

**Research Article****Hybrid Performances and Line-by-Tester Analysis of Highland Maize Inbred Lines for Grain Yield and Other Related Traits**

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**ABSTRACT**

The current study was conducted to evaluate the performance of test-cross hybrids and to estimate the combining ability of highland maize inbred lines for grain yield and yield related traits. 48 test crosses together with two standard checks were evaluated using alpha lattice design with two replications at two high-altitude sub-humid agro-ecology representing trial sites (Ambo and Holeta) in Ethiopia during 2018 main cropping season. Combined analysis of variance showed highly significant differences among the two locations for all the studied traits except EH, indicating the presence of considerable variation among locations for genotype performance. The interaction between locations and genotypes, were significant for GY, DA, DS and EA. The significance of both GCA and SCA mean squares for some traits indicates the role of additive and non-additive gene action in the inheritance of the traits. The contribution of GCA variance for all the traits was greater than the contribution of SCA variance. L1, T3 and T4 had significant positive GCA effects and are considered as good combiners for grain yield. Likewise, L4, L8, L9, T2 and T3 were identified as parents good for short plant stature. On the other hand, the study identified two best cross combinations L9xT4 and L11xT4 that exceeded the standard checks in mean GY for further use in breeding and cultivar development process.

**Key words:** GCA, Grain yield, Lines, SCA, Testers.

**INTRODUCTION**

Maize (*Zea mays* L.;  $2n=2x=20$ ) is an important food security crop in the developing world, especially in sub-Saharan Africa (SSA) and Latin America. In Africa, maize is produced on a total area of 38.7 million hectares; with the production of 78.9 million metric tons which is about 19.96% of the total maize area of the world and 6.88% of the global production respectively (FAOSTAT, 2019). Lack of congruence between the proportion of production and the cultivated area is due to the low productivity of maize in Africa ( $<2t\ ha^{-1}$ ) as compared to a global average of  $5.6\ t\ ha^{-1}$ .

Maize is cultivated in all of the major agro-ecological zones in Ethiopia. The production and productivity of maize in all agro-ecologies are constrained by several biotic and abiotic stresses. The importance of the constraints varies from agro-ecology to agro-ecology and from location to location within the same agro-ecology. In response to the constraints, the highland maize

improvement project was launched back in 1998 in Ethiopia in partnership between the International Maize and Wheat Improvement Center (CIMMYT) and the National Agricultural Research Systems (NARS) of east and central African (ECA) countries (Twumasi *et al.*, 2002). This initiative has resulted in the development of seven improved highland maize varieties for the transitional-highland to highland agro-ecologies of Ethiopia to date. To keep this momentum moving forward, the process of developing new highland maize inbred lines has been progressing well at the main breeding station of Ambo Agricultural Research Center. In the process of developing new maize inbred lines, information on combining ability of parental maize inbred lines, i.e., general combining ability (GCA) and specific combining ability (SCA), is an important input for designing breeding strategy aimed at exploiting the genetic potential of maize for achieving higher productivity (Chawla and Gupta, 1984).

Several studies on combining ability of highland maize inbred lines for grain yield and yield related traits were

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conducted for different sets of locally developed/introduced inbred lines (Legesse *et al.*, 2009, Elmyhum 2013, Gudeta *et al.*, 2015, Shimelis *et al.*, 2019, Zeleke *et al.*, 2020). However, it is always necessary for any breeding program to generate such information for any new batch of inbred lines generated locally or received from exotic sources. The focus of the current study was, therefore, to generate information on combining ability of newly developed highland maize inbred lines for grain yield and yield related traits using line-by-tester mating scheme.

## MATERIALS AND METHODS

### Description of Experimental Sites

The study was conducted at two locations in the highland sub-humid agro ecology of Ethiopia, namely, Ambo and Holetta Agricultural Research Centers, in the main cropping season of 2018 (Table 1).

### Experimental Materials

A total of 50 entries composed of 48 test crosses, formed by crossing 12 highland maize inbred lines with four-line testers (referred to as heterotic testers A and B), and two standard checks (Jibat, and Kolba,) were studied. The inbred lines were previously developed by Ambo highland maize breeding program and CIMMYT from the crosses of elite-by-elite inbred lines. The list and the pedigrees of the inbred lines used in the line x tester crosses and testers are given in Table 2. Two of the line testers are CIMMYT developed testers and widely used in Ethiopian maize breeding programs, while the other two are locally developed line testers commonly used by the highland maize breeding program at Ambo.

