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Combining ability of maize (Zea mays l.) inbred lines adapted to sub-humid central highland of Ethiopia

Takele Mitiku[1+]
Gudeta Nepir[2]
Demoz Negera[3]

[1] *Bako National Maize Research Center, Ethiopia.*
Email: takelemitku202@gmail.com
[2] *Ambo University Guder Compus, Ethiopia.*
Email: gudetangt@gmail.com
[3] *Ambo Agricultural Research Center, Ethiopia.*
Email: dworeti@gmail.com

(+ Corresponding author)

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ABSTRACT

The production of maize, a primary food crop in Africa, is hampered by a lack of high-yielding cultivars, biotic and abiotic stressors. In order to create high-yielding maize varieties, choosing promising germ plasm that have good combining ability, and heterotic groups is so important. Estimating the GCA and SCA of grain yield and other yield-related traits of maize inbred lines was the goal of this work. In 2019 using line by tester mating design, 26 inbred lines were crossed with two testers to produce 52 F1 hybrids. The experiment was carried out in the Ambo and Kulumsa Agricultural Research Centres in the 2020 cropping season using an alpha lattice design with two replications. Analysis of variance revealed significant mean squares attributable to crosses and lines in each location and across locations for targeted traits. The finding of the line x tester ANOVA showed significant mean squares for lines, testers, and cross for grain yield, anthesis date, silking date, plant height, ear height, kernel row per ear, and number of ears per plant. This show inconsistency of inbred lines traits across testing sites. While crossings L1xT2, L17xT1, L8xT1, L10xT1, L14xT1, L20xT2, L24xT2, and L26xT1 were effective particular combiners, inbred L2, L4, L5, L7, L10, and L13 were strong general combiners for grain yield. The best particular combiners for plant and ear height traits were L11xT1, L17xT1, and L11xT1, L26xT2, while L14, L21, and L22 worked well for EPP and L14 for KPR with T1.

Contribution/Originality: The originality of this study is to demonstrate potential genetic transfer of traits from parents to offspring. This finding contribute the improvement of hybrid parental line's genetic variability so that enhance heterosis and yield potential.

1. INTRODUCTION

Maize (Zea mays L., 2n=20) is a significant cereal crop that is a member of the Maydeae tribe and the Poaceae grass family, Genus Zea, Species mays. It is the most frequently cultivated cereal grain in the world and the main staple meal in many poor nations. The world produced 1,124 MT of maize during the 2018/2019 cropping season, with the United States producing 366.287 MT, China 257.330 MT, Brazil 94.500 MT, and the European Union 83.185 MT [1].

In Africa, Egypt (5.45 t ha-1), South Africa (5.45 tha-1) and Ethiopia (3.74 t ha-1) are the top three maize producers in 2020/2021 cropping season. However, report revealed that, in Ethiopia, maize productivity is 4.18 tha-

1 which is relatively higher than report, though both reports indicate that maize productivity is still lower than the world maize average (5.65 t ha-1) in Ethiopia.

With 10.56 million tonnes produced, maize is the most productive cereal crop in Ethiopia, followed by tef (5.51 million tonnes) and wheat (5.78 million tonnes). Maize is a major crop for Ethiopian farmers' overall food security and economic development because 75% of all maize production is used by farming households [2]. In Ethiopia, maize is consumed by each person on an annual basis in amounts of 50 kilogrammes [3]. The most significant staple crop for the rural Ethiopian population in terms of caloric intake is maize [4]. According to CSA data, of the total grain crop area in Ethiopia for the 2019–20 main cropping season, 81.46% (10,478,218.03 hectares) were under cereals. The grain crop area was divided between teff, maize, sorghum, and wheat, which accounted for 24.11% (or roughly 3,101,177.38 hectares), 17.68% (or roughly 2,274,305.93 hectares), 14.21% (1,828,182.49 hectares), and 13.91% (or roughly 1,789,372.23 hectares) of the total. The total amount of maize produced in Ethiopia during the 2018/19 crop season was 8.6 MT, with an average yield of 3.7 t ha-1 (FAOSTAT, 2018/19). Cereals made up 88.52% (29,672,647,694 tonnes) of the grain yield production on an annual basis. In that order, the grain production was made up of 28.75% (9,635,734.5 tonnes) of maize, 17.11% (5,735,710.187 tonnes) of teff, 15.86% (5,315,270.328 tonnes) of wheat, and 15.71% (5,265,580.059 tonnes) of sorghum [5].

