Combining Ability Study for Grain Yield and Agronomic Traits of Quality Protein Maize (*Zea mays* L.) Inbred Lines Adapted to Mid-Altitude Agroecology of Ethiopia

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Abstract. In spite of the importance of quality protein maize to alleviate protein deficiency, almost all maize varieties cultivated in Ethiopia are normal maize varieties, which are devoid of lysine and tryptophan. Perusing the combining ability of QPM inbred for grain yield and its components is vital to design appropriate breeding strategies for the development of nutritionally enhanced maize cultivars. A line x tester analysis involving 36 crosses generated by crossing 9 elite maize inbred lines with 4 testers were evaluated for different desirable agronomic traits during the 2019 main season at BNMRC and JARC. The experiment was conducted using alpha lattice design with 3 replications. The objectives were to determine the combining ability of quality protein maize inbred lines, adapted to mid altitude agroecology of Ethiopia for agronomic traits. The crosses were evaluated in alpha lattice design replicated 3 times. Analyses of variances showed significant mean squares due to crosses for almost all the traits studied. GCA mean squares due to lines and testers were significant (P<0.05 or P<0.01) for most studied traits. SCA mean squares were also significant for most attributes across locations. The comparative importance of GCA and SCA variances observed in the current study for most studied traits indicated the preponderance of additive genetic variance in governing these attributes. Only L3 was the best general combiner for grain yield. Inbred line L3, for days to anthesis and L5 for days to silking had negative and significant GCA effects. L5 and L6 displayed negative and significant GCA effects for plant and ear height. Crosses, L2xT4, L3xT4, L4xT4, L5xT2, L6xT3, L7xT2, L9xT1 and L9xT4 were good specific combiners for grain yield. In general, these genotypes help as a source of promising alleles that could be used for forthcoming breeding work in the development of quality protein maize cultivars with desirable traits.

Keywords: combining ability; GCA effect; line by testers; SCA effect; quality protein maize

INTRODUCTION

Maize (*Zea mays* L.) is among the most important cereals for both human and animal consumption, where used as food, feed, and fodder. In addition, many products such as oil, starch, gluten, alcohol, glucose, and ethanol are obtained as a maize product (El-Shamarka *et al*.,2015). Quality protein maize (QPM), which are more important for both humans and monogastric animals since they have high lysine and tryptophan among. QPM is described as nutritionally superior maize with high lysine and tryptophan contents and desired kernel characteristics as compared to its normal maize counterparts. Biological value of QPM was almost equivalent to egg protein. Breeding of maize for quality protein is based on three genetic systems like opaque-2 genetic system, endosperm modifier genetic system and associated gene systems(Maqbool *et al*.,2021). Maize, which we call, QPM, can significantly improve the nutritional status of groups whose main staple is maize and who cannot afford protein-rich foods to supplement their diet (Priya *et al*.,2015). In Ethiopia, maize has become one of the 5 major cereals crops (including wheat, teff, barley and sorghum) in terms of production volume, area coverage and household consumption (Abate *et al*., 2015). It occupies about 2 million ha, the 2nd largest production area next to teff. Approximately 9 million smallholders account for 95% of the national maize production (Taffesse *et al*., 2012). However, yet, the actual maize yield is still lag on-farm and on station trial yields (Kassie *et al.,* 2014). This is attributed due to shortage of high yielding varieties, biotic and abiotic stresses (Mosisa *et al*., 2012) are the foremost contributors for low yield.

In contrast, population growth and changing consumption patterns have increased global food demand and are threatening food security in the developing world (Dzanku *et al*.