### Experimental Design and Field Managements

The experimental design was alpha lattice design (0, 1) (Patterson and Williams, 1976) with 5 plots per an incomplete block and 10 incomplete blocks with two replicates. Each entry was planted in a one row 5.25 m long plot with spacing of 0.75 m between rows and 0.25 m between plants within a row. The experimental materials were hand planted with two seeds per hill, which were later thinned to one plant to get the recommended planting density for the testing sites, 53,333 plants per hectare. Planting was conducted on the onset of the main rainy season after an adequate soil moisture level was reached to ensure good germination and seedling development. Other agronomic practices were carried out as per the recommendation for the test areas.

### Data Collection

Data on grain yield and other important agronomic traits were collected on a plot and sampled plants bases. Data collected on a plot basis include days to 50% anthesis, days to 50% silking, number of ears per plant, field weight (kg/plot), plant aspects, ear aspects, and bad husk cover; while data recorded on sampled plants basis were ear height (cm) and plant height (cm). Yield in t/ha was calculated using CIMMYT fieldbook software (Banziger and Vivek, 2007).

### Data Analysis

All Data collected for this study were subjected to analyses of variance (ANOVA) using the PROC GLM

**Table 1:** Description of testing locations

Location	Altitude (masl)	Rainfall (mm)	Temp (°C)		Latitude	Longitude	Soil type
			Min	Max			
Ambo	2225	1050	10.4	26.3	8°57'N	38°7'E	Black vertisol
Holeta	2400	1102	6	22	09°04'N	38°29'E	Nitosols and vertisols

\*Rainfall and Temp; were taken as averages of many years for each locations

**Table 2:** List of highland maize inbred lines and testers used for test-cross formation.

S/N	Lines Code	Genotype name	Source (Origin)
1	L1	MH1307001-4-2-1-1	EIAR- HMBP
2	L2	MH1307002-3-3-3-1	EIAR- HMBP
3	L3	MH1307002-4-1-1-2	EIAR- HMBP
4	L4	MH1307002-4-2-2-1	EIAR- HMBP
5	L5	MH1307002-9-1-1-1	EIAR- HMBP
6	L6	MH1307002-9-2-1-2	EIAR- HMBP
7	L7	MH1307002-10-1-2-1	EIAR- HMBP
8	L8	MH1307002-10-1-2-2	EIAR- HMBP
9	L9	MH1307002-10-1-2-3	EIAR- HMBP
10	L10	MH1307002-10-2-3-2	EIAR- HMBP
11	L11	MH1307002-10-2-3-3	EIAR- HMBP
12	L12	MH1307002-10-3-2-2	EIAR- HMBP
13	T1	HLM0001	EIAR- HMBP
14	T2	HLF0002	EIAR- HMBP
15	T3	CML312	CIMMYT
16	T4	CML395	CIMMYT

\*EIAR-HMBP = Ethiopian Institute of Agricultural Research - Highland Maize Breeding Program

procedure in SAS® computer program (SAS Institute, 2004). Least significant difference (LSD) was used for mean comparisons. For traits that displayed significant differences among crosses, line by tester analysis was performed to further partition the variances due to crosses into lines, tester and line by tester effects using SAS program (SAS institute, 2004).

### Line by Tester Analysis

Line by tester analyses was performed for traits that showed significant differences among crosses as suggested by Dabholkar (1999) and Singh and Chaudhary (1985) to partition the mean square due to crosses into lines, testers and line x tester interactions. The following mathematical model was used for the combining ability analysis of individual locations:

$$Y_{ijk} = \mu + r_k + g_i + g_j + S_{ij} + e_{ijk}$$

Where,  $Y_{ijk}$  = the value of a character measured on cross of line  $i$  by tester  $j$  in  $k^{\text{th}}$  replication;  $\mu$  = population mean;  $r_k$  = effect of  $k^{\text{th}}$  replication;  $g_i$  = general combining ability (GCA) effects of  $i^{\text{th}}$  line;  $g_j$  = general combining ability (GCA) effect of the  $j^{\text{th}}$  tester;  $S_{ij}$  = specific combining ability (SCA) of  $i^{\text{th}}$  line and  $j^{\text{th}}$  testers such that  $S_{ij}$  equals  $S_{ji}$ ;  $e_{ijk}$  = experimental error for  $ijk^{\text{th}}$  observation.