Low yields in Ethiopia's maize agroecology are caused by unimproved varieties combined with biotic problems like turcicum leaf blight, common leaf rust, stalk lodging, stalk borers, and storage pests, as well as abiotic stresses like frost, hailstorm, and low soil fertility [6].

Future crop productivity is significantly at risk from climate change due to rising temperatures, changing rainfall patterns, and increased pest and disease pressures [7]. In the past forty years, drought and famine have both posed a danger to Ethiopia's maize production [8]. In comparison to the average yield per hectare for the world (5.2 t/ha) and that of industrialised nations (7.2 t/ha), Ethiopia's average national maize productivity is extremely low [9]. The most significant abiotic factors that have an impact on maize productivity are drought and low soil fertility [10-12].

It is absolutely necessary to improve germplasm and continue intensification to raise and stabilise yields in order to narrow production gaps in order to lessen these important issues Foley, et al. [13]. Legesse, et al. [14] also found that to adapt to the constantly shifting environmental conditions and growing population pressure, maize breeding programmes must incorporate genetically variable germplasm.

Combining ability investigations show the kind and extent of different types of gene activity involved in the development of quantitative traits, which is helpful information for choosing ideal parents for successful hybridization programmes. Crop breeders typically employ combining ability analysis to choose parents with high general combining ability (GCA) and hybrids with high specific combining ability (SCA) effects. Combining ability analysis is a key technique for understanding gene activities. Understanding the genetic potential of a population and choosing the breeding strategy to be used in a particular population depend on knowledge of the nature and amount of gene action.

2. MATERIALS AND METHODS

2.1. Description of Experimental Site

The main cropping season of 2020 was used to perform this study at the Kulumsa and Ambo Agriculture Research Centres in Ethiopia's central highland agroecology. The Ambo Agriculture Research Centre is situated at an altitude of 2225 masl at 8 57 N latitude and 38 07 E longitude. The majority of the topsoil (0–30 cm) has a pH of 7.8 and is a heavy clay soil type (vertisoils) [15]. The average minimum and maximum temperatures are 11.7 °C and 25.5 °C, respectively, with an average value of 18.6 °C. The long-term total annual rainfall is 1115 mm. At a height of 2200 masl, Kulumsa is situated at 8° 5' N latitude and 39° 10' E longitude. Luvisol/eutric nitosols, with good drainage and pH, are the most common form of soil. The total long-term annual rainfall is 830 mm. The mean minimum and maximum temperatures are 10 oC and 23.2 oC, respectively with an average value of 16.6 oC.

2.2. Experimental Materials

Twenty-six maize inbred lines and two single cross testers (Table 1) were used in this study. The materials were developed at Ambo highland maize breeding program. The inbred lines were test crossed to two single cross testers following line × tester mating design as described by Kempthorne [16] during the main season of 2019 at Ambo Agricultural research center to generate 52 F1 hybrids.

Table 1. List of lines and testers used in the experiment.

S/N	Coded parent lines	Type of materials	Generation	Source
1	CEL17289	Inbred lines	S5	CIMMYT
2	CEL17295	Inbred lines	S5	CIMMYT
3	CEL17298	Inbred lines	S5	CIMMYT
4	CEL17301	Inbred lines	S5	CIMMYT
5	CEL17310	Inbred lines	S5	CIMMYT
6	CEL17312	Inbred lines	S5	CIMMYT
7	CEL17314	Inbred lines	S5	CIMMYT
8	CEL17315	Inbred lines	S5	CIMMYT
9	CEL17316	Inbred lines	S5	CIMMYT
10	CEL17329	Inbred lines	S5	CIMMYT
11	CEL17330	Inbred lines	S5	CIMMYT
12	CEL17331	Inbred lines	S5	CIMMYT
13	CEL17333	Inbred lines	S5	CIMMYT
14	CEL17334	Inbred lines	S5	CIMMYT
15	CEL17335	Inbred lines	S5	CIMMYT
16	CEL17336	Inbred lines	S5	CIMMYT
17	CEL17351	Inbred lines	S5	CIMMYT
18	CEL17353	Inbred lines	S5	CIMMYT
19	CEL17357	Inbred lines	S5	CIMMYT
20	CEL17371	Inbred lines	S5	CIMMYT
21	CEL17372	Inbred lines	S5	CIMMYT
22	CEL17377	Inbred lines	S5	CIMMYT
23	CEL17378	Inbred lines	S5	CIMMYT
24	CEL17379	Inbred lines	S5	CIMMYT
25	CEL17380	Inbred lines	S5	CIMMYT
26	CEL17404	Inbred lines	S5	CIMMYT
Testers				
1	CEL08008/CEL08047	Single cross tester	S5	CIMMYT
2	CEL08024/CML561	Single cross tester	S5	CIMMYT