2015). Additionally, most maize cultivated in Ethiopia is Conventional maize which is inadequate levels of tryptophan and lysine and therefore its consumption without a balanced protein source, especially by infants, could result in initial growth failures such as 'kwashiorkor,' reduced immune system and consequently, death (Sultana *et al*., 2019). These imply that the production is unsatisfactory to meet the demands of a rapidly increasing population of the country principally in nourishment cases. To solve and for narrowing the yield gap requires the identification and explanation of factors (Assefa *et al*., 2020). Hence, plant breeders always have an objective to advance the yield and quality of maize which require continuous development and release of higher yielding, glowing qualified and well adapted varieties having better advantage over the existing commercial varieties (Pandit *et al*., 2019).

To develop new maize genotypes, breeders need acquaintance regarding the gene actions and comparative combining ability of the inbred lines. Combining ability is the ability of an inbred to transmit a favorable performance to its hybrid offspring. Combining ability analysis is an important genetic tool used to estimate the estimates of general combining ability (GCA) of parents and specific combining ability (SCA) of crosses and facilitated selection of the desired parents and crosses (Ahmed *et al*., 2017). This might include information about general and specific combining ability of inbred lines in yield and its components. The two main genetic parameters, GCA and SCA are vibrant in developing maize breeding approaches. The advantage of parental inbred lines having good GCA is twofold: 1) they can be used for development of new inbred lines and 2) they can be used as parents of new hybrids. GCA and SCA effects are important indicators of the level of usefulness of the inbred lines in hybrid combinations and in categorizing materials into heterotic groups (Tolera *et al*., 2017). The

variance due to general combining ability (GCA) is usually considered to be an indicator of the extent of additive type of gene action, whereas specific combining ability (SCA) is taken as the measure of non-additive type of gene actions in heterosis breeding (Kanagarasu *et al*., 2010). One of the most revealing procedures in this concern line is tester mating design, which is widely used for assessing the types of gene action and combining ability since it provides reliable information on GCA and SCA (Sharma *et al*., 2004). Therefore, this study was conducted to determine inbred lines with good general and specific combining ability effects for quality protein maize for future uses in hybrid maize breeding programs.

METHODS

1. Descriptions of experimental sites

The experiment was conducted at Bako National Maize Research Center (BNMRC) and Jimma Agricultural Research Center (JARC) during the 2019 cropping season. BNMRC is in the East Wollega zone of the Oromia National Regional State, Western Ethiopia. BNMRC lies between 9°06' north latitude and 37°09' east longitude in the sub-humid agro-ecology, at an altitude of 1650 meters above sea level. The mean minimum and maximum temperatures of the location are 19.7°C and 22.7°C, respectively. The long-term annual rainfall of the site is 1245 mm per year and relative humidity of 63.55%. The soil type at BNMRC is characterized by reddish brown in color and clay and loam in texture (nitisols) with pH of 6.0 and 5.9 (Girma *et al*., 2015). JARC is in the Jimma zone, Oromia National Regional State, South Western of Ethiopia. The center is located between 7°40'37'N and 36°49'47'E and at an altitude of 1753 m.a.s.l. The average maximum and minimum temperatures are 11.9 and 26.2°C, respectively. It receives an average annual rainfall of 1532 mm. The long-term annual rainfall of the site is 1572 mm per year with an RH of 67%. The soil type at JARC is

characterized by reddish brown/ nitisols with pH of 5.20 (Lemi *et al.,* 2018).

2. Experimental materials

The experiment consisted of 36 F_1 hybrids and 13 parental lines. The 36 F1 hybrids were generated by using design-II in 2018/2019 cropping season at Bako National Maize Research Center from 13 parental lines (9 females and 4 males) (Table-1) introduced from CIMMYT and IITA for QPM germplasm development.

Table 1. List of parental inbred lines used in experiment to generate the single cross hybrids using Mating design-II.