The proportional contributions of lines ( $GCA_L$ ), testers ( $GCA_T$ ) and their interaction ( $SCA_{L \times T}$ ) with the sum square of crosses were calculated as the ratio between sum of squares of each component and the cross sum of squares expressed in percentage following Singh and Chaudary (1985) as follows:

$$\text{Contribution of lines (L)} = \frac{SS(L)}{SS(\text{Crosses})} * 100$$

$$\text{Contribution of testers (T)} = \frac{SS(t)}{SS(\text{Crosses})} * 100$$

$$\text{Contribution of line by tester (L x T)} = \frac{SS(L \times T)}{SS(\text{crosses})} * 100$$

**Table 3:** Mean squares from line x tester analysis of variance for yield and yield related traits over two locations in Ethiopia in 2018

Source of var.	DF	GY	DA	DS	PH	EH	PA	EA	EPP
Location(Loc)	1	84.97**	9856.08**	13744.82**	1404.50*	169.28	16.65**	15.96**	0.96**
Rep(Loc)	1	3.65	27.38	0.98	54.08	237.62	0.01	0.28*	0.001
BLK(Rep))	18	2.19	16.20	3.19603	264.82	192.08	0.09	0.08	0.04
Genotype (G)	49	13.83**	41.54**	31.96**	1266.55**	664.93**	0.19**	0.67**	0.11**
Crosses(Cr)	47	15.56**	48.73**	37.75**	1336.83**	761.16**	0.21**	0.72**	0.13**
G*Loc	49	2.71*	25.19*	13.06**	240.04	108.46	0.12	0.18**	0.04
Cr*Loc	47	3.12**	24.75*	14.60**	298.95	121.29	0.13*	0.20**	0.05*
GCA(L)	11	10.66**	8.88*	10.51**	853.91**	365.14**	0.15*	0.66**	0.20**
GCA(T)	3	155.31**	518.35**	469.62**	10716.47**	7400.74**	1.27**	6.90**	0.66**
SCA(L*T)	33	4.49**	19.32	7.57**	645.10**	289.57**	0.13*	0.17**	0.06**
GCA(L)*Loc	11	4.53**	11.30	9.71**	484.89*	78.89	0.09	0.38**	0.05
GCA(T)*Loc	3	7.65**	122.59**	118.42**	395.39	159.93	0.57**	0.07	0.05
SCA(L*T)*Loc	33	2.22	20.34	6.79**	228.2	131.9	0.1	0.15**	0.04
Pooled Error Cr	94	1.56	16.34	3.02	219.36	145.81	0.08	0.07	0.03
Pooled Error G	80	1.57	15.59	2.91	103.18	134.1	0.08	0.07	0.03
CV		16.31	3.81	1.61	6.87	10.82	9.73	8.7	13.98
Cont. of GCA		79.72	72.16	85.92	66.12	73.29	56.85	82.89	67.10
Cont. of SCA		20.28	27.84	14.08	33.88	26.71	43.26	17.11	32.90

\*=0.05 and \*\*= 0.01 significant probability level respectively. GY=Grain yield, DA = Days to anthesis, DS = Days to silking, EH = Ear height, PH = Plant height, PA=Plant aspect, EA=Ear aspect, EPP = Number of ears per plant, DF = degrees of freedom, Cont. of GCA = contribution of general combining ability of lines and testers, Cont. of SCA = contribution of specific combining ability of line by tester

The significance of GCA and SCA effects were tested by dividing the corresponding SCA and GCA values by their respective standard error, to obtain the calculated t values, and comparing the calculated t value with tabular t-value at the error degree of freedom.

## RESULTS AND DISCUSSION

### Analysis of Variance

Combined analysis of variance showed significant differences among the two locations for all the studied traits except EH (Table 3). The result also showed highly significant ( $P > 0.01$ ) mean squares due to genotypes for all traits studied. The interaction between locations and genotypes (Loc x G), were highly significant and significant ( $P < 0.05$ ) for GY, DA, DS, and EA, indicating that the performances of the genotypes were not consistent across locations for these traits and there is adequate genetic variability among the inbred lines to allow good progress from selection for improvements of the traits. Similar results were reported for GY by different authors (Badu-Apraku *et al.*, 2011, Gudeta *et al.*, 2017, Zeleke *et al.*, 2020). However, non-significant interaction effects of Loc x G were observed for PH, EH, PA and EPP, indicating that the genotypes were performed uniformly across sites for those traits. In line with this finding, Tesfaye *et al.* (2019) reported non-significant Loc x G interaction for PH, EH and EPP in their study.