2.3. Experimental Design and Agronomic Practices

In an Alpha Lattice design, 52 F1 hybrids created through line-by-tester mating were repeated twice. The trial was carried out at the Agricultural Research Station in Ambo and Kulumsa. Each entry was planted in a single row plot of 4 metres long, with 0.75 metres between rows and 0.25 metres between plants. To achieve a density of 53,333 maize plants per hectare, the experimental materials were manually planted with two seeds per hill, which were then thinned out to one plant/hill. DAP and UREA were used at the prescribed rates of 150 and 200 kg/ha, respectively.

At planting time, a band application of diammonium phosphate (DAP), a phosphorous fertiliser, was made. At 40 days and 70 days following planting, UREA was administered in two splits. Other agronomic management procedures were carried out in accordance with local recommendations.

3. RESULTS AND DISCUSSION

3.1. Analysis of Variance

Overall ANOVA result of the current investigation displayed in (Table 2). Analysis of variance was made on yield and yield-related traits of grain yield (GY), anthesis of date (AD),1000-kernel weight (TW), anthesis silking interval (ASI), silking date (SD), plant height (PH), and ear height (EH), number of ears per plant (EPP), number of kernel rows per ear (KRPE), number of kernels per row (KPR), ear length (EL) and ear diameter (ED) for each location and across the locations.

Table 2. Analysis of variance for yield and yield related traits for testcross across location.

Traits	L df=1	Re(L) df=2	B(L*R) df=12	Ent df=51	Ent*L df=51	Error df=90	Mean±SE(m)	CV%	R^2
GY	73.8***	36.64***	2.72***	5.28**	2.85***	0.948	7.44±0.97	13.08	0.88
AD	68.08***	15.64*	5.36	11.77**	4.14	5.02	97.02±2.24	2.31	0.7
SD	10.17	5.7	6.29	12.65**	5.07	5.37	98.79±2.32	2.35	0.69
ASI	12.62***	4.64	1.13	1.96	1.28	1.73	1.76±1.32	74.55	0.63
PH	510.9	1707***	442***	397.7**	212.5	156.78	225.4±12.52	5.56	0.76
EH	3894***	1611***	302*	406.2**	229.8**	130.08	125.73±11.41	9.07	0.79
EPP	0.93***	0.2*	0.03	0.11***	0.08*	0.05	1.39±0.22	15.51	0.73
EL	0.81	19.16**	4.24	3.24	3.18	3.1	17.38±1.76	10.14	0.59
ED	2.77	19.16	3.2*	7.13	6.41	5.13	46.68±2.26	4.86	0.63
KRPE	1.56	2.4	1.77	1.18	1	0.99	12.61±0.99	7.3	0.6
KPR	218.12***	27.98	12.16	21.11*	10.49	14.35	36.66±3.8	10.33	0.62
TSW	22.89	4429.93	3286.43	1707.25	1547.88	1862.03	350.51±43.15	12.31	0.53

Note: L=Location, Re=Replication, Ent=Entry, SE= Standard error, CV= Coefficient of variation, R2=Coefficient of determination. *= significance at 0.1 level, **= significant at 0.05, and ***= significance at 0.01 level.

This implies that there is sufficient diversity to select from among the genotypes that have been examined. Amiruzzaman, et al. [17]; Amare, et al. [18]; Ziggiju, et al. [19] and Tulu, et al. [20] are among the authors who have identified substantial genotype differences for yield-related metrics and grain yield of different sets of maize genotypes. The interaction between location and entrance (Location x entry) was significant (p 0.05) and highly significant (P<0.01) for grain yield, ear height, and ear per plant. However, non-significant interaction effects of (Location x entry) were detected for parameters such as the anthesis date, silking date, anthesis silking interval, plant height, ear length, ear diameter, kernel row per ear, kernel per row, and thousand seed weight Bayisa, et al. [21] and Dagne, et al. [22] discovered that this attribute performed consistently across experiments, which is in line with the conclusions of the present inquiry. Grain yield, anthesis date, silking date, plant height, ear height, and number of ears per plant are highly significant at (p<0.01) and kernel row per ear significant at (p<0.05) for genotype, whereas the remaining variables were not significant.

