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Combining Ability Analysis of Maize Inbred Lines in Ethiopia

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Abstract

The study was initiated to estimate combining ability of maize inbred lines and crosses using line by tester analysis. Fifty entries consists 48 F1 single crosses developed from 24 inbred lines and 2 testers using line x tester design and two commercial check hybrids used in the study. The experiment was conducted using alpha lattice design with two replications. Analysis of variance revealed existence of significant genetic variation among genotypes for all studied traits except for plant aspect (PA). Location x entry interaction for most of the traits was not significant which suggests hybrid performance was consistent across tested locations. Line x tester analysis of variance showed that mean squares due to GCA of lines were significant ($p< 0.01$ or $p< 0.05$) for all studied traits. Mean squares of tester GCA and SCA were significant for most of studied traits. This indicates that both additive and non-additive gene effects had contributed for the variation of the crosses. However, higher proportional contribution of additive gene action for all studied traits was obtained. Several lines and crosses were identified as good general and specific combiners for yield and yield related traits. Lines L23, L11, L15 and crosses L2xT1, L3xT1, L8xT1, L11xT1, L23xT1 and L13xT2 were found to be good general and specific combiners, respectively. In conclusion, the stated inbred lines with desirable gca effects and cross combinations with desirable sca effects for grain yield and yield related traits could be used as useful genetic material.

Keywords: Combining ability, General combining ability, Specific combining ability, Inbred lines, Line by tester, Maize.

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Contents

Contribution of this paper to the literature

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1. Introduction

Maize (*Zea mays* L.) is a diploid (2n = 20) crop belongs to the family of grasses *Poaceae* and tribes *Maydeae* and naturally it is cross pollinated crop. The crop is grown over a wide range of environmental conditions. Maize has great world-wide importance as human food, industrial raw material and animal feed. Because of its high yield potential and wider adaptation, maize is one of the strategic crops for the achievement of food security. Prasanna, et al. [1] noted that the crop is a vital source of calorie, protein, and some important vitamins and minerals to billions of people world-wide, particularly in Africa, South America and Asia. Approximately 88% of maize produced in Ethiopia is consumed as food, both as green and dry grain. The per capita consumption is 50 kg per annum [2].

Maize is cultivated globally as one of most important cereal crops and ranks third next to wheat and rice. The total world production of maize is 1,068.79 MT, with the United States producing 384.78 MT, China 219.55 MT, Brazil 97.00 MT, European Union 60.71 MT, South Africa 16.40 MT and Ethiopia harvesting 6.35 MT of the total production of maize Foreign Agricultural Service (FAS) [3]. Central Statistical Agency (CSA) [4] reported that in Ethiopia by 2016/17 main cropping season out of the total grain crop area (12,574,107.33 hectare), 81.27% was under cereals of which maize share as large area as 16.98%, after tef (24%). Regarding total annual production, cereals contributed 87.42% (253,847,239.63 quintals) in which maize ranked first 27.02% (78,471,746.57 quintals) [4]. Over 5.8 million hectares of potential suitable land was identified for the highland maize hybrids in the country [5]. The crop is increasingly grown to the highlands of Ethiopia where it has been a minor crop in the past. Zeng, et al. [6] pointed out that increased productivity and production of maize has significant positive impact on poverty reduction in sub-Saharan African countries including Ethiopia.

Considering its importance, wide adaptation, total production and productivity, maize is one of the high priority crops to feed the increasing population of the country. However, national average yield in Ethiopia is still as low as 3.675t ha^{-1}[4] compared to that of the developed world 10.96t ha^{-1}[3] and this warrants the increasing maize productivity as high national priority issue. For such yield gap, a number of production constraints are responsible. The shortages of high yielding varieties or potential parent materials and the effect of biotic and abiotic stresses are the major constraints limiting maize production and productivity [2]. This implies the need for developing high yielding maize varieties from suitable parents and crosses which will perform well under stress and non-stress conditions.

Identification of suitable inbred lines and superior cross combinations require knowledge of combining ability. Information from combining ability (GCA and SCA) analysis can show the type of gene action involved in controlling quantitative characters thereby assisting breeders in selecting suitable parent materials and crosses [7]. Parental lines selection can be performed by particular mating designs such as line x tester, North Carolina (NC) designs I, II and III, and diallel. Line x tester analysis as suggested by Kempthorne [8]is useful in deciding the relative ability of female and male lines to produce desirable hybrid combinations [9]. Lines x tester programs have been applied to provide a systematic approach for the detection of suitable parents and crosses for investigated characters [10].

Combining ability has been studied in Ethiopia for different sets of new maize inbred lines [9, 11]. However, it is always mandatory for any breeding program to generate such information for any new batch of inbred lines developed or received outside of the program. In line with this, highland maize breeding program at Ambo Agricultural Research Center (AARC) in collaboration with CIMMYT recently developed inbred lines and crosses whose genetic information has not been studied. Hence, the study was conducted to evaluate the combing ability of inbred lines and their testcrosses.

2. Materials and Method

Description of Study Site: The experiment was conducted at Ambo and Holeta Agricultural Research Centers of the Ethiopian Institute of Agricultural Research (EIAR) during the main cropping season of 2017. Holeta Agricultural research center (HARC) is located at 09°04'12"N latitude and 38°29'45"E longitudes and an elevation of 2400 m.a.s.l. The center receives an average rainfall of 1102 mm per annum. The maximum and minimum temperatures of this site are 6°C and 22°C, respectively. The center has nitosols and vertisols soil types with pH of 6.0 [12].

Ambo Agricultural Research Center (AARC) is located at 8°57' N l and 37° 51' E and the elevation is 2225 m.a.s.l. The site receives an average rainfall of 1115mm. The maximum and minimum temperatures of this site are 11.7°C and 25.4°C, respectively. The soil type of Ambo is clay (heavy vertisols) with a pH of 7.8 [13].

2.1. Experimental Materials

The experiment consisted of 50 maize entries which include 48 testcrosses and two hybrid checks (AMH853 Kolba and AMH851-Jibat). The testcrosses (48) were generated from crossing of 24 inbred lines (female parents) with two testers (male parents) in line x tester mating design during 2015/2016 cropping season at Ambo Agricultural Research Center. The inbred lines were developed at Ambo Agricultural Research Center from CYMMYT materials using ear-to-row selection and subsequent selfing until they attain homozygosity. The testers used for the formation of the testcrosses were FS59 (Tester 1) and FS67 (Tester 2) Table 1. The first tester was from heterotic group "B", while the second was from heterotic group "A". The checks used in the study were AMH851 (Jibat) and AMH853 (Kolba) which are three-way cross hybrid varieties released by Ambo Agricultural Research Center, highland maize breeding program in 2011 and 2015, respectively. They take about 178 days for grain mature at Ambo and similar environments. Besides, hybrid checks are high yielding, tolerant/resistance to major maize disease in the country and well adapted to the altitude ranging from 1800-2600m in the highland sub-humid agro-ecological conditions of the country [14].

Table-1. List and pedigree of parents and hybrid checks used for the study.