The combined analysis of variance for grain yield and other related traits also showed highly significant and significant differences (Table 3) ( $P < 0.01$  and  $P < 0.05$ ) among crosses,  $GCA_L$ ,  $GCA_T$  and  $SCA_{(L \times T)}$  for all studied traits except DA in  $SCA_{(L \times T)}$ . The interactions of  $GCA_L * Loc$  showed significant differences for GY, DS, PH and EA; whereas the mean squares of  $GCA_T * Loc$  revealed highly significant differences for GY, DA, DS and PA. On the other hand, significant differences were observed in  $SCA_{(L \times T)} * Loc$  only for DS and EA (Table 3). The significance of both GCA and SCA mean squares for most of the traits indicates the role of additive and non-additive gene action in the inheritance of the traits. Various

scientists (Dagne *et al.*, 2011, Tolera *et al.*, 2017) also reported similar findings in other groups of inbred lines they studied. Similarly, for all of the traits, the contribution of GCA variances were greater than the contribution of SCA variances (Table 3), revealing the predominance of additive gene action in the inheritance of all traits. This showed that parents with good GCA and *per se* performance could be used to predict the performance of their crosses. Therefore, these parents can be crossed to develop high-yielding hybrids that can potentially be used in further breeding work (inbred line development) and/or directly released for commercial use. Similar results were reported by other authors in their study on combining ability for yield and yield related traits in maize (Seyoum *et al.*, 2016, Dufera *et al.*, 2018). The significance of the interaction of GCA of parents (lines and testers) with the environment and SCA of the crosses with the environment revealed that the GCA effects of the parents and SCA of the crosses over the test environments were different.

### Mean Performance of Genotypes

The mean performances of the genotypes (the 48 hybrid progenies and two checks) across site are given in Table 4. The mean grain yields (GY) of the genotypes across sites ranged from 3.65 to 11.53 t/ha with overall mean of 7.68 t/ha. Among the 48 test crosses the highest yielding crosses L11 x T4 (11.53 t/ha) and L9 x T4 (11.26t/ha) out yielded the standard checks, Kolba by 6.86 and 4.36% and Jibat by 12.49 and 9.85% respectively. The presence of crosses having mean values better than the standard checks indicate the possibility of obtaining good hybrid (s) for future use in breeding program. DA and DS ranged from 99.00 to 109.50 and 100.00 to 111.50 days, with overall means of 103.88, and 105.95 days, respectively. The lowest mean values for both DA and DS were observed in cross L2 x T3, while the highest mean values were observed in the crosses L6xT4 and L2 x T4 for DA and DS respectively (Table 4). As a result, most of the crosses showed longest number of days to anthesis and silking as compared to standard checks, indicating that those crosses could be grouped as late maturing types.

**Table 4:** Mean grain yield and agronomic traits of top-twenty genotypes and standard checks evaluated across two locations of highland agro-ecologies in Ethiopia.