Table 3. Analyses of variance for line by tester for grain yield and yield related traits of 52 test crosses and 26 inbred lines evaluated in across location.

SV	Df	GY	AD	SD	ASI	PH	EH	EPP	EL	ED	KRPE	KPR	TSW
Site	1	73.8***	68.1***	10.2ns	0.04***	510.94*	3894.23***	0.928***	0.81	2.77	1.56	218.12***	22.89
Rep(Site)	2	36.64***	15.64	5.70ns	0.007	1706.53***	1610.55***	0.20*	19.16***	19.16*	2.40	27.98	4429.93
Blk(rep)	7	11.15***	13.45*	10.36ns	0.003	1410.94***	837.44***	0.023	11.57***	10.22*	2.39*	21.31	3601.91
Cross	51	5.28***	12.00***	12.52***	0.003	397.75***	406.16***	0.11***	3.24	7.13	1.19	21.11*	1707ns
Line	25	5.48***	22.08***	23.66***	0.004	457.69***	277.66***	0.11***	2.53	7.04	0.89	23.27*	1028.37
Tester	1	12.26***	0.12***	3.77ns	0.005	3706.17***	8581.23***	1.01***	20.31***	8.48	0.17	55.043*	190.38
Line*tester	25	5.09***	4.64	5.28ns	0.003	281.99***	241.70***	0.08*	2.90	7.98*	1.24	17.62	2207.49
Site*line	25	2.92***	4.76	4.12ns	0.003	246.34***	182.38*	0.08*	3.18	7.33*	1.25	8.32	1418.21
Site*tester	1	20.75***	4.62	12.02ns	0.004	1173.25***	1969.23***	0.26*	5.24	22.23*	0.48	10.62	3336
Site*cross	51	2.72***	4.14	5.07	0.006	212.45	246.89***	0.08***	3.17	6.41	1.00	10.49	1547.89
Site*line*tester	25	1.94***	3.18	5.00ns	0.004	202.05***	242.90***	0.08*	3.16	4.91	0.83	14.12	870.51ns
Error	95	0.42	4.44	5.13	0.003	100.4	99.67	0.046	17.38	4.51	0.99	13.56	1913.75
Mean		7.44	97.02	98.79	1.23	225.35	125.73	1.39	2.62	46.57	12.61	36.66	350.51
CV		8.70	2.17	2.29	4.21	4.45	7.4	15.41	9.32	4.56	7.91	10.05	12.48
R^2		0.95	0.72	0.69	0.63	0.83	0.83	0.72	0.64	0.66	0.58	0.62	0.49
LSD		1.37	1.15	3.26	1.85	17.59	16.02	0.31	2.48	3.18	1.41	5.32	60.62
Proportional contribution													
%L(GCA)		49.55	82.62	81.33	56.66	51.52	32.19	46.57	40.56	45.84	41.78	54	31.71
%T(GCA)		4.43	0.02	0.52	2.43	16.7	39.79	37.22	13	2.21	0.32	5.11	0.23
%LXT(SCA)		46.02	17.36	18.15	40.91	31.77	28.02	36.1	46.44	51.95	57.9	40.89	68.06

Note: *= significance at 0.1 level and ***= significance at 0.01 level.

3.2. Combined Analysis for Combining Ability

As a consequence of the combined analysis, highly significant mean squares resulting from crossings were found for GY, AD, SD, PH, EH, and EPP, as well as significant mean squares for KPR, indicating the potential of computing combining ability analysis and dividing into GCA and SCA. The findings also indicated the existence of statistically significant variations among GCA of lines for GY, AD, SD, PH, EH, EPP, and KPR. For GY, AD, PH, EH, EPP, EL, and KPR, highly significant mean squares of testers were also obtained ($P < 0.05$). Similar results were seen across sites, with extremely significant mean squares resulting from SCA for GY, PH, EH, and EPP as well as ED (P 0.05) in Table 3. The current finding indicated the presence of a site x line interaction that was highly significant for GY and significant ($P < 0.05$) for EH, EPP, and ED. However, for AD, SD, ASI, EL, KRPE, KPR, and TSW, the interaction of S x L was shown to be non-significant. For GY, PH, and EH, the across-site interaction of Site x Tester (SxT) was very significant ($P < 0.01$), while for EPP and ED, it was significant. For EH and EPP, site x crosses also exhibited extremely significant interaction, but non-significant interaction for the majority of characteristics.