SN	Line Code	Pedigree	Origin
1	L1	(CML442*/OFP4)-B-4-2-2-B-B-B-#	AMB16N42-29/AMB16N42-144
2	L2	(CML495*/OFP14)-7-1-5-1-1-B-B-#	AMB16N42-107/AMB16N42-144
3	L3	(CML442*/OFP4)-B-17-1-1-B-B-B-#	AMB16N42-32/AMB16N42-144
4	L4	(CML495*/OFP6)-B-27-1-1-B-#	AMB16N42-142/AMB16N42-144
5	L5	(CML539*/OFP14)-2-1-1-2-2-B-B-#	AMB16N42-16/AMB16N42-144
6	L6	(CML442*/OFP4)-B-17-5-1-B-B-B-#	AMB16N42-36/AMB16N42-144
7	L7	(CML395*/OFP105)-1-1-1-1-1-B-B-#	AMB16N42-38/AMB16N42-144
8	L8	(CML395*/OFP105)-1-2-3-1-1-B-B-#	AMB16N42-39/AMB16N42-144
9	L9	CML539*/OFP1)-B-11-2-2-B-B-B-#	AMB16N42-20/AMB16N42-144
10	L10	(CML444*/OFP23)-6-3-1-1-1-B-B-#	AMB16N42-44/AMB16N42-144
11	L11	(LPSC7-F96-1-2-1-1-B-B-B*/OFP9)-3-2-1-1-1-	AMB16N42-2/AMB16N42-144
12	L12	(CML444*/OFP14)-3-2-4-1-2-B-B-#	AMB16N42-47/AMB16N42-144
13	L13	(CML444*/OFP4)-B-4-1-1-B-B-B-#	AMB16N42-50/AMB16N42-144
14	L14	(CML444*/OFP4)-B-6-1-1-B-B-B-#	AMB16N42-51/AMB16N42-144
15	L15	(CML537*/OFP106)-6-1-3-1-2-B-B-#	AMB16N42-53/AMB16N42-144
16	L16	(CML537*/OFP106)-7-1-2-1-2-B-B-#	AMB16N42-56/AMB16N42-144
17	L17	(CML491*/OFP4)-B-10-1-2-B-B-B-#	AMB16N42-88/AMB16N42-144
18	L18	CML546-#	AMB16N42-61/AMB16N42-144
19	L19	([SYN-USAB2/SYN-ELIB2]-12-1-1-1-B*4-B-	AMB16N42-62/AMB16N42-144
20	L20	([CML312/[TUxPSEQ]C1F2/P49-SR]F2-	AMB16N42-75/AMB16N42-144
21	L21	([CML444/CML395//DTPWC8F31-1-1-2-2-	AMB16N42-65/AMB16N42-144
22	L22	([CML444/CML395//DTPWC8F31-1-1-2-2-	AMB16N42-66/AMB16N42-144
23	L23	(LPSC7-F71-1-2-1-2-B-B-B*/OFP2)-B-1-3-2-	AMB16N42-8/AMB16N42-144
24	L24	[CML444/CML395//DTPWC8F31-1-1-2-2-	AMB16N42-69/AMB16N42-144
		Tester	
25	T1	FS59	Heterotic group
26	T2	FS67	Heterotic group
		Checks	
27		JIBAT	3-way hybrids
28		KOLBA	3-way hybrids

2.2. Experimental Design and Procedure

The experimental materials along with two hybrid checks were grown during the 2016/2017 main cropping season using alpha lattice design [15] with two replications, 10 incomplete blocks and 5 plots per the incomplete blocks at both locations. Each entry was planted in a single row plot of 5.25m length with a spacing of 75cm between rows and 25cm between plants. Seeds were planted with two seeds per hill and later thinned to one plant at four leaf stage.

2.3. Data Collection and Analysis

Data were collected days to 50% anthesis (AD), days to 50% silking (SD), anthesis-silking interval (ASI), ear aspect (EA), plant aspect (PA), grain yield (GY), number of ear per plant (EPP) and thousand kernel weight (TKW) on plot basis. On plant basis data were collected on plant height (PH), ear height (EH), ear length (EL), ear diameter (ED), number of kernel rows per ear (KRPE) and number of kernels per row (KPR). Plant aspect and ear aspect were measured in 1 to 5 scales.

The data obtained for different traits from field measurements were organized and analyzed using SAS statistical package [16]. Analysis of variance across location was conducted with PROC GLM procedure by considering location, replication and blocks as random and entry/genotype as fixed factors with statement of RONDOM and TEST option. The significance of mean squares for entries, crosses, and location in combined analysis were tested against the mean squares for their corresponding interaction with location as error term, while their interaction with location were tested against their corresponding pooled error. Based on general analysis of variance, traits that showed significant differences among the entries were further analyzed according to line x tester analysis [8] using analysis of genetic designs with R (AGD-R) version 3.0 procedures for individual and combined data [17].

2.4. Estimation of Combining Ability Effects

Genotypic means of individual locations were used for the determination of GCA and SCA. The GCA effects of lines (L) and testers (T), the SCA effect of LxT, and their interactions with the environment were determined following the method stated by Kempthorne [8] assuming the following model.

Yijke= μ + Le + R (L) ke +Vij+ (LV) ije +Ɛijke Where, Yijke = observed value from each experimental unit; μ = grand mean; Le = location effect; Rke = replication effect within each location Vij = F_1 hybrid effect = gi+gj+sij, where, gi = general combining ability of i^{th} lines; gj = general combining ability of j^{th} tester; sij = specific combining ability of $ij^{th}F_1$ hybrids; (LV) ije = interaction effect of ij^{th} F_1 hybrid and e^{th} location Ɛijke = residual effect.

The Significance of GCA and SCA effects were performed computing the standard error for lines, testers and crosses and then tested against t-test by taking the degree of freedom of pooled error mean square [18, 19]. The proportional contributions of lines (GCAL), testers (GCAT), and their interaction (SCA LxT) to the sum square of crosses were calculated as the ratio between sum of squares of each component and the cross sum of squares as given [19].

3. Results and Discussion

The analysis of variance and general and specific combining ability effects were computed and the results are discussed below.

3.1. Analysis of Variance

The analysis of variances for yield and yield related traits for individual and combined location are presented in Appendix 1, 2 and Table 2. Significant differences were detected between the two locations for all of the studied traits except for ear length, indicating that the two locations differed in the environmental conditions to cause variation which agreed with the finding of Aly and Khalil [20]. Entry difference were significant (p<0.01 or p<0.05) for all traits except for plant aspect Table 2. Entries differed in their performance from one location to another for variable like grain yield, plant and ear height, ear diameter and 1000 kernels as entry x location interaction was significant. Beyene, et al. [21] and Murtadha, et al. [22] also reported significant entry x location interaction effect for some yield and its components in maize and indicated presence of wide variability with regard to tested entry and locations. The result showed the location played significant role in the variation of these traits. If significant genotype x location interaction mean squares existed, different genes involved in controlling the traits show the inconsistency of the genes over locations [23]. The interaction of entry with location suggests further evaluation of the genotypes across more number of locations to minimize environmental effect from computation genetic variance.

Table-2. Analysis of variance for yield and yield related traits of 48 testcross and two hybrid checks evaluated at Holeta and Ambo, 2017.

