1.68*	1.92**	0.27	-4.94	-7.18*
L ₅ × T ₁	1.15	1.20	0.85	5.77	17.39**
L ₅ × T ₂	1.50*	1.05	1.55	-7.04	-5.08
L ₅ × T ₃	-2.65**	-2.25**	-2.40**	1.27	-12.31**
L ₆ × T ₁	2.48**	2.53**	1.52	6.73	0.64
L ₆ × T ₂	-1.17	-1.12	-1.78*	0.11	-0.23
L ₆ × T ₃	-1.32	-1.42*	0.27	-6.84	-0.41
L ₇ × T ₁	-0.18	-0.13	0.18	7.54	-2.81
L ₇ × T ₂	1.17	1.22	0.88	-10.77*	-1.93
L ₇ × T ₃	-0.98	-1.08	-1.07	3.23	4.74
L ₈ × T ₁	-1.85**	-1.47*	0.02	9.61*	5.31
L ₈ × T ₂	2.50**	2.38**	1.72*	-1.11	-8.71*
L ₈ × T ₃	-0.65	-0.92	-1.73*	-8.50	3.40
L ₉ × T ₁	0.65	0.53	0.18	-28.32**	-23.10**
L ₉ × T ₂	0.50	0.88	-1.12	17.51**	15.78**
L ₉ × T ₃	-1.15	-1.42*	0.93	10.81*	7.32*
L ₁₀ × T ₁	-1.68*	-1.63*	0.52	-0.56	6.01
L ₁₀ × T ₂	0.67	0.22	-0.28	-0.17	-8.21*
L ₁₀ × T ₃	1.02	1.42*	-0.23	-0.73	2.20
SE (Sij)±	0.67	0.63	0.77	4.45	3.39
SE (Sij-Skl) ±	0.94	0.89	1.09	6.29	4.79
CD(5%)	1.93	1.84	2.22	12.90	9.81
CD(1%)	2.59	2.48	2.99	17.37	13.21

Crosses	100 seed weight	Grain yield/plant	Cob length (cm)	Cob girth (cm)	Kernel rows/cob	Protein (%)	Tryptophan	Iron	Zinc
L ₁ × T ₁	2.28	4.87	0.46	-1.25	-0.28	0.71*	0.02	2.38	1.01
L ₁ × T ₂	0.38	21.51**	0.42	1.11	0.16	-0.24	0.00	-3.73*	-0.49
L ₁ × T ₃	-2.66	-26.38**	-0.88	0.14	0.11	-0.46	-0.02	1.35	-0.52
L ₂ × T ₁	-1.05	-37.93**	-0.50	-0.73	-0.19	-0.01	0.01	-0.28	-1.00
L ₂ × T ₂	0.67	9.16*	1.10	0.13	-0.02	0.08	-0.03*	1.24	2.59
L ₂ × T ₃	0.38	28.77**	-0.60	0.61	0.22	-0.07	0.02	-0.96	-1.58
L ₃ × T ₁	1.20	-1.79	-1.44	-0.63	-0.41	0.01	-0.03*	-1.17	-2.95*
L ₃ × T ₂	-0.60	1.48	0.87	0.53	-0.05	-0.20	0.01	-1.84	-1.21
L ₃ × T ₃	0.60	0.31	0.57	0.11	0.45	0.18	0.02	3.01	4.16**
L ₄ × T ₁	0.83	27.91**	0.36	1.97*	0.27	-0.21	-0.03	0.99	-0.06
L ₄ × T ₂	1.51	-15.86**	-0.73	-0.37	0.74	0.12	0.01	-2.18	-1.91
L ₄ × T ₃	-2.35	-12.41**	0.37	-1.59*	-1.02	0.08	-0.01	1.19	1.97
L ₅ × T ₁	-4.54**	-14.07**	-0.84	0.62	-0.57	-0.19	0.02	-1.01	-2.18
L ₅ × T ₂	1.99	12.41**	-0.53	-0.02	0.24	-0.37	-0.01	1.53	0.74
L ₅ × T ₃	2.56	1.67	1.37	-0.61	0.33	0.56	0.02	-0.52	1.45
L ₆ × T ₁	0.56	0.93	-0.50	1.51	1.51*	0.69*	-0.01	-0.17	4.07**
L ₆ × T ₂	-0.98	2.29	-0.20	-0.03	-0.88	0.05	-0.01	-1.26	-2.05
L ₆ × T ₃	0.42	-3.22	0.70	-1.47	-0.63	-0.74*	-0.02	1.42	-2.02
L ₇ × T ₁	3.75*	20.73**	-0.64	1.07	0.58	-0.01	0.02	2.51	2.57
L ₇ × T ₂	-1.74	-31.12**	-0.33	-1.67*	-1.03	0.15	0.01	0.7	3.35*
L ₇ × T ₃	-2.02	10.39*	0.97	0.61	0.46	-0.15	0.02	-3.30*	-5.92**
L ₈ × T ₁	-0.86	11.87**	2.96**	0.39	0.57	-0.12	-0.03*	-2.61	-0.48
L ₈ × T ₂	-1.02	-11.52**	-0.53	-0.34	0.20	-0.13	0.07**	2.56	0.07
L ₈ × T ₃	1.88	-0.35	-2.43**	-0.06	-0.76	0.25	-0.04**	0.05	0.40
L ₉ × T ₁	-0.34	-21.91**	-0.30	-2.07*	-1.18	-0.24	-0.03	-0.19	-1.14
L ₉ × T ₂	-0.33	8.35	0.00	0.72	0.23	-0.07	0.00	0.77	-1.83