Crosses	GY (t/ha)	DA (days)	DS (days)	PH (cm)	EH (cm)	PA (1-5)	EPP (num)	EA (1-5)
L11xT4	11.53	106.75	107.00	228.51	117.08	2.7	1.30	2.4
L9xT4	11.26	106.25	108.50	225.15	116.17	2.5	1.23	2.5
L10xT4	10.80	105.50	108.25	215.92	121.23	2.8	1.22	2.6
L12xT4	10.59	107.50	108.50	237.20	122.47	2.9	1.51	2.9
L5xT4	10.32	108.00	111.00	231.60	118.53	3.0	1.17	3.1
L1xT3	10.15	100.50	101.00	192.10	93.88	2.8	1.35	2.3
L8xT4	10.01	106.75	110.25	208.81	131.18	2.3	1.07	2.3
L7xT4	9.84	107.50	110.25	218.09	123.14	2.8	1.32	2.7
L2xT3	9.53	99.00	100.00	178.54	79.52	2.9	1.36	3.1
L9xT3	9.16	101.00	102.50	189.20	83.62	3.0	1.18	3.0
L10xT3	9.04	100.75	101.50	204.83	92.66	2.8	1.22	2.6
L1xT4	8.88	108.25	110.25	244.04	129.97	2.6	0.96	2.4
L3xT4	8.70	107.00	109.00	217.39	110.47	2.7	1.04	2.9
L1xT2	8.61	102.50	103.00	191.07	93.94	2.7	1.33	2.6
L12xT3	8.58	99.75	100.75	196.74	95.41	3.0	1.47	3.0
L6xT3	8.46	100.25	102.25	209.36	81.80	2.7	1.23	2.4
L11xT3	8.43	101.50	104.25	183.72	97.14	2.8	1.40	2.8
L2xT4	8.33	108.25	111.50	239.12	117.96	2.9	1.00	2.8
L5xT3	8.28	100.75	102.25	212.29	104.81	3.0	1.22	2.8
L8xT3	8.17	100.75	103.50	186.29	77.27	3.0	1.23	2.7
KOLBA	10.79	101.00	103.00	229.93	103.82	3.1	1.37	2.6
JIBAT	10.25	103.25	104.25	234.54	117.88	2.8	1.51	3.0
LSD	2.04	6	3.60	21.73	16.45	0.4	0.26	0.5
Mean	7.68	103.88	105.95	207.57	107.04	2.88	1.23	3.04
Min	3.65	99.00	100.00	163.37	77.27	2.34	0.80	2.27
Max	11.53	109.50	111.50	244.04	131.18	3.27	1.64	3.74

GY=Grain Yield, DA=Days to anthesis, DS = Days Silking PH=Plant height, EH=Ear height, PA=Plant Aspect, EA=Ear Aspect, EPP=Ears Per Plant, LSD=Least Significant Difference

**Table 5:** Estimates of GCA effects for grain yield and other agronomic traits of 12 highland maize inbred lines and four testers crossed using line x tester mating design and evaluated across site in 2018 main cropping season.

Lines	Traits							
	GY	DA	DS	PH	EH	PA	EA	EPP
L1	1.23*	-0.27	-1.23	5.85	5.38*	-0.13	-0.52**	-0.02
L2	0.01	0.61	0.33	2.79	-0.87	0.09	0.26	0.03
L3	-0.50	0.11	0.20	0.79	-1.62	0.09	0.10	-0.01
L4	-1.28*	-0.39	0.08	-9.21	-9.62**	0.12	0.20	-0.11*
L5	-0.02	1.05	0.77	6.73	0.19	0.12	0.10	-0.06
L6	-1.35**	-1.77*	0.70	4.73	-0.18	-0.10	-0.11	-0.19**
L7	-0.26	0.55	0.77	-5.65	4.01	0.06	0.14	-0.04
L8	-0.35	0.30	1.20	-14.21**	-3.31	-0.04	-0.08	-0.01
L9	0.90	-0.33	-0.55	-8.15	-5.81**	-0.02	0.01	0.06
L10	0.72	-0.58	-0.92	4.17	1.51	-0.04	-0.02	0.04
L11	0.76	0.67	-0.23	6.67	7.38**	-0.16*	-0.11	0.04
L12	0.14	0.05	-1.11	5.48	2.94	0.02	0.04	0.27**
SE(gi)	0.51	0.80	0.75	5.27	2.13	0.07	0.15	0.06
SE(gi-gj)	0.62	2.02	0.87	7.41	6.04	0.14	0.13	0.09
Testers								
T1	-1.91**	-0.22	0.66	-3.35	0.03	0.16	0.31**	-0.10**
T2	-1.07**	0.82	-0.32	-10.31**	-3.66*	0.05	0.33**	0.14**
T3	0.99**	-4.27**	-3.96**	-8.31**	-13.06**	0.01	-0.24**	0.05
T4	1.99**	3.67**	3.62**	21.98**	16.69**	-0.23*	-0.41**	-0.10**
SE(gi)	0.35	1.38	1.36	2.49	1.58	0.09	0.03	0.03
SE(gi-gj)	0.36	1.17	0.50	4.28	3.49	0.08	0.08	0.05

\*=0.05 and \*\*= 0.01 significant probability level respectively: GY=grain yield, DA = days to anthesis, DS = days to silking, EH = ear height, PH = plant height, EA=Ear Aspect, PA=Plant Aspect, EPP = number of ears per plant, SE(gi) = standard error of general combining ability effects of lines and testers, SE (gi-gj)=standard error of the difference of general combining ability effects of lines and testers.