Trait	L, df=1	Re(L)df=2	B(L*R) df=36	Ent df=49	Ent*L df=49	Error df=62	Mean±SE(m)	CV%	R^2
GY	8.38*	0.03	1.29	4.41*	2.63**	1.1	7.53± 0.52	13.9	0.86
AD	14162.4**	24.23**	2.96	13.33**	2.77	3.18	104.52±0.89	1.71	0.99
SD	18489.6**	19.34**	2.60	15.66**	2.51	3.31	105.15±0.91	1.73	0.99
ASI	0.63**	0.001	0.005	0.007*	0.005	0.004	1.2± 0.03	5.52	0.86
PH	574.6**	779.0**	161.6	1631.89**	237.4*	139.1	251.07±5.9	4.70	0.93
EH	5724.5**	398.33**	45.04	943.11**	85.85*	54.64	136.66±3.7	5.41	0.95
EPO	0.07**	0.0002	0.001	0.004**	0.0007	0.002	0.54±0.02	7.33	0.79
EPP	1.49**	0.007	0.03	0.13**	0.05	0.03	1.70±0.09	10.18	0.86
EA	0.78*	0.91**	0.13	0.43**	0.19	0.13	3.12±0.18	11.56	0.84
PA	2.88**	0.75*	0.15	0.20	0.14	0.20	3.30±0.22	13.69	0.70
EL	1.69	8.82**	0.98	3.61**	1.21	0.81	15.47±0.45	5.82	0.88
ED	1.62**	0.004	0.03	0.10**	0.03**	0.03	4.32±0.09	3.84	0.86
KRPE	10.76**	0.58	0.63*	1.21**	0.47	0.37	12.86±0.3	4.74	0.86
KPR	19.22*	25.22**	7.43*	8.51**	6.50	4.22	32.3±1.03	6.37	0.83
TKW	193827.8**	27.26	743.1	3102.2**	1603.9*	947.3	305.0±15.39	10.09	0.90

3.2. Combining Ability Analysis

Significant differences (p<0.01, or p<0.05) were observed among the crosses for all traits except for anthesis-silking interval at Holetta and for number of kernels per row at Ambo Appendix 3 and 4. At Ambo, GCA mean squares due to lines were significant (p<0.01, or p<0.05) for most of the studied traits except for ear position and ear aspect, while tester GCA mean squares were significant (p<0.01, or p<0.05) for days to 50% silking, anthesis- silking interval, plant and ear height, ear aspect and 1000 kernels weight Appendix 3. Similarly, SCA mean squares for line x tester were significant for grain yield, ear height, ear position and ear aspect. At Holetta, GCA mean squares of lines and testers were significant (p<0.01, p<0.05) for all traits except for ear length, anthesis silking interval and number of kernels per row and GCA of tester for days to 50% anthesis, number of kernels per row and 1000 kernels weight. The mean squares of SCA line x testers were also significant (p<0.01, or p<0.05) for seven traits and non-significant for other seven studied traits Appendix 4. This indicates both additive and non-additive gene actions with different level from location to location were involved in the inheritance of these traits. The observed differences in the level of significance of GCA and SCA mean squares with changing locations were an indication of environmental effect on the preponderance of additive and non-additive gene action. Zare, et al. [24] reported the different level of GCA and SCA mean square for different testing environment. In contrast, Haddadi, et al. [25] found no environmental effect on the preponderance of additive and non-additive gene action. The significance of mean squares due to lines and testers indicated inbred lines variation among the lines and tester in their performance. Meanwhile, significant line x tester interaction suggests that inbred lines performed differently according to the testers to which they were crossed.

Combined analysis of line x tester showed highly significant (p<0.01) difference among cross for all studied traits Table 3a and 3b. Cross x location interaction were significant (p<0.01, or p<0.05) for most traits except for days to 50% anthesis, anthesis silking interval and ear position. This indicates the presence of wide genetic variations among the studied materials. These findings are in agreement with those reported by Aly and Hassan [26]; Aly and Khalil [20] and Mousa [27]. The mean squares of GCA lines and testers and SCA were significant (p<0.01, or p<0.05) for all traits except GCA of testers for days to 50% anthesis, number of ear per plant and ears aspect, and SCA for anthesis silking interval, number of ears per plant, number of kernel rows per ear and ear diameter, which confirms to the finding of Mohammad, et al. [28] and Dar, et al. [29]. Significant GCA and SCA mean squares indicate that both additive and non-additive gene effects were involved for the variation of crosses through all studied traits. However, higher GCA proportional contribution and GCA/SCA ratio greater than unit indicated predominance of additive gene action for all studied traits. This indicates that variations among crosses through all the studied traits were mainly due to additive gene effect which was in accordance with the finding of Amare, et al. [30]. Adebayo and Menkir [31];Satyanvesh [32];Tolera, et al. [11] have earlier reported that additive gene actions were more important than non-additive gene actions for inheritance of grain yield and yield related traits. However, Aminu, et al. [33] and Arsode, et al. [34] reported that non-additive gene action was predominated in the inheritance of these traits. Based on current findings, the inheritance of all traits was governed by additive gene effect, suggesting selection would be effective in improving yield and yield related traits.

GCA line x location interaction was significant ($p<0.01$, or $p<0.05$) for traits such as grain yield, ear height, number of ears per plant, ear length and number of kernels row/ear, while GCA tester x location interaction effect showed significant for all studied traits except for days to 50% anthesis and silking, ear position and ear length Table 3aand 3b. These suggest that the lines and testers were depended on the location in which they were grown and limited number of testing location would be insufficient. Comparable results were reported Aly [35]; Fan, et al. [36] and Noelle, et al. [37] for the materials they studied. On the contrary, non-significant GCA x location interaction mean squares were reported by Alemeshet [38]. Significant GCA x location interaction implies that the trend of variation of GCA of lines and testers were different across location and selection for good combining lines would be effective if based on hybrid performance across a range of environment. This also suggests the need for selecting inbred lines at specific locations. However, mean squares of SCA x location interaction were non-significant for all investigated traits which were in agreement with the finding of Dagne, et al. [39]; Adebayo and Menkir [31] and Fan, et al. [36]. But, Tulu, et al. [40] for grain yield and ear per plant, Noelle, et al. [37] for days to 50% silking and ear aspect and Mosa, et al. [41] for ear length, number of rows per ear and number of kernels per row found significant SCA x location interaction.

Table-3a. Analysis of variance and heritability for yield and yield related traits of 48 testcrosses and two commercial hybrid checks evaluated at Ambo and Holeta, 2017.