Code	Genotype name	Origin of germplasms lines	Source of lines
L1	CML511	CIMMYT-Zimbabwe	BNMRC
L2	CZLQ2	CIMMYT-Zimbabwe	>>>
L3	CZLQ3	CIMMYT-Zimbabwe	>>>
L4	TZMI818	IITA-Nigeria	>>>
L5	TZMI819	IITA-Nigeria	>>>
L6	TZMI820	IITA-Nigeria	>>>
L7	TZMI825	IITA-Nigeria	>>>
L8	TZMI829	IITA-Nigeria	>>>
L9	TZMI833	IITA-Nigeria	>>>
Testers	Tester's name	Origin of germplasms testers	Source of testers
T1	CML144	CIMMYT-Zimbabwe	BNMRC
T2	CZLQ1	CIMMYT-Zimbabwe	>>>
T3	CZLQ5	CIMMYT-Zimbabwe	>>>
T4	TZMI809	IITA-Nigeria	>>>

3. Experimental Design and Field Managements

At the main cropping season of 2018, both the hybrid (36F1) and 13 parental lines with a total of 49 entries were planted by laid out in 5x8 alpha lattice experimental design (Patterson and Williams, 1976) with 3 replications. Each entry was planted in one row per plot of 5m long with spacing of 0.75 m between rows and 0.25 m between plants within a row. Hybrid and parental trials were planted adjacent to each other in the same field to avoid the shade effect. Two seeds were planted per hill to ensure uniform and enough stand and then thinning was performed at the 3 to 5 leaf stages to attain a final plant density of 53333 plants per hectare as EIAR recommendations.

Planting was conducted on the onset of the main rainy season once adequate soil moisture level was reached in order to ensure good germination and seedling development. Pre-emergence herbicide. NPS and urea fertilizers were applied at the rate of 150 kg/ha and 250 kg/ha, respectively. The other remaining agronomic practices were carried out as per the recommendation for the areas.

4. Data Collected

Data on grain yield and other important agronomic traits were collected on a plot and sampled plant bases. Data collected on a plot basis include days to 50% silking (DS), number of ears per plant (EPP), field weight

(FW) (kg/plot), plant aspects (PA), ear aspects (EA) and bad husk cover (HC); while data recorded on sampled plants basis were ear height (EH) (cm) and plant height (PH) (cm), number of rows per ear (NRPE), number of kernels per row(NKPR), ear diameter (ED), ear length (EL), thousand kernels weight (TKW), root Lodging (RL), stock Lodging (SL) and major diseases such as gray leaf spot (GLS), turcicum leaf blight (TLB) and common leaf rust (CLR).

5. Statistical analysis
5.1 Analysis of variance (ANOVA)

Analysis of variance (ANOVA) were computed for grain yield and other agronomic traits for individual location. Prior to combined data analysis across locations, Bartlett's test for grain yield and related traits were conducted to test homogeneity of error variances (Gomez and Gomez, 1984). As a result, combined analysis over the 2 locations was carried out for these traits by using PROC GLM and PROC MIXED in SAS (SAS, 2014). Further, analyses were performed according to the line x tester analysis to partition the mean square due to crosses into lines, tester, and line by tester effects (Dabholkar, 1999 and Singh and Chaudhary, 1985) using SAS program for the traits with significant differences among crosses. The combining abilities were investigated; GCA and SCA effects were estimated according to the formula given in the following section.

5.2 Combining ability analysis

5.2.1 Estimation of GCA effects

Line x tester analysis was done for traits that showed statistically significant differences among crosses in each environment and across environments using the adjusted means based on the method described by Kempthorne (1957). General combining ability (GCA) and specific combining ability (SCA) effects for grain yield and other agronomic traits were calculated using the line x tester model.

$$Y_{ijk} = \lceil + r_k + g_i + g_j + S_{ij} + e_{ijk} \text{......equation}(1)$$

Where, Y_{ijk} = the value of a character measured on cross of line i by tester j in kth replication μ = Population means, r_k = Effect of kth replication, g_i = General combining ability (GCA) effects of ith line, g_j = General combining ability (GCA) effect of the jth tester, S_{ij} = Specific combining ability (SCA) of ith line and jth testers such that Sij equal to Sji, and e_{ijk} = Experimental error for ijkth observation. General and specific combining abilities of lines were computed for characters that showed significant differences among crosses following line by tester (LxT) analysis as suggested by Singh and Chaudhary (1985).