$L_9 \times T_3$	0.67	13.56**	0.30	1.35	0.94	0.41	0.02	-0.58	2.97*
$L_{10} \times T_1$	-1.82	9.38*	0.43	-0.88	-0.29	-0.54	-0.02	-0.46	0.17
$L_{10} \times T_2$	0.13	3.31	-0.07	-0.05	0.40	0.61	-0.01	2.12	0.73
$L_{10} \times T_3$	1.70	-12.70**	-0.37	0.93	-0.11	-0.07	0.03	-1.66	-0.91
SE (Sij)±	1.38	4.11	0.73	0.77	0.62	0.30	0.01	1.58	1.31
SE (Sij-Skl) ±	1.95	5.81	1.03	1.08	0.88	0.43	0.02	2.23	1.85
CD(5%)	3.99	11.91	2.10	2.21	1.79	0.88	0.04	4.57	3.80
CD(1%)	5.37	16.03	2.83	2.98	2.41	1.19	0.05	6.15	5.12

*Significant at $P \leq 0.05$, **Significant at $P \leq 0.01$

Estimation of genetic components of variance

The estimates of analysis of variance were confirmed from the study of additive (σ^2A), dominant (σ^2D) components of variance and proportional contribution of lines, testers and their interactions to the total variances of respective traits are presented in table 1.6. Dominance component (σ^2D) were greater than the additive component (σ^2A) for the all the traits. Higher σ^2D than σ^2A indicates the role of non-additive gene action. Similar findings were observed by Melkamu (2013) [10]. It was further clear from the ratio of additive to

dominance variance which is less than unity exhibited for most of the traits studied confirmed the non additive gene action. Average degree of dominance which exceeded one clearly indicated the over dominance of the traits under studied. The preponderance of non-additive gene action in the inheritance of all the traits studied clearly suggested exploitation of heterosis breeding for the improvement of these traits and the presence of sufficient hybrid vigour in different cross combinations. Similar findings were reported by Atif *et al.* (2012).

Table 1.6: Estimates of genetic components of variance

Traits	σ^2A	σ^2D	σ^2A / σ^2D	Average Degree of Dominance
Days to 50 % Pollen shed	0.38	3.25	0.11	8.53
Days to 50% silking	0.39	2.96	0.14	7.63
Days to 75% maturity	0.24	1.97	0.12	8.27
Plant height (cm)	30.65	103.08	0.29	3.36
Cob placement height (cm)	13.41	99.21	0.14	7.39
100 seed weight (g)	0.33	3.15	0.10	9.65
Grain yield/plant (g)	8.72	419.70	0.02	48.11
Cob length (cm)	0.02	1.00	0.02	52.15
Cob girth (cm)	0.04	1.03	0.03	28.66
Kernel rows /cob	0.05	0.25	0.22	4.56
Protein (%)	0.01	0.10	0.12	8.16
Tryptophan (%)	0.0006	0.0008	0.75	1.33
Iron (mg/kg)	0.23	2.61	0.09	11.13
Zinc (mg/kg)	0.17	6.45	0.03	37.56

Conclusion

The present study identified inbred lines with good GCA and cross combinations with desirable SCA for the traits studied. Considerable diversity was observed in treatments and hybrids that show selection process is desirable. The estimates of GCA effects revealed that the inbred lines L_7 , L_8 and L_{10} tester T_1 had good GCA for grain yield and most of the yield component and nutritional traits therefore, these promising lines may be successfully used in hybrid development programme. The hybrid $L_2 \times T_3$ with the highest SCA effect did not involve either of the parent with significant positive GCA effects. Similarly, hybrid combinations *viz.*, $L_1 \times T_2$ and $L_5 \times T_3$ with significant negative SCA effects for earliness but their parents were poor combiners. This indicated wide diversity in nicking to produce hybrid vigour. In general, there was no generalized order of nicking among the parents to produce desirable combinations. Any sort of combinations could give hybrid vigour over the parents which might be due to favorable dominant genes or over dominance. The magnitude of dominance variance was higher than additive variance for all the traits which indicates the preponderance of non-additive gene action suggesting the exploitation of hybrid vigour in maize. Hence, the information from this study may possibly be useful for researchers who would like to develop high yielding varieties of maize for yield and nutritional traits.

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