Source	df	GY t/ha	AD day	SD day	ASI day	PH cm	EH cm	EPO %
Loc	1	7.76*	12661**	17787**	193**	351.72	5184 **	0.067**
Rep(Loc)	2	0.06	23.07**	18.89**	0.32	403.86	357.6 **	0.000
Cross	47	5.20**	13.92**	18.23**	3.03*	1952.07**	1208.2 **	0.005**
Line(GCA)	23	5.92**	21.48**	25.75**	2.30*	1019.01**	772.4**	0.006**
Tester(GCA)	1	22.07**	10.45	105.02**	47.51**	59791.93**	33769 **	0.033**
Line xTester	23	3.75**	6.50*	6.94**	1.82	370.08**	228**	0.002
Cross x Loc	47	2.57**	3.90	4.38*	1.90	221.59*	96.49*	0.001
Line x Loc	23	2.81**	4.08	4.60	1.39	205.39	93.50 *	0.001
Tester x Loc	1	20.90**	0.31	14.08*	17.06**	2665.16**	1307**	0.001
L x T x Loc	23	1.54	3.87	3.75	1.75	131.55	46.84	0.001
GCA/SCA		1.83	3.38	4.37	2.40	9.78	9.82	4.67
Error	58	1.07	3.14	3.16	1.65	129.31	52.26	0.001
Pro. Cont (%)								
L		55.66	75.55	69.11	37.20	25.55	31.29	67.33
T		9.02	1.60	12.25	33.38	65.17	59.47	15.04
LxT		35.32	22.85	18.64	29.42	9.28	9.24	17.63
h^2_b		28.19	68.26	71.21	34.45	84.65	88.76	80

Table-3b. Analysis of variance and heritability for yield and yield related traits of 48 testcrosses and two commercial hybrid checks evaluated at Ambo and Holeta, 2017.

Source	df	EPP no	EA scale	EL cm	ED cm	KRPE no	KPR no	TKW gm
Loc	1	1.35**	1.01**	1.88**	1.08**	4.20**	5.83	186083**
Rep(Loc)	2	0.006	0.67*	6.69**	0.01	0.18	7.21	14.33
Cross	47	0.147**	0.51**	4.74**	0.11**	1.30**	9.43**	3885.10**
Line(GCA)	23	0.229**	0.80**	7.36**	0.18**	1.53**	11.68**	5356.10**
Tester(GCA)	1	0.193*	0.05	0.88	0.34**	11.79**	10.46	34114.7**
Cross x Loc	47	0.050*	0.21*	1.33*	0.04*	0.57*	6.31*	1909.8**
Line x Loc	23	0.055*	0.18	1.55*	0.04	0.62*	6.84	1256.1
Tester x loc	1	0.188*	1.94*	2.59	0.65**	1.87*	1.90	26660.1**
LxT x Loc	23	0.039	0.17	1.05	0.02	0.47	5.96	1486.45
GCA/SCA		3.45	3.28	3.23	5.09	3.37	1.70	6.21
Error	58	0.031	0.13	0.85	0.02	0.36	3.96	820.01
Pro.cont (%)								
L		74.55	76.39	76.027	77.16	57.76	60.65	67.46
T		2.99	0.22	0.003	6.42	19.32	2.36	18.68
LxT		22.45	23.39	23.64	16.42	22.89	37.04	13.86
h^2_b		58.43	50.85	65.33	53.85	48.34	26.49	39.72

3.3. General Combining Ability Effect

Estimates of *gca* effects of 24 inbred lines and two testers for combined data of yield and yield related traits are presented in Table 4aand 4b. Out of 24 lines, three of them had positive and highly significant *gca* effects and six lines exhibited negative and significant ($p<0.01$, or $p<0.05$) *gca* effects for grain yield. Line L23 showed maximum *gca* effect (1.64t ha^{-1}) followed by L11 (1.50t ha^{-1}), whereas L13 revealed lowest *gca* effect (-1.57t ha^{-1}) followed by L3 (-1.31t ha^{-1}). This depicts the presence of best and poorest general combiners in the group of the studied inbred lines. L23, L11 and L15 found to be good general combiners suggesting their ability to transmit additive genes in desirable direction for grain yield. L3, L7, L13, L21, L18 and L19 found to be poor general combiners as they had tendency to reduce grain yield. Among the testers, FS59 revealed significantly positive *gca* effect. Several researchers Girma, et al. [9]; Natol [42] reported both positive and negative significant *gca* effects for maize grain yield in different set of materials. High GCA effects are attributed to additive or additive x additive gene effects which denote the fixable genetic components of variance [43]. The inbred lines with good general combining ability can make complementary single cross which can be used as seed parent for three-way or double cross hybrid development.

For days to 50% anthesis and silking, *gca* effects of inbred lines ranged from -2.81 to 2.70 and -2.89 to 3.49 Table 4a, respectively. L3, L7, L10, L13, L14 and L22 showed positive *gca* effects, while lines L1, L4, L5, L9 and L18 had negative *gca* effects for both traits. Lines *gca* effect for anthesis- silking interval ranged from -1.41 (L12) to 1.06 (L3) and tester *gca* effects for anthesis-silking interval were -0.5 (T2) to 0.5 (T1). Despite the importance of negative *gca* effects for anthesis-silking interval, only L12 was found to be good general combiner. Negative and significant line *gca* affects for days to 50% anthesis and silking, and anthesis silking interval suggests the possibility of exploiting favorable genes for earliness to maturity and narrower anthesis silking interval in future breeding work. Similarly, Sundararajan and Kumar [44] and Demissew [13] suggested the importance of the negative *gca* effects for days to 50% anthesis and silking to develop early maturing varieties.

For plant and ear height, L1, L5, L10, L12, and L14 revealed positive and significant lines *gca* effect, while L2, L8, L13, L18 and L22 showed negative and significant *gca* effects. Inbred lines with negative *gca* effects are good general combiners for plant and ear height. Girma, et al. [9] concluded that shorter plant height with lower ear placement is desirable. Inbred lines with negative *gca* effect had tendency to reduce plant and ear height, hence genotypes with shorter plant height with lower ear placement can be good for lodging resistance. Ji, et al. [45] also noted that cultivars with high ear positions are prone to root and stalk lodging and suggested that negative significant lines *gca* effects are desirable shorter stature and lower ear placement.

Significant *gca* effects of inbred lines ranged from -0.37 (L18) to 0.40 (L23) for number of ear per plant, -1.71 (L13) to 2.06 (L15) for ear length, -0.24 (L7) to 0.27 (L10) for ear diameter, -0.83 (L17) to 0.73 (L20) for number of kernel rows per ear and -3.02 (L1) to 2.27 (L4) for number of kernels per rows Table 4b. L1, L9, L23 and L24 for number of ears per plant, L4, L7, L8, L10, L12, L14, L15 and L24 for ear length, L4, L10, L11, L12, L14, L20 and L21 for ear diameter and L8, L10, L11, L14, L20 for number of kernel rows per ear and L4 and L15 for number of kernels per rows showed positive and significant *gca* effects. On the other hand, L4, L8, L13, L18, L20 and L21 for number of ears per plant, L1, L9, L11, L13 and L19 for ear length, L1, L7, L16, L17, L19, L22, L23 and L24 for ear diameter, L2, L5, L16, L17, L21 and L22 for number of kernel rows per ear and L1, L3 and L9 for number of kernels per row revealed negative and significant line *gca* effect. Ejigu, et al. [46] also reported certain inbred lines with good general combing ability and suggested the possibility of improving these traits through selection. The present study also identified inbred lines with good general combing ability which could be used for the improvement of traits of interest as these lines had potential to transfer favorable genes to their progenies.

The range of lines *gca* effect for 1000 kernels weight varied from -45.84 (L7) to 77.36 (L21). Inbred lines L11, L14, L21 and L22 had positive and significant line *gca* effects, while L2, L7, L9, L13, L15 and L19 showed negative and significant line *gca* effects. Hence, L11, L14, L21 and L22 were good general combinersand had favorable allele frequency for developing varieties with heavy grain weight.