The main effects due to females and males were considered as GCA effects while, male x female interaction effects were represented as the SCA. Then the combining ability mean squares were calculated based on cross means of each genotype from each location, error mean squares calculated for crosses above were used to test the significance of GCA and SCA interactions with location (Singh and Chaudhary, 1985).

This was computed based on formula recommended by Singh and Chaudary (1985) as follows:

a) Lines: $g_i = \dfrac{X_i..}{tr} - \dfrac{X...}{ltr}$ ………….equation (2)

b) Testers: $g_j = \dfrac{X._j.}{lr} - \dfrac{X...}{ltr}$ ………equation (3)

Where, gi☐ GCA effect for ith line, g$_j$☐ GCA effect for jth tester, X.$_j$.= sum of the jth tester, X.$_i$...☐ Sum of the ith line, X...☐ grand sum, l☐ number of lines, t☐ number of testers and r ☐ number of replications

$$\sum g_i = \sum g_j = 0 \quad \ldots\ldots\text{equation (4)}$$

5.2.2. Estimation of SCA effects

SCA effect was calculated as a deviation of each cross mean from all hybrids' mean adjusted for corresponding GCA effects of parents. They were computed as follows as given by Singh and Chaudary (1985).

$$S_{ij} = \frac{X_{ij\cdot}}{r} - \frac{X_{i\cdot\cdot}}{tr} - \frac{X_{\cdot j\cdot}}{lr} + \frac{X_{\ldots}}{ltr} \quad \ldots\ldots\ldots\text{equation (5)}$$

Where, S$_{ij}$ = SCA effect of the ijth crosses, X$_{ij\cdot}$ = i x j cross sum, X$_{i\cdot\cdot}$ = ith line sum, X$_{\cdot j\cdot}$ = jth tester sum, l = number of lines, t = number of testers and r = number of replications

Standard errors for combining ability effects were calculated as follow:

1. Standard error for general combining ability effects

a) Line: SE (GCA for line) = $\sqrt{Mse(l-1)/ltr}$……..equation (6)

b) Tester: SE (GCA of tester) = $\sqrt{Mse(t-1)/ltr}$…….equation (7)

2. Standard error for specific combining ability effects

SE (SCA effects) = $\sqrt{Mse(l-r)(t-r)/ltr}$……equation (8)

3. Standard error of the difference between combining ability effects

a) Standard error of the differences between general combining ability effects

SE (g$_i$-g$_j$) line = $\sqrt{2Mse/rt}$..........equation (9)

SE (g$_i$-g$_j$) tester = $\sqrt{2Mse/rl}$......equation (10)

b) Standard error of the differences between specific combining ability effects

SE (S$_{ji}$-S$_{kl}$) = $\sqrt{2Mse/r}$ ....equation (11)

The significance of GCA and SCA effects were estimated by dividing the corresponding SCA and GCA values by their respective standard error and comparing the obtained t value with tabular t-value at error degree of freedom. The values of GCA(males), GCA(females) and SCA effects were evaluated based on the procedure as recommended by Singh and Chaudhary (1977).The significance of general and specific combining ability effects was tested using the formula of Cox and Frey (1984).

(a) General Combining ability effect:

$$t = \frac{GCA}{SE\ gca(male)} \text{where, S.E (GCA male)} = \frac{(mse)1/2}{r*f} \ldots\ldots\text{equation (12)}$$

$$t = \frac{GCA}{SE\ gca(females)} \text{ where, S.E (GCA female)} = \frac{(mse)1/2}{r*m} \ldots\ldots\text{equation (13)}$$

Where:- Mse = error mean square, r = number of replications, f = number of females, m = number of males, S.E = standard error