But for GY, PH, and EH as well as significant ($P < 0.05$) for EPP, the current investigation revealed a very significant interaction of site x line x tester. Site, line, and tester interactions were not significant for other attributes. This might mean that both sites are anticipating similar performance from those features. According to the most recent genetic investigation, for variables including GY, AD, SD, ASI, PH, EH, and EPP, the total of squares attributable to GCA was more than that owing to SCA. These findings suggest that the additive gene type contributes primarily, and that these features may be improved by selection. However, for features like KRPE, TSW, and ED, the sum of squares attributable to GCA was lower, indicating that these qualities are controlled by non-additive gene types and might be utilised through hybrid development.

3.3. General Combining Ability Effect Across Locations

Inbred lines L2, L4, L5, L7, L10, and L13 had significant and positive GCA estimates for GY. Given that inbred lines made effective general combiners for grain yield across locations, it is possible that they may be used to create synthetic varieties. For L1, L6, L12, L17, L21, L22, and L24, the GCA for GY was highly significant and significantly negative. This demonstrates that the lines were inefficient general combiners, which implies that they failed to disperse additive genes in the intended manner. L4, L5, and L18 were significant and negative for the anthesis date, but L4, L5, L11, L14, L18, and L19 were significant and positive for the silking date. The lines can be used in breeding programs to enhance hybrid early-maturing cultivars for drought-prone areas. For SD, L2, L3, L6, L7, L8, L9, L10, L12, L17, L22, L24, and L25 showed the similar results, whereas L3 and L12 showed positive and significant outcomes for AD. These lines were inadequate general combiners for the associated attributes. Numerous authors, including Shushay, et al. [23] and Yazachew, et al. [24] have found significant and both positive and negative lines GCA impacts.

The plant's GCA falls from -12.38 cm (L16) to 17.33 cm (L24). Strong negative and positive GCA were found in the 26 lines L1, L16, L21, L22, and L9, making L23, L24, and L26 from those 26 lines good and terrible general combiners for this trait, respectively. The GCA effect for ear height runs from L21 to L12, 12.22cm, starting at -10.96cm. Significantly negative GCA values were found for L18, L21, and L22, but significant positive GCA values were found for L12. L12 was a bad general combiner for this trait since maize is sought after for its small ear height. Kamara, et al. [25]; Girma, et al. [26] and Ahmed, et al. [27] found substantial positive and negative GCA effects of inbred lines for plant and ear height by claiming that shorter plant height with lower ear placement was preferable.

Inbred lines' GCA impacts on the number of ears per plant ranged from -0.23 (L11) to 0.17 (L26), with L3 and L11 having significantly negative GCA values and L18 and L26 having significantly positive GCA values. As a result, it was clear that L3 and L11 were ineffective general combiners for the qualities, however L18 and L26 performed well. The GCA estimates for L1, L5, L6, L7, L8, L9, L10, L11, L12, L15, and L26 in the case of KPR were significant and positive, demonstrating that these loci support additive genes that improve traits through selection. L2, L3, L13, L16, L17, L19, and L26 have negative and significant GCA estimations, which makes them poor general combiners for the attributes. The tester's negative and positive values were noted in regard to the GCA effect even though significant positive and negative results weren't attained. The following Table 4 represent GCA of inbred lines and two testers.

Table 4. General combining ability of inbred lines and two testers across location.