Concerning testers, FS59 was a good general combiner for grain yield, ear diameter, number of kernels row per ear and 1000 kernels weight. Likewise, FS67 found to be good general combiner for days to 50% silking, anthesis-silking interval, plant height, ear height and ear position. Generally, inbred lines and testers with good general combiners could be utilized in the improvement of traits of interest either during hybrid or synthetic variety development.

Table-4a. Estimates of general combining ability (*gca*) effect of lines and testers for yield and yield related traits across two locations, 2017.

Lines	GY t/ha	AD days	SD days	ASI days	PH cm	EH cm	EPO ratio
L1	0.45	-2.05**	-2.26**	-0.30	10.26*	7.72**	0.01
L2	-0.30	-1.06	-1.01	0.13	-15.83**	-11.77**	-0.01
L3	-1.31**	2.57**	3.49**	1.06*	-5.15	-3.65	0.00
L4	-0.08	-2.05**	-1.64*	0.85	10.30*	2.10	-0.02
L5	0.72	-2.81**	-2.39**	-0.08	27.22**	11.86**	-0.01
L6	-0.64	-0.68	-1.51*	-0.83	-2.32	1.71	0.01
L7	-0.86*	2.70**	2.99**	0.23	-5.81	4.72	0.04**
L8	-0.07	-0.17	0.61	0.74	-10.37*	-8.79**	-0.02
L9	0.39	-2.30**	-2.89**	-0.57	1.82	-9.02**	-0.04**
L10	0.68	1.57*	1.61*	0.05	13.92**	8.72**	0.00
L11	1.50**	1.58*	1.24	-0.29	3.97	8.97**	0.03*
L12	0.37	1.95**	0.61	-1.41**	9.59*	21.11**	0.06**
L13	-1.57**	1.95**	2.11*	0.13	-14.11**	-13.40**	-0.02
L14	0.31	2.32**	2.74**	0.47	13.19**	5.97*	0.00
L15	1.26**	0.33	0.86	0.49	3.42	4.83	0.01
L16	0.05	-0.68	-0.89	-0.24	6.50	11.37**	0.03*
L17	-0.08	-1.18	-1.39*	-0.26	7.62	6.10*	0.01
L18	-0.78*	-1.55*	-1.64*	-0.11	-16.52**	-8.65**	0.00
L19	-1.13**	-0.31	-0.26	0.09	-20.87**	-2.90	0.05**
L20	0.22	-0.30	-0.14	0.35	-4.47	-1.27	0.00
L21	-1.15**	0.20	-0.39	-0.64	5.51	5.22*	0.01
L22	-0.16	1.57*	1.74**	0.28	-10.03*	-12.52**	-0.03*
L23	1.64**	-1.05	-1.14	-0.16	-4.89	-12.52**	-0.04**
L24	0.57	-0.56	-0.51	0.06	-2.17	-15.91**	-0.06**
SE	0.36	0.63	0.63	0.45	4.02	2.56	0.01
Tester							
T1	0.34**	0.24	0.74**	0.51**	18.39**	13.28**	0.01**
T2	-0.33**	-0.24	-0.74*	-0.51 **	-18.33**	-13.28**	-0.01**
SE	0.11	0.26	0.18	0.13	1.16	0.74	0.004

Note: **Significant ($p<0.01$), *significant ($p<0.05$), L=line, T=tester, SE= standard error, GY=grain yield, AD=anthesis days, SD=silking days, ASI=anthesissilking interval, PH=plant height, EH=ear height, EPO=ear position.

Table-4b. Estimates of general combining ability (*gca*) effect of lines and testers for yield and yield related traits across two locations, 2017.

LINES	EPP no	EA scale	EL cm	ED cm	KRPE no	KPR no	TKW gm
L1	0.24**	-0.26*	-1.54**	-0.13**	-0.21	-3.02**	-12.62
L2	0.11	0.55**	-0.58	-0.08	-0.44*	0.59	-24.07*
L3	-0.05	0.06	-0.56	-0.11	0.38	-1.98**	-4.06
L4	-0.14*	-0.38**	0.81*	0.16**	0.36	2.27**	4.85
L5	0.06	-0.32*	0.29	0.02	-0.63**	0.38	1.95
L6	0.05	-0.56**	-0.41	0.09	0.35	-0.38	-8.94
L7	-0.02	0.56**	1.05**	-0.24**	-0.07	0.51	-45.84**
L8	-0.16*	0.00	0.98**	0.01	0.50*	0.91	18.04
L9	0.16*	0.32*	-1.64**	0.03	0.37	-2.14**	-26.96**
L10	-0.05	-0.44**	0.92**	0.27**	0.48*	1.02	7.06
L11	0.05	0.62**	-1.34**	0.19**	0.54*	-0.30	31.41**
L12	0.04	0.18	0.73*	0.11*	-0.12	1.20	29.04**
L13	-0.19**	0.06	-1.71**	0.10	-0.07	-0.75	-21.20*
L14	0.02	-0.13	0.97**	0.11*	0.54*	0.57	-12.61
L15	0.01	-0.32*	2.06**	0.06	0.39	2.10**	-21.46*
L16	0.05	0.25	-0.44	-0.11*	-0.66**	-0.48	-15.47
L17	0.03	0.05	-0.08	-0.16**	-0.83**	-1.23	12.36
L18	-0.37**	-0.38**	0.19	0.10	-0.01	0.50	-3.44
L19	-0.13	-0.01	-0.85*	-0.21**	0.18	-0.02	-35.00**
L20	-0.18**	0.06	0.42	0.20**	0.78**	0.73	14.49
L21	-0.19**	0.06	0.04	0.13**	-0.64**	-1.06	77.36**
L22	0.07	0.12	0.16	-0.22**	-0.65**	-0.83	22.73*
L23	0.40**	0.00	-0.27	-0.15**	-0.27	0.64	3.06
L24	0.15*	-0.12	0.82*	-0.18**	-0.31	1.19	9.30
SE	0.06	0.13	0.32	0.05	0.21	0.70	10.12
Tester							
T1	0.03	-0.02	0.06	0.04**	0.26**	0.25	-13.33**
T2	-0.03	0.02	-0.06	-0.04**	-0.26**	-0.21	13.33**
SE				0.02	0.06		2.92

Note: **Significant (p<0.01), *significant (p<0.05), L=line, T=tester, SE= standard error, EPP=ear per plant EA=ear aspect EL=ear length ED=ear diameter, KRPE=kernel rows per ear, KPR=kernels per rows, TKW=thousand kernels weight.