(b) Similarly, significance of SCA effect:

$$t = \frac{SCA}{SE\ sca(line*tester)} \quad \text{where, S.E (SCA)} = \frac{(mse)1/2}{r} \ldots\ldots\text{equation (14)}$$

Where: Mse= error mean square and r = number of replications

4. Proportional contribution of line, tester, and line by tester estimations

The proportion contribution of lines, tester, and line x tester to the sum square of crosses were assessed with the ratio between sum of squares of each component and the cross sum of squares according to given by (Singh and Chaudhry, 1985) as the following formulas:-

$$\text{Contribution of lines} = \frac{Sum\ square\ of\ line}{Sum\ square\ of\ Cross} \times 100 \ldots\ldots\ldots\text{equation (15}$$

$$\text{Contribution of tester} = \frac{Sum\ square\ of\ tester}{Sum\ square\ of\ Cross} \times 100 \ldots\ldots\ldots\text{equation (16)}$$

$$\text{Contributions of line by tester} = \frac{Sum\ square\ of\ Line\ x\ Testers}{Sum\ square\ of\ crosses} \times 100 \ldots\ldots\text{equation (17)}$$

RESULTS AND DISCUSSION

Mean squares due to sites, lines, testers, testcrosses/ genotypes, and their interaction for the studied attributes of both individual and combined locations were estimated to describe the observed variation. All traits across locations, due to crossing, showed significant difference for both GCA and SCA ($p<0.05$ or $p<0.01$). This result showed the existence of adequate genetic variability in the experimental genotypes under study and used to curtain the importance of both additive and non-additive components of genetic discrepancy in inheritance of these characters. The combined analysis, the mean square of line and tester GCA showed significant difference ($p<0.01$ or $p<0.05$) for the most of studied traits (Table-2).The mean square of SCA also showed significant difference ($p<0.01$ or $p<0.05$) for all traits except anthesis silking interval, ear length, ear rot, stock lodging and root lodging. The results of analysis of combining abilities obtained from this study indicated the importance of both additive gene actions in controlling these agronomically important traits. In line with this study, many maize researchers also have reported significant differences in GCA for grain yield and yield-related traits in different maize genotypes studied. Legesse *et al.* (2017), Tolera *et al.* (2017), Bitew *et al.* (2017) and Gemechu *et al.* (2020) in separate study suggested that both GCA and SCA effects are significant and important for grain yield and most other traits studied.

GCA × Loc mean squares were significant for grain yield, turcium leaf blight, common leaf rust, number of kernels per row, ear length, ear diameter, thousand kernel weights, ear per plant, and bad husk cover which indicating that GCA effects associated with parents were not reliable for these traits over the two environments (Table-2). But the interaction was not significant for days to anthesis, days to silking, and days to maturity, plant and ear height, number of kernels per ear, gray leaf spot, ear rot, Phaeosphaeria leaf spot, stock, and root lodging, indicating that GCA effects related with parents were consistent over the 2 environments. Dagne *et al.* (2014), and Bitew *et al.* (2018) observed significant GCA × location interaction in QPM inbred lines for grain yield and other agronomic traits in independent studies. SCA × Loc mean squares were significant for anthesis silking interval and common leaf rust displaying that SCA effects of these traits associated with crosses were not consistent over the two environments, while, SCA × Loc showed non-significant mean squares for most of the traits, showing that SCA effects related with crosses were consistent over the 2 environments. Significant differences were observed in

checks x location and crosses vs check x location for grain yield, plant and ear height, number of kernels per ear, ear rot, husk cover, stock, and root lodging. Similar findings were reported by Dagne *et al*. (2007) in their study on combining ability for grain yield and its component in selected maize inbred lines. Tolera *et al*. (2017) obtained highly significant variances between interactions GCAL, GCAT and SCA with the locations for grain yield, days to anthesis, days to silking, plant and ear height and ear aspect characters studied except ear aspect and grain yield in line GCA, for days to anthesis in line by tester (SCA) x locations, whereas Assefa *et al*. (2017) observed GCA × L (both for lines and testers) for days to maturity, 1000-seed weight and grain yield while significant SCA × L interaction for all characters except number of kernel rows per ear, ear length and ear diameter.