PH and EH ranged from 163.37 to 244.04 and 77.27 to 131.18 cm with mean values of 207.57 and 107.04 cm, respectively. The two high yielding crosses (L11 x T4 and L9 x T4) were tall with acceptable PA and EA. In line with this finding, Dufera *et al.* (2018) reported higher GY from taller plants and the authors also suggested that this could be attributed to high photosynthetic products accumulation during long period for grain filling.

EPP ranged from 0.8 (L6 x T4) to 1.64 (L9 x T2) (data not shown), with an overall mean of 1.23. The high yielding crosses had EPP value greater than or equal to the overall mean, indicating that EPP trait contributes for having high grain yield. The genotypes ranged from 2.27 to 3.74 for their EA with a mean of 3.04. The highest and lowest mean values for ear aspect were observed in crosses L2 x T1 and L6 x T4 (data not shown). L6 x T4 cross was preferred for this trait because of smaller value of EA which is desirable.

**Table 6:** Estimates of specific combining ability (SCA) effects for grain yield and other agronomic traits of 12 highland maize inbred lines crossed in line x tester mating design and evaluated across sites in 2018 main cropping season.

Crosses	Traits						
	GY	DS	PH	EH	PA	EA	EPP
L1xT1	0.65	-0.47	8.48	5.35	0.22	-0.09	0.05
L1xT2	0.88	-1.49	-9.06	-11.21*	-0.18	-0.24	0.00
L1xT3	0.37	0.15	-9.06	0.43	-0.01	0.08	0.12
L1xT4	-1.90**	1.82	9.65	5.43	-0.02	0.25	-0.17*
L2xT1	-0.13	-0.04	7.04	4.60	0.00	0.13	-0.05
L2xT2	0.41	0.94	2.50	5.04	-0.02	-0.15	0.13
L2xT3	0.96	-2.41*	-17.50**	-6.57	-0.11	0.05	0.09
L2xT4	-1.24*	1.51	7.96	-3.07	0.13	-0.03	-0.17*
L3xT1	0.60	0.34	-0.96	-0.15	-0.13	-0.22	0.07
L3xT2	0.34	0.57	9.50	12.04*	-0.02	0.01	0.06
L3xT3	-0.58	-0.04	2.75	-2.82	0.14	0.08	-0.07
L3xT4	-0.36	-0.87	-11.29	-9.07	0.01	0.13	-0.06
L4xT1	0.69	1.96	0.54	8.10	0.09	0.06	0.06
L4xT2	-0.21	-0.81	-23.50**	-11.21*	0.07	-0.08	-0.05
L4xT3	0.04	-1.41	19.00**	7.68	0.11	-0.01	0.04
L4xT4	-0.52	0.26	3.96	-4.57	-0.27*	0.03	-0.06
L5xT1	-0.66	0.03	-10.90	-7.46	-0.03	0.16	0.07
L5xT2	0.12	0.01	5.81	-4.78	-0.18	-0.24	-0.11
L5xT3	-0.25	-0.60	7.81	13.62**	-0.01	-0.17	-0.04
L5xT4	0.79	0.57	-2.73	-1.38	0.23	0.25	0.08
L6xT1	-0.58	-0.41	-25.40**	-13.34**	0.18	0.38*	-0.01
L6xT2	0.86	0.07	12.81*	11.35*	-0.08	0.23	0.02
L6xT3	1.26*	-0.54	8.56	-6.26	-0.17	-0.32*	0.16
L6xT4	-1.54*	0.88	4.02	8.24	0.07	-0.28	-0.17
L7xT1	-0.84	0.28	-11.02	-0.03	0.15	0.13	-0.04
L7xT2	0.54	-1.24	5.94	-0.34	0.01	-0.15	-0.13
L7xT3	-0.25	1.15	6.19	2.56	-0.08	0.05	-0.05
L7xT4	0.54	-0.18	-1.10	-2.19	-0.09	-0.03	0.22*
L8xT1	-1.66**	2.34*	-11.21	-12.96**	0.25	0.09	-0.09
L8xT2	0.89	-1.93	9.50	7.22	-0.15	0.07	0.16
L8xT3	-0.03	0.21	5.75	-7.38	0.14	0.02	-0.05
L8xT4	0.80	-0.62	-4.04	13.12**	-0.24	-0.19	-0.03
L9xT1	-1.11	-0.16	-3.52	-3.96	0.10	0.00	-0.12
L9xT2	0.60	-0.43	-3.06	2.72	0.04	-0.02	0.22*
L9xT3	-0.29	0.96	0.69	-0.88	0.00	0.18	-0.15
L9xT4	0.80	-0.37	5.90	2.12	-0.14	-0.16	0.04
L10xT1	0.78	-0.79	14.67*	5.22	-0.25	0.03	0.03
L10xT2	-1.07	0.94	-3.88	-4.84	0.23	0.14	0.01
L10xT3	-0.23	0.34	2.88	-1.19	-0.11	-0.17	-0.08
L10xT4	0.52	-0.49	-13.67	0.81	0.13	0.00	0.03
L11xT1	1.55*	-1.72	24.42**	12.85**	-0.38**	-0.25	-0.03
L11xT2	-1.88**	1.76	2.88	1.54	0.10	0.35*	-0.19*
L11xT3	-0.88	2.40*	-22.88**	-3.32	0.14	0.05	0.07
L11xT4	1.22	-2.43*	-4.42	-11.07*	0.13	-0.16	0.16
L12xT1	0.71	-1.35	7.85	1.79	-0.19	-0.41*	0.04
L12xT2	-1.48*	1.63	-9.44	-7.53	0.17	0.07	-0.12
L12xT3	-0.11	-0.22	-4.19	4.12	-0.05	0.15	-0.05
L12xT4	0.89	-0.06	5.77	1.62	0.07	0.19	0.13
SE	0.62	1.08	6.26	4.76	0.13	0.16	0.08
SE(Sji-Skl)	1.25	1.74	14.81	12.08	0.28	0.26	0.17