3.4. Specific Combining Ability Effect

Estimates of specific combining ability (*sca*) effects for grain yield and yield related traits for all hybrids computed across locations are presented in Table 5aand 5b. Crosses L2 x T1 (1.03), L3 x T1 (1.04), L8 x T1 (1.10), L11 x T1 (1.14), L13 x T2 (1.64) and L23 x T1 (1.64) are exhibited significant positive *sca* effects for grain yield. Crosses like L2 x T2 (-1.03), L3 x T2 (-1.04), L8 x T2 (-1.10), L11 x T2 (-1.14), L13 x T1 (-1.64) and L23 x T2 (-1.64) found to be poor specific combiners which could be due to the presence of unfavorable gene combinations in the parents. The positive *sca* effects indicate lines were from opposite heterotic group, while negative sca affects refer lines were from the same heterotic group. For instance, cross L2 x T1 showed significant positive *sca* effect, but had lower grain yield than standard checks. The high positive and significant *sca* effects were manifested by crosses of low x low (L13 x T2 and L3 x T2), low x high (L2 x T1 and L8 x T1) and high x high (L23 x T1, L11 x T1), indicating the presence of complementary gene action for grain yield. Inbred lines L3, L2, L13 and T2 had poor general combining ability, but resulted in hybrids with higher *sca* effects for grain yield. This signifies that inbred lines with poor general combining ability might produce better hybrids depending on the other parent with which it combines.

The *sca* effects of days to 50% anthesis (AD) and silking (AD) ranged from -1.98 (L16 x T1) to 1.98 (L16 x T1) and -2.14 (L21 x T2) to 2.14 (L22 x T1), respectively. Crosses such as L13 x T2, L16 x T1 and L21 x T2 revealed negative and significant *sca* effects for days to 50% anthesis and silking, while L13 x T1, L16 x T2 and L21 x T1 showed positive *sca* effects. Crosses with negative and significant *sca* effects for these traits are considered as good specific combiners, which indicate the earliness of the hybrids. On the other hand, crosses with positive and significant *sca* effects were found to be poor specific combiners, mainly for highland condition due to lateness. Inbred lines with negative and significant *gca* effects did not necessarily produced crosses with negative and significant *sca* effects. But, tester FS59 had negative and significant *gca* effect and interacted well with L21 and L13 in cross combination thereby resulted in crosses with negative and significant *sca* effects. The interactions involved in the crosses were poor x good general combiners (L13 x T1 and L21 x T1) and poor x poor (T16 x T2).

Crosses L9 x T1, L16 x T2 and L21 x T1 had negative and significant *sca* effects for plant and ear height considered as good specific combinations. These crosses involved parents with general combiners of good x poor, poor x good and poor x poor *gca* effects. L13 x T2, L16 x T1 and L21 x T2 for plant height and L9 x T2, L10 x T1, L12 x T2, L16 x T2 and L21 x T1 for ear height showed positive and significant *sca* effects, indicating that these crosses were poor specific combination for these traits. Accordingly, good specific combination could be utilized in developing lodging resistance hybrids. Positive *sca* effects for plant and ear height indicates crosses had tendency to increase height in undesirable direction.

Crosses L8 x T1 for number of ears per plant, L9 x T1, L10 x T2 and L14 x T1 for ear length and L11 x T2 for number of kernels per row had significant and positive *sca* effects. The crosses involved parent interaction of poor x poor, good x poor and good x poor based on their *gca* effects. L8 x T2 for number of ears per plant, L9 x T2, L10 x T1 and L14 x T2 for ear length and L11 x T1 for number of kernels per row showed significant and negative *sca* effects. The crosses exhibiting significant and positive *sca* effects are considered as good specific combiners. The crosses that showed significant and negative *sca* effects found to be poor specific combiners. Moreover, crosses with positive and significant *sca* effects had inbred lines with positive (L10 and L14) and negative (L9) *gca* effect.

Finally, based on the *gca* effects of parents, and *sca* effects hybrids for different traits, it is evident that high specific combinations involved, Inbred lines with high x high, high x low and low x low *gca* effects. The *sca* effects of crosses combinations exhibited no specific trends in cross combinations between parents having good and poor *gca* effects. This indicates high specific combiners were not only obtained from the combination of good x good general combiners, but also resulted from good x poor and poor x poor general combiners. The superiority of hybrids resulted from the crosses of high x low combiners could be due to interactions between positive alleles and negative alleles from good and poor combiners, respectively. The best performance of these combination may be caused by additive x additive (high x high), additive x dominance (high x low), or dominance x dominance (low x low) gene interactions Dey, et al. [47]; Talukder, et al. [48]. Zhang, et al. [49] suggested that hybrids with high *sca* effects from parents with low *gca* effects might be primarily due to non-additive gene action which includes dominance and epistasis. For some of the studied traits, high *gca* effect parents resulted into hybrids with low *sca* effect which might be due to the lack of complementary of gene action. On the other hand, low*gca* effect parents produced hybrids with high *sca* effects which might be caused by complementation of gene actions. Generally, the crosses identified were best specific combiners for yield and yield related traits which can be used in the heterosis breeding.

Table-5a. Estimates of specific combining abilities of line x tester for yield and yield related traits across two location, 2017.

S/N	CODE	GY t/ha	AD days	SD days	PH cm	EH cm	EPP no
1	L1xT1	-0.14	-0.11	0.01	-0.91	2.22	-0.03
2	L1xT2	0.13	0.11	-0.01	0.85	-2.22	0.03
3	L2xT1	1.03*	1.12	0.26	1.86	-4.52	-0.02
4	L2xT2	-1.03*	-1.12	-0.26	-1.93	4.52	0.02
5	L3xT1	-1.04*	-0.12	-0.24	-4.16	-2.41	-0.01
6	L3xT2	1.04*	0.12	0.24	4.09	2.41	0.01
7	L4xT1	-0.17	0.03	-0.11	-4.46	-0.63	0.09
8	L4xT2	0.17	-0.03	0.11	4.40	0.63	-0.09
9	L5xT1	0.30	0.39	-0.11	-3.85	0.34	-0.07
10	L5xT2	-0.31	-0.39	0.11	3.78	-0.34	0.07
11	L6xT1	0.56	0.02	-0.74	-3.13	-4.54	0.00
12	L6xT2	-0.56	-0.02	0.74	3.06	4.54	0.00
13	L7xT1	-0.58	-0.85	-0.24	2.10	-2.03	-0.13
14	L7xT2	0.58	0.85	0.24	-2.17	2.02	0.13
15	L8xT1	1.10*	0.01	0.14	7.63	2.97	0.26**
16	L8xT2	-1.10*	-0.01	-0.14	-7.70	-2.97	-0.26**
17	L9xT1	0.18	-0.86	-0.11	-10.57**	-9.27**	0.05
18	L9xT2	-0.18	0.86	0.11	10.51**	9.27**	-0.05
19	L10xT1	-0.72	0.76	0.89	5.60	7.72*	-0.03
20	L10xT2	0.72	-0.76	-0.89	-5.66	-7.72*	0.03
21	L11xT1	1.14**	0.00	0.51	4.01	2.48	0.01
22	L11xT2	-1.14	0.00	-0.51	-4.07	-2.48	-0.01
23	L12xT1	0.34	0.64	0.89	2.29	12.86**	0.03
24	L12xT2	-0.34	-0.64	-0.89	-2.36	-12.86**	-0.03
25	L13xT1	-1.64**	1.88*	1.89*	-11.57**	-5.67	-0.04
26	L13xT2	1.64**	-1.88*	-1.89*	11.51**	5.66	0.04
27	L14xT1	0.55	-0.23	-0.49	4.36	3.48	0.08
28	L14xT2	-0.55	0.23	0.49	-4.43	-3.48	-0.08
29	L15xT1	-0.04	0.76	0.14	1.56	2.61	-0.06
30	L15xT2	0.04	-0.76	-0.14	-1.63	-2.61	0.06
31	L16xT1	0.94	-1.98*	-2.11*	14.87**	9.61**	-0.05
32	L16xT2	-0.94	1.98*	2.11*	-14.93**	-9.61**	0.05
33	L17xT1	-0.73	-0.27	-0.11	4.03	0.09	-0.15
34	L17xT2	0.72	0.27	0.11	-4.09	-0.09	0.15
35	L18xT1	0.53	-0.87	0.39	9.55	2.35	0.00
36	L18xT2	-0.53	0.87	-0.39	-9.62	-2.35	0.00
37	L19xT1	0.03	-0.86	-1.24	-5.79	-4.90	0.04
38	L19xT2	-0.03	0.86	1.24	5.72	4.90	-0.04
39	L20xT1	0.29	-0.88	-1.11	7.64	1.97	0.10
40	L20xT2	-0.30	0.88	1.11	-7.70	-1.97	-0.10
41	L21xT1	-0.56	1.62*	2.14*	-12.70**	-8.02*	-0.11
42	L21xT2	0.56	-1.62*	-2.14*	12.63**	8.02*	0.11
43	L22xT1	-0.17	1.03	0.76	3.72	-5.26	0.09
44	L22xT2	0.17	-1.03	-0.76	-3.79	5.26	-0.09
45	L23xT1	1.64**	-0.37	-0.86	-4.70	0.96	0.06
46	L23xT2	-1.64**	0.37	0.86	4.64	-0.97	-0.06
47	L24xT1	-0.87	-0.87	-0.49	-8.17	-2.41	-0.08
48	L24xT2	0.87	0.87	0.49	8.11	2.41	0.08
SE(d)		0.52	0.89	0.89	5.69	3.23	0.09