The contribution of GCA variances was greater than that of SCA variances for most of the traits except for anthesis silking interval, days to maturity, gray leaf spot, ear rot and Phaeosphaeria leaf spot across locations. The proportional sum square contribution across location of line and tester GCA (sum of line GCA and tester GCA) to the cross sum of square for grain yield was 13.4% and 50.5%, respectively, whereas proportional sum square contribution across of SCA (line by tester) to the cross sum of square for grain yield was 36% (Table-2). Among the studied traits, grain yields, days to anthesis, days to silking, plant and ear height, turcicum leaf blight, common leaf rust, ear diameter and ears per plant indicated that additive gene action was contributing superior traits in the performance of the attributes (Table-2). These indicate that contributions of GCA difference were greater than SCA difference for the majority of the traits. The higher percentage relative contribution of GCA sum of square over SCA sum of square revealed the major role of additive gene action over non-additive action in the inheritance of traits studied.

Generally, the contribution of GCA variance was much greater than that of SCA variance for all the characters except days to maturity, gray leaf spot, ear rust and phaeosphaeria leaf spot indicating the predominance of additive gene action in the inheritance of traits (Table-2). Similar findings were reported by Berhanu (2009) that the contribution of GCA for the total variation was higher than SCA. Anderson *et al*. (2012) also observed that the main percentage of genetic variation in maize is because of additive genetic effects. Fan *et al,* (2016) suggested that general combining ability effects of specific lines are controlled by genes with additive effects and these effects can be transferred to the next generation.

General combining ability effect estimates

The estimated general combining ability of inbred lines across locations is presented in Table-3. For grain yield, combined across locations estimated GCA effect of line L3 exhibited positive and significant that is reflected as anticipated good combiner; whereas L6 and L9 displayed negative significant GCA effects and this indicates that it is a poor combiner while the other lines had positive and negative non-significant GCA effects for grain yield. The significant positive GCA effect of inbred lines displayed the potential advantage of the parents for developing high-yielding crosses. Fan *et al*. (2008), suggested that selecting inbred lines with positive GCA effects in all or most of the yield components traits will have greater chance to obtain crosses with higher grain yield. In another suggestion, positive significant GCA effects for maize lines indicated that they are desirable parents for maize hybrid development and involvement in the maize breeding program as they can be a good allele source in the process of varietal development (Rawi, 2016).

Table-2. Analysis of variance for combining ability combined across the two locations and proportional contribution of GCA and SCA in hybrids evaluated in 2019.

Source of Variations	DF	Mean square											
		GY	DA	DS	ASI	DM	PH	EH	EPO	TLB	NKPE	PA	EA
Locations(L)	1	711**	320**	75.9*	0.26**	68.26*	0.13	0.94	0.13**	4.13**	8.36*	40.1**	7.9**
Rep(Site)	4	5.65*	4.69	4.67	3.29	885.8*	455.6	529.5*	0.006*	0.39*	0.71	0.49	1.96**
Lines	8	4.7**	43**	58.3**	0.005	58.24*	1684**	1001**	0.017**	0.33**	1.95*	2.09**	3.04
Testers	3	47.2**	92.2**	108**	0.02*	44.16*	4815**	2228**	0.017**	1.09**	16.8**	2.85**	1.16**
Lines*Testers	24	4.2**	16.4**	20.2**	0.005	29.27*	591**	261**	0.002	0.16*	0.85*	0.403	0.64*
Lines*L	8	11.9**	6.18	0.88	0.02	14.42	22.89	1.04	0.003**	0.32*	1.33	0.57	0.18
Testers*L	3	1.09	0.55	0.19	0.008*	15.93	6.88	0.58	0.00005*	0.224*	0.84	0.15	0.34
Lines*Tester*L	24	0.90	1.16	0.62	0.006*	24.9	13.79	0.58	0.00005	0.07	0.45	0.12	0.24
Error	140	1.02	6.1	5.95	0.0037	22.9	185.4	93.4	0.0014	0.076	0.63	0.16	0.27
Line GCA (%)		13.4	33.9	36.6	16.2	40.4	32.0	38.2	59.4	27.3	18.0	28.3	47.5
Testers GCA (%)		50.5	27.3	25.4	19.4	35.8	34.3	31.9	17.5	33.5	58.4	47.9	11.9
GCA %(T+L)		63.9	61.2	62	44.7	46.0	66.3	70.1	76.9	60.8	76.4	76.2	59.4
LxT SCA (%)		36.0	38.9	38.0	55.3	54.0	33.7	29.9	23.1	39.2	23.6	23.8	40.6
GCA/SCA		1.8	1.6	1.6	1	1	2.0	2.3	3.3	1.6	3.2	3.2	1.5