\*=0.05 and \*\*= 0.01 significant probability level respectively: GY=grain yield, DS = days to silking, EH = ear height, PH = plant height, EA=Ear Aspect, PA=Plant Aspect, EPP = number of ears per plant, SE = standard error, SE (sji-Skl) = standard error of the difference of specific combining ability effects of line by testers.

### General Combining Ability Effects

The GCA effects of the 12 inbred lines and 4 testers for GY and related traits are presented in Table 5. Among the 12 inbred lines, only L1 was with significantly positive mean GCA effects for GY. Similarly, among the four testers T3 and T4 were showed highly significant positive GCA effects for this trait. Therefore, the inbred line and the testers with positive and significant GCA effects are good combiner for improving GY. On other hand, L4 and L6; T1 and T2 were showed significantly negative GCA effects for

GY, indicating, that these inbred lines and testers were not good combiner within this group of inbred lines and may not be exploited for GY improvement.

In line with the current study, several authors reported either positive or negative significant GCA effects of inbred lines for GY in other group of inbred lines (Legesse *et al.*, 2009, Tolera *et al.*, 2017, Dufera *et al.*, 2018, Tesfaye *et al.*, 2019).

For DA, only L6 showed negative significant GCA effects, while none of the inbred lines were showed neither

positive nor negative significant GCA effects for DS. Line with negative GCA effects for DA is desirable line, as this line tends to flower earlier than other lines. Desirability of negative GCA for DA and DS was suggested by various authors' (Abrha *et al.*, 2013, Dufera *et al.*, 2018). In addition, T4 had positive and highly significant GCA effects on both DA and DS, while T3 revealed negative and highly significant GCA effects for both DA and DS, indicating T3 is a desirable tester for making intermediate maturing and T4 is a desirable tester for making lateness and high yielding crosses when crossed with other inbred lines.