Note: **Significant (p<0.01), *significant (p<0.05), SE= standard error, GY=grain yield, AD=anthesis days, SD=silking days, PH=plant height, EH=ear height,

Table-5b. Estimates of specific combining abilities of line x tester for yield and yield related traits across two location, 2017.

S/N	CODE	EA scale	EL cm	KPR no	S/N	CODE	EA scale	EL cm	KPR no
1	L1xT1	0.02	-0.45	0.73	25	L13xT1	-0.05	-0.42	0.60
2	L1xT2	-0.01	0.45	0.73	26	L13xT2	0.05	0.42	-0.60
3	L2xT1	-0.04	0.27	-0.21	27	L14xT1	-0.10	1.03*	1.54
4	L2xT2	0.04	-0.27	0.21	28	L14xT2	0.10	-1.03*	-1.54
5	L3xT1	-0.05	0.26	0.16	29	L15xT1	-0.05	-0.80	0.52
6	L3xT2	0.05	-0.26	-0.16	30	L15xT2	0.05	0.80	-0.52
7	L4xT1	0.02	-0.13	0.08	31	L16xT1	-0.11	0.27	0.42
8	L4xT2	-0.02	0.13	-0.8	32	L16xT2	0.11	-0.27	-0.42
9	L5xT1	-0.42*	-0.03	0.22	33	L17xT1	-0.04	0.75	0.91
10	L5xT2	0.42*	0.03	-0.22	34	L17xT2	0.04	-0.75	-0.91
11	L6xT1	0.08	0.09	0.13	35	L18xT1	0.02	0.14	1.08
12	L6xT2	-0.08	-0.09	-0.13	36	L18xT2	-0.02	-0.14	-1.08
13	L7xT1	0.08	0.18	-1.08	37	L19xT1	0.02	0.03	1.48
14	L7xT2	-0.08	-0.18	1.08	38	L19xT2	-0.02	-0.03	-1.48
15	L8xT1	-0.23	-0.03	-0.01	39	L20xT1	-0.29	-0.22	0.65
16	L8xT2	0.23	0.03	-0.01	40	L20xT2	0.29	0.22	-0.65
17	L9xT1	0.21	1.25**	1.76	41	L21xT1	0.08	-0.55	-1.04
18	L9xT2	-0.21	-1.25**	-1.76	42	L21xT2	-0.08	0.55	1.04
19	L10xT1	0.08	-0.99*	-0.96	43	L22xT1	-0.10	-0.08	-0.99
20	L10xT2	-0.08	0.99*	0.96	44	L22xT2	0.10	0.08	0.999
21	L11xT1	0.27	-0.84	-2.39*	45	L23xT1	0.02	0.10	-1.13
22	L11xT2	-0.27	0.84	2.36*	46	L23xT2	-0.02	-0.10	1.13
23	L12xT1	0.45*	-0.24	-0.50	47	L24xT1	0.15	0.39	-0.69
24	L12xT2	-0.45*	0.24	0.50	48	L24xT2	-0..15	-0.39	0.69
SE						0.18	0.46	0.99	

Note: ** highly significant (p<0.01),*significant (p<0.05), EA=ear aspect, EL=ear length, ED=ear diameter, KRPE=kernel rows per ear, KPR=kernels per rows, TKW=thousand kernels weight.

4. Conclusion

Analysis of variance revealed the presence of significant variation among the genotypes for all studied traits except for plant aspect. Mean square of entry x location interaction for most of studied traits showed non-significant, indicating that hybrid performance was consistent across locations. Nevertheless, genotype x location interaction was significant for some traits, suggesting further evaluation of selected genotypes over a number of locations. Mean squares of GCA and SCA were significant for most of studied traits, implying that both additive and non-additive gene action were involved in the control of the inheritance of these traits. However, the proportional contribution of GCA effect was higher and GCA/SCA ratio was greater than unit for all studied traits, suggesting that additive gene action was more important than non-additive gene action for these traits.

Estimation of gca and sca effects identified lines and crosses with good general and specific combiners for studied traits respectively. Inbred lines L23, L11 and L15 for grain yield, L1, L9, L23 and L24 for number of ears per plant, L8, L14 and L15 for ear length, L8, L14 and L20 for number of kernels row per ear and L4 and L15 for number of kernels per row were the top good general combiners for the respective traits. Crosses such as L11xT1, L13xT2 and L23xT1 for grain yield, L6xT2 for number of ear per plant, L9xT1, L10xT2 and L14xT1 for ear length and L11xT2 for number of kernels per row revealed good specific combining ability. Finally, better performing testcrosses, inbred lines with desirable gca effects and cross combinations with desirable sca effects for grain yield and yield related traits could be used as source of useful genetic material for future maize breeding.

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Appendix

Appendix-1. Analysis of variance for grain yield and yield related traits of 50 maize genotypes evaluated at Ambo, 2017.