SN	Lines	GY	AD	SD	PH	EH	EPP	KPR
1	L1	-0.63**	-0.27	-0.49	-8.85*	-5.74	0.11	2.24***
2	L2	0.69**	1.00	1.81***	-0.36	3.09	-0.03	-1.27***
3	L3	0.02	2.08**	2.06***	-0.40	-2.66	-0.21**	-2.16***
4	L4	0.98***	-4.14***	-3.88**	-0.74	4.52	-0.06	0.10
5	L5	0.85***	-2.79**	-2.84***	-6.40	-4.53	0.10	0.73*
6	L6	-0.82***	0.36	1.08***	1.44	5.47	0.12	0.82*
7	L7	1.08***	1.47	1.56***	0.01	6.09	0.12	1.23*
8	L8	0.31	0.99	1.22***	-4.68	-7.46	-0.08	2.25***
9	L9	0.30	0.84	0.94***	8.25*	6.17	0.20	0.20
10	L10	0.69**	0.23	0.57*	-4.74	0.12	-0.12	1.69**
11	L11	-0.06	-0.53	-0.62*	-1.97	-4.20	-0.23**	0.84*
12	L12	-0.55*	1.60*	1.85***	-6.75	12.22***	-0.10	1.45***
13	L13	0.88**	0.33	-0.37	6.79	2.87	0.12	-1.39***
14	L14	0.41	0.11	-0.75**	-3.38	2.26	0.05	-0.29
15	L15	-0.15	0.21	0.01	0.48	2.09	-0.09	1.84***
16	L16	0.07	0.60	-0.51	-12.38***	-2.12	0.08	-1.93***
17	L17	-1.26***	1.35	0.91***	4.85	0.44	-0.02	-2.02***
18	L18	0.26	-4.89***	-4.35***	-8.26	-10.18**	0.16*	0.58
19	L19	0.10	-1.28	-1.64***	5.91	-1.52	-0.02	-1.42***
20	L20	0.37	-0.39	0.02	5.43	4.32	-0.08	0.59
21	L21	-0.68**	0.61	0.27	-7.56*	-10.96***	-0.01	0.09
22	L22	-2.69***	1.24	2.18***	-7.69*	-7.89*	-0.10	-5.37***
23	L23	0.01	-0.40	-1.25***	14.36***	5.88	-0.04	-0.58
24	L24	-0.94***	1.21	0.89***	17.33***	4.37	0.07	-0.28
25	L25	0.24	0.24	1.24***	-5.45	-4.86	-0.09	0.57
26	L26	0.37	0.23	0.13	12.98***	0.95	0.17*	1.48*
	SE	0.23	0.74	0.25	3.54	3.53	0.08	0.35
	T1	0.24	-0.03	-0.15	4.20	6.51	0.07	-0.52
	T2	-0.25	0.03	0.15	-4.34	-6.60	-0.07	0.51
	SE	0.27	0.03	0.15	4.06	5.60	0.07	0.51

Note: Line, T=Tester, SE=Standard error, GY=Grain yield, AD=Anthesis days, SD=Silking date, PH=Plant height, EH=Ear height, EPP=Ear per plant KPR=Kernels per rows, TSW=Thousand seed weight. *= significance at 0.1 level, **= significant at 0.05, and ***= significance at 0.01 level.

3.4. Specific Combining Ability of Across Location

Specific combining ability across locations were listed in General combining ability across location value listed in Table 5. Grain yield had a favourable and significant across-location SCA effect in crosses like L1xT2, L14xT1, L17xT1, L8xT1, L10xT1, L14xT1, L17xT1, L20xT2, L24xT2, and L26xT1. This suggests that the two parents' genes significantly positively interacted and served as an effective combiner for this trait. These gene interactions cause heterosis to manifest, which can be used to create hybrid types. Cross L1xT1, L14xT2, L17xT2, L8xT2, L10xT2, L14xT2, L17xT2, L20xT1, L24xT1, and L26xT2 are subpar specific combiners for GY and showed negative significant SCA estimations. The results of Kamara, et al. [25]; Girma, et al. [26]; Ram, et al. [28] and Bullo and Dagne [29] others who observed substantial positive and negative SCA for grain yield, are consistent with the current conclusion. They proposed that SCA effects might aid in the selection of parental material for hybridization when high yielding particular combinations are sought. Jumbo and Carena [30] and Pswarayi and Vivek [31] revealed non-significant positive and negative SCA effects for grain yield, in contrast.

Different crosses, including L10xT1 (-1.46), L10xT2 (1.46), L19xT1 (-1.48), and L19xT2 (1.48), demonstrated both positive and negative SCA estimates for AD, while L10xT1 (-1.66) and L10xT2 (1.65), respectively, demonstrated the highest levels of both negative and positive SCA estimates for SD. Good particular combiners for the two qualities in the desired direction were L10 and L19 with T1. While L10 and L19 with T2 may be used for late maturity in regions with sufficient rainfall, this cross may be utilised for early maturity in locations with insufficient rainfall. Numerous researchers have documented both significant positive and negative SCA effects for AD and SD, which is consistent with our conclusion [19, 32-34].