Mean GCA effects of inbred lines for PH and EH ranged from -14.21 to 6.73 and -9.62 to 7.38 respectively (Table 5). Only L8 showed negative and highly significant mean GCA effects for PH, while L4 and L9 showed negative and highly significant GCA effects for EH, implying the tendency of these lines to reduce plant height, which is important for the development of genotypes resistant to lodging. On the other hand, L1 and L11 showed positive and significant mean GCA effects for EH (Table 4), indicating that these inbred lines were poor combiner in making genotypes with good ear position. Similarly, T4 showed positive and highly significant mean GCA effects for both PH and EH, whereas T2 and T3 revealed negative and highly significant mean GCA effects for these traits. In line with the present study, Demissew *et al.* (2011) and Tolera *et al.* (2017) found significant positive and negative GCA effects for PH and EH in inbred lines and testers they studied. Among the inbred lines, only L1 and L11 were with significantly negative mean GCA effects for EA and PA respectively. Similarly, among the four testers T3 and T4 were showed highly significant negative mean GCA effects for these traits. On other hand T1 and T2 showed positive and highly significant mean GCA effects for EA, indicating that the testers with positive and significant GCA effects are poor combiner for improving EA and the inbred lines and testers with negative GCA effects for both traits were good combiners in improving these traits.

In case of EPP L4 and L6 showed negative and significant GCA effects, while positive and significant GCA effects were observed for L12. The positive and significant GCA effect for EPP indicates prolificacy, which is a desirable trait in increasing maize productivity to some extent (Alamerew and Warsi, 2015). In addition, T2 had positive and highly significant GCA effects, while T1 and T4 revealed negative and highly significant GCA effects for this trait, indicating T2 is a desirable tester for improving this trait when crossed with other inbred lines.

### Specific Combining Ability Effects

Specific combining ability effects computed for grain yield and other agronomic traits are presented in Table 6. L6 and L11 had significantly positive SCA effects when crossed to T1 and T3 for GY implying that there was significant positive interaction of genes between the two parents for this trait. Such gene interactions lead to the expression of heterosis, which can be exploited in the development of hybrid varieties. Therefore, these crosses could be selected for their specific combining ability for higher grain yield. In line with this finding, Bullo and Dagne (2016) reported highly significant positive and negative SCA effects for GY and they suggested that, when

high yielding specific combinations are desired, especially in hybrid maize development, SCA effects could help in the selection of parental material for maximum exploitation of heterosis. In contrast, L1xT4, L2xT4, L6xT4, L8xT1, L11xT2 and L12xT2 had significantly negative SCA effects for GY indicating that these crosses were poor specific combiners for grain yield. For DS, only a few crosses showed significant SCA effects in both directions. L8 x T1 and L11 x T3 showed significant and positive SCA effects, while L2 x T3 and L11 x T4 showed negative and significant SCA effects for this trait. The hybrids with low SCA for DS are desirable as they have earlier silking days than what is expected based on GCA of their parents.

Of the 48 test crosses, some of them showed significant SCA effects for PH and EH (Table 6). The crosses L2xT3, L4xT2, L6xT1 and L11x T3 had significant negative SCA effects for PH and could be considered the best cross combinations in view of having relative potential of tolerating lodging. Likewise, L1xT2, L4xT2, L6xT1, L8xT1 and L11xT4 had significant negative SCA effects for EH indicating that these cross combinations may be exploited for tolerance to lodging. L4xT4 and L11xT1 showed negative and significant SCA effects for PA, while L6xT3 and L12xT1 revealed positive and significant SCA effects for EA. The crosses that had negative values of SCA for EA and PA were considered as desirable crosses, as the higher scores of these traits indicates bad ear and plant characteristics. The crosses L7 x T4 and L9 x T2 showed positive and significant SCA effects for EPP. Thus, these crosses could be selected for their specific combining ability to improve EPP. In contrast, L1xT4, L2xT4 and L11xT2 showed negative SCA effects, indicating that these cross combinations are in undesired direction for prolificacy.

### Conclusion

This study identified one new inbred line and two tester inbred lines (L1, T3 and T4) that were good combiners for improvement of GY for highland maize breeding program. The three inbred lines and two inbred testers (L4, L8, L9, T2 and T3) having significant negative GCA effects for PH and EH identified in the current study can also be used as parents for short stature to reduce the grain yield loss caused by lodging. This study also identified two best cross combinations (L9xT4 and L11xT4) that exceeded the standard checks (Jibat and Kolba) in mean GY for further evaluation. The selected inbred lines from this study could be crossed to more testers and evaluated under more testing locations in order to get more information on Genotype x environment interactions of the lines for further use in the highland maize breeding program.

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