Traits	Rep(df=1)	Blk(rep)df=18	Entry(df=49)	Error df=31	Mean	CV %
GY	0.06	0.904	4.26**	1.19	7.74	14.08
AD	16.0*	1.01	6.23*	3.38	96.10	1.91
SD	13.69	2.75	9.63**	3.9	95.53	2.07
ASI	0.0002	0.003	0.008**	0.002	1.1	4.24
PH	501.76	224.06	776.49**	207.71	207.71	5.70
EH	272.25*	32.20	399.64**	50.28	142.01	4.99
EPO	0.00004	0.001	0.002	0.003	0.56	9.17
EPP	0.01	0.027	0.094**	0.029	1.62	10.47
EA	0.12	0.059	0.20**	0.095	3.056	7.66
PA	0.49	0.16	0.19	0.18	3.42	12.52
EL	8.82**	1.01	2.51**	1.09	15.37	6.78
ED	0.004	0.04	0.07**	0.03	4.41	4.05
KRPE	0.37	0.93**	0.56	0.35	12.63	4.68
KPR	6.35	8.97	7.20**	5.68	32.56	7.32
TKW	22.37	987.20	3282.45**	1024.25	336.13	7.52

Note: **Significant (p<0.01),*significant (p<0.05), Rep=replication, Blk=block, CV=correlation variation.

Appendix I2. Analysis of variance for grain yield and yield related traits of 50 maize genotypes evaluated at Holetta, 2017.

Traits	Rep(df=1)	Blk(rep)df=18	Entry(df=49)	Error df=31	mean	CV%
GY	0.006	1.67	3.12**	1.01	7.33	13.73
AD	32.49 **	4.91	11.19**	2.98	112.93	1.53
SD	25.0**	2.43	10.23**	2.71	114.76	1.44
ASI	0.001	0.006	0.004*	0.006	1.22	6.37
PH	1056.25**	99.13	1136.63**	70.54	249.37	3.37
EH	524.41**	57.88	650.52**	59.0	131.31	5.85
EPO	0.0003	0.0004	0.002**	0.0005	0.52	4.35
EPP	0.004	0.03	0.08**	0.04	1.79	10.5
EA	1.69**	0.20	0.44**	0.21	3.18	14.33
PA	1.0*	0.14	0.17	0.22	3.18	14.9
EL	8.82**	0.95	2.53**	0.53	15.56	4.70
ED	0.004	0.01	0.08**	0.02	4.23	3.59
KRPE	0.79	0.34	1.17**	0.39	13.08	4.79
KPR	44.08**	5.87*	7.92**	2.74	31.94	5.19
TKW	32.15	498.92	1742.34*	870.39		

Note: **Significant (p<0.01),*significant (p<0.05), Rep=replication, Blk=block, CV=correlation variation.

Appendix-3. Mean squares, and proportional contribution of lines, tester and line x tester of yield and yield related traits 48 maize testcross at Ambo, 2017.

Source	DF	GY	AD	SD	ASI	PH	EH	EPO
Rep	1	0.03	15.84*	12.76	0.11**	408.38	260.04*	0.0013
Cross	47	4.76**	6.49**	10.89**	2.81(0.009)**	902.75**	511.62**	0.0025**
Line	23	6.23**	9.73**	13.11**	1.95(0.006)	687.48*	422.09**	0.003
Tester	1	0.09	3.76	98.01**	59.32(0.18)**	19877.41**	10922.67**	0.0047
Line x	23	3.48**	3.37	4.88	1.20(0.004)	293.04	148.49**	0.002*
Error	29	1.01	2.57	3.61	0.77(0.002)	211.96	44.85	0.0008
Proportion contribution								
Line		64.12	73.36	58.91	34.07	37.27	40.37	58.44
Tester		0.04	1.23	19.15	44.98	46.85	45.42	3.92
Line x		35.84	25.41	21.93	20.95	15.89	14.2	37.65
		EA	**ED**	**EL**	**EPP**	**KRPE**	**KPR**	**TKW**
Rep	1	0.09	0.01	6.48**	0.01	0.06	0.68	7.23
Cross	47	0.22**	0.07**	2.66**	0.11**	0.65*	7.18	3590.20**
Line	23	0.28	0.12**	4.48**	0.16**	0.73*	7.54	3535.40**
Tester	1	0.67**	0.01	0.44	0	2.62**	9.01	57934.13**
Line x	23	0.15*	0.02	0.93	0.06	0.27	6.73	1282.22
Error	29	0.06	0.03	1.06	0.03	0.36	5.04	857.51
Proportion contribution								
Line		60.68	88.45	82.47	74.35	65.43	51.45	48.19
Tester		6.36	0.33	0.36	0	10.19	2.67	34.33
Line x		32.97	11.22	17.18	25.65	24.38	45.88	17.48

Note: **Significant (p<0.01), *significant (p<0.05), GY=grain yield, AD=anthesis days, SD=silking days, ASI=anthesissilking interval, PH=plant height, EH=ear height, EPO =ear position, EPP=ear per plant, EA=ear aspect, EL=ear length, ED=ear diameter, KRPE=kernel rows per ear, KPR=kernels per rows, TKW=thousand kernels weight.

Appendix-4. Mean squares, and proportional contribution of lines, tester and line x tester of yield and yield related traits of 48 maize testcross Holetta, 2017.

Source	DF	GY	AD	SD	ASI	PH	EH	EPO
Rep	1	0.05	15.66**	25.01**	0.55	247.00**	320.26**	0.0005
Cross	47	3.05**	10.57**	11.73**	2.04	1226.24**	755.60**	0.0024*
Line(GCA)	23	2.96**	15.71**	17.24**	1.67	587.61**	434.46**	0.0032**
Tester(GCA)	1	37.79**	3.32	21.09**	3.43	39148.12**	22634.84**	0.0241**
Line x Tester(SCA)	23	1.63	5.74	5.81*	2.34	216.10**	125.48*	0.0007
Error	29	0.97	3.1	2.71	2.50	46.94	55.52	0.0005
Proportional contribution (%)								
Line		47.5	72.75	71.93	40.11	23.45	28.14	64.69
Tester		26.35	0.01	3.83	3.58	67.93	63.74	21.43
Line x Testers		26.15	26.58	24.25	56.31	8.62	8.13	13.88
		EA	**ED**	**EL**	**EPP**	**KRPE**	**KPR**	**TKW**
Rep	1	1.17**	0	4.70**	0.001	0.54	10.54	23.21
Cross	47	0.50*	0.09**	3.17**	0.09*	1.48**	8.45**	2074.04**
Line(GCA)	23	0.70**	0.09**	4.09	0.11*	1.55**	11	3015.38*
Tester(GCA)	1	1.27**	1.02**	3.56	0.38**	12.98**	1.27	229.4
Line x Tester(GCA)	23	0.26	0.04*	2.23**	0.05	0.91*	6.22*	1212.9
Error	29	0.2	0.02	0.6	0.04	0.36	2.81	745.02
Proportional contribution (%)								
Line		69.15	51.46	63.17	62.95	51.22	63.69	71.15
Tester		5.44	25.17	2.39	9.46	18.69	0.89	0.24
Line x Testers		25.41	23.36	34.44	27.59	30.1	36	28.62

Note: **Significant ($p<0.01$), *significant ($p<0.05$), GY=grain yield, AD=anthesis days, SD=silking days, ASI=anthesissilking interval, PH=plant height, EH=ear height, EPO =ear position, EPP=ear per plant, EA=ear aspect, EL=ear length, ED=ear diameter, KRPE=kernel rows per ear, KPR=kernels per rows, TKW=thousand kernels weight.