L11xT1, L17xT1 and L11xT1, L26xT2 are negative and significant for grain plant height for the PH and EH crosses, respectively. These crosses are effective general combiners for these features since the short plant is desired to prevent lodging. The positive and substantial SCA values for the PH cross L11xT2, L17xT2, the EH cross L11xT2, and L26xT2 are poor specific combiners. This suggests that the combination was controlled by non-additive gene activation.

Because of this, heterosis breeding may be used to enhance the qualities. In their tests on the combining ability and heterotic orientation of mid-altitude sub-humid tropical maize inbred lines for grain yield and associated variables. L14xT1, L21xT1, and L22xT1 were crosses with substantial positive SCA effects for EPP traits, whereas L14xT2, L21xT2, and L22xT2 were crosses with significant negative SCA effects. L14xT1 (3.09) and L14xT2 (-3.09) for KPR cross with contrasting SCA values. For EPP, L14, L21, and L22 worked well as specifiec combiners, as did L14 for KPR with T1. These features could be enhanced by heterosis breeding to produce more kernels and ears per row. The following Table. 5 represent SCA of inbred lines with their two testers.

Table 5. Specific combining ability of crosses across locations.

SN	Genotype	GY	AD	SD	PH	EH	EPP	KPR
1	L1XT1	-1.36***	0.78	1.15	2.44	-1.06	0.02	2.15
2	L1XT2	1.37***	-0.78	-1.16	-2.30	1.16	-0.02	-2.15
3	L2XT1	0.13	0.02	-0.16	-0.96	6.42	0.00	0.90
4	L2XT2	-0.12	-0.02	0.16	1.10	-6.32	0.00	-0.89
5	L3XT1	0.19	0.40	1.13	-8.95	-2.98	0.02	-0.22
6	L3XT2	-0.17	-0.40	-1.13	9.09	3.08	-0.02	0.22
7	L4XT1	-0.21	-0.84	-0.40	-1.85	-1.56	-0.05	-1.50
8	L4XT2	0.22	0.83	0.39	1.99	1.65	0.05	1.50
9	L5XT1	0.02	1.02	0.68	3.37	1.14	-0.03	1.64
10	L5XT2	-0.01	-1.02	-0.68	-3.23	-1.04	0.03	-1.64
11	L6XT1	-0.24	-0.08	0.36	-6.16	-3.33	0.10	0.54
12	L6XT2	0.25	0.08	-0.36	6.30	3.43	-0.10	-0.54
13	L7XT1	-0.50	0.75	0.40	0.85	-3.32	-0.04	0.90
14	L7XT2	0.51	-0.75	-0.40	-0.71	3.42	0.04	-0.89
15	L8XT1	0.74**	-0.23	-0.61	4.52	-0.38	0.01	0.91
16	L8XT2	-0.74**	0.23	0.61	-4.38	0.48	-0.01	-0.90
17	L9XT1	0.12	-0.36	-0.18	6.31	4.52	0.16	-0.10
18	L9XT2	-0.11	0.36	0.18	-6.17	-4.43	-0.16	0.10
19	L10XT1	0.76**	-1.46	-1.66	7.70	6.44	0.05	1.14
20	L10XT2	-0.76**	1.46	1.65	-7.56	-6.35	-0.05	-1.14
21	L11XT1	-0.28	0.03	-0.30	-13.69**	-11.80*	-0.02	0.77
22	L11XT2	0.29	-0.03	0.29	13.69**	11.80*	0.02	-0.77
23	L12XT1	0.45	-1.35	-0.93	-6.92	-8.56	0.01	-1.34

Table 5. Continued.

SN	Genotype	GY	AD	SD	PH	EH	EPP	KPR
24	L12XT2	-0.44	1.34	0.92	7.06	8.65	-0.01	1.34
25	L13XT1	-0.54	0.38	0.55	1.96	1.92	-0.10	-1.20
26	L13XT2	0.55	-0.39	-0.55	-1.82	-1.82	0.10	1.21
27	L14XT1	1.90***	-0.60	-0.42	1.53	3.63	0.23*	-3.09
28	L14XT2	-1.90***	0.60	0.41	-1.39	-3.53	-0.23*	3.09
29	L15XT1	-0.35	-0.24	-1.07	-2.37	-2.22	-0.09	0.76
30	L15XT2	0.36	0.24	1.07	2.51	2.32	0.09	-0.75
31	L16XT1	-0.02	0.92	0.74	-0.25	-8.01	-0.06	-2.50
32	L16XT2	0.03	-0.93	-0.75	0.39	8.11	0.06	2.51
33	L17XT1	1.46***	0.65	1.36	10.06*	6.36	0.03	1.36
34	L17XT2	-1.45***	-0.65	-1.36	-10.06*	-6.26	-0.03	-1.36
35	L18XT1	-0.22	0.65	0.75	5.21	4.12	-0.04	0.23
36	L18XT2	0.24	-0.65	-0.76	-5.07	-4.03	0.04	-0.23
37	L19XT1	0.10	-1.48	-0.96	-6.45	-6.45	-0.01	0.28
38	L19XT2	-0.09	1.48	0.96	6.59	6.55	0.01	-0.28
39	L20XT1	0.76*	0.14	0.86	1.39	2.29	0.01	-1.99
40	L20XT2	-0.76*	-0.15	-0.86	-1.25	-2.19	-0.01	1.99
41	L21XT1	-0.46	-0.60	-1.05	3.40	3.52	0.25*	1.77
42	L21XT2	0.46	0.60	1.05	-3.26	-3.42	-0.25*	-1.77
43	L22XT1	-1.50***	1.28	0.30	-0.65	-0.54	-0.20	-2.74
44	L22XT2	1.50***	-1.28	-0.30	0.79	0.64	0.20	2.74
45	L23XT1	-0.30	0.65	0.41	-6.27	-4.89	0.08	1.88
46	L23XT2	0.31	-0.65	-0.41	6.41	4.98	-0.08	-1.88
47	L24XT1	-1.36***	-0.23	-0.71	1.45	3.42	-0.19	-0.63
48	L24XT2	1.36***	0.23	0.70	-1.31	-3.32	0.19	0.63
49	L25XT1	-0.28	0.27	0.30	-0.87	0.44	-0.06	-0.49
50	L25XT2	0.29	-0.27	-0.31	1.01	-0.34	0.06	0.50
51	L26XT1	1.12***	-0.48	-0.59	6.88	12.06*	-0.09	0.61
52	L26XT2	-1.12***	0.48	0.58	-6.75	-12.06*	0.09	-0.60
	SE	0.32	1.05	1.13	5.00	4.98	0.11	1.83

Note: Line, T=Tester, SE=Standard Error, GY=Grain yield, AD=Anthesis days, SD=Silking date, PH=Plant height, EH=Ear height, EPP=Ear per plant KPR=Kernels per rows, TSW=Thousand kernels weight. *= significance at 0.1 level, **= significant at 0.05, and ***= significance at 0.01 level.

4. CONCLUSION

The goal of the current study was to conduct the GCA and SCA of traditional highland maize inbred lines. In 2019–2020, two single cross testers were used to cross 26 inbred lines using the LxT mating pattern. As a result, 52 maize single cross hybrids were tested in Ambo and Kulumsa using an alpha lattice design and two replications. The majority of the examined traits had considerable genotype-to-genotype variation, according to analysis of variance. For the majority of the examined qualities, testers found highly significant variations between inbred lines and lines, indicating the involvement of additive and non-additive gene activity in regulating the inheritance of the traits. Thus, the current study implies that most qualities can be improved by selection. The current study highlighted crosses L14x T1 (10.13 t/ha), L26 x T1, L10xT1, L7x T1), (L7 xT2), and L20 x T1 for additional multi-location evaluation based on the grain yield performance at two locations. Additionally, lines L2, L4, L5, L7, L10, and L10 were found to be effective positive general combiners that could aid in the creation of synthetic varieties. Genes were responsible for the inheritance of yield, and features related to yield were greatly influenced by the environment, according to significant GCA and SCA mean sum of square in various environments. Programmes for the production of maize varieties may use inbred lines with favourable GCA effects for desired features. Good general combiner lines L4, L5, L7, L10, and L13 were used to select for the trait and increase grain production. Crosses including L1xT2, L14xT1, L17xT1, L8xT1, L10xT1, L14xT1, L17xT1, L20xT2, L24xT2, and L26xT1 had notable favourable impacts on grain yield. They were regulated by non-additive action and could be increased by hybrid breeding. L3, L4, L4, L11, L14, L18, L19, and L23 were effective general combiners for the silking date and the anthesis date, respectively, so that the inheritance was governed by additive gene effect and could be enhanced through selection.

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