*=Significance level at 0.05, **=Significance level at 0.01 no asterisk of */**=non-significance at 0.05 and 0.01 levels, GCA=general combining ability SCA=specific combining ability, Df=degree of freedom, GY=grain yield, DA=days to anthesis, DS=days to silking, ASI=anthesis silking interval, DM= days to maturity, PH=plant height, EH=ear height, EPO= ear position, TLB= turcicum leaf blight, NRE=number of row per ear, NKR=number of kernels per row, EL=ear length, ED=ear diameter, TKW= thousand kernels weight, GLS=gray leaf spot, EPP=ear per plant, PA=plant aspect, EA=ear aspect, EPO=ear position.

Table-2. …..(Continued)

Sources of variations		Mean square											
	DF	CLR	NKPR	EL	ED	TKW	GLS	EPP	ER	HC	PLS	SL	RL
Locations(L)	1	5.6**	6513**	874**	33.1**	0.24**	5**	28.3**	21.2**	9.6**	0.45	12.3**	9.2**
Rep(Site)	4	0.53*	8.8	9.11*	0.57**	0.004	0.37*	0.18*	4.14*	13.8**	0.67*	1.01	10.2**
Lines	8	0.38*	88.9**	8.87*	0.52**	0.01**	0.21*	0.19*	0.36*	1.06**	0.298	0.29*	0.28**
Testers	3	2.57**	98.2**	8.78*	0.29*	0.01*	0.39*	1.1**	0.25	0.68*	0.593	0.37*	0.22
Lines*Testers	24	0.25*	24.47*	3.24	0.11*	0.003*	0.14*	0.12*	0.14	0.22*	0.34*	0.08	0.106
Lines*L	8	2.10**	38.23	9.24*	0.092	0.003	0.059	1.15**	0.31	0.84*	0.13	0.24	0.06
Testers*L	3	0.14	28.60*	7.99*	0.27**	0.005*	0.062	0.09	0.25	0.84**	0.1	0.16	0.08
Lines*Tester*L	24	0.21*	16.36	1.99	0.075	0.0014	0.12	0.11	0.16	0.23	0.07	0.15	0.04
Error	140	0.122	11.2	2.22	0.056	0.002	0.083	0.05	0.12	0.14	0.17	0.07	0.076
Line GCA (%)		18.2	44.6	40.5	54.7	45.7	26.9	19.3	38.6	48.9	19.4	42.2	39.5
Testers GCA (%)		45.7	18.5	15.0	11.5	12.0	18.5	42.0	7.1	15.3	14.5	16.8	11.7
GCA %(T+L)		63.9	63.1	55.5	66.2	57.7	45.4	61.3	45.7	64.2	33.9	59.0	51.2
LxT SCA (%)		36.1	36.9	44.4	33.8	42.3	54.5	38.8	54.3	35.8	66.1	41.0	48.8
GCA/SCA		1.8	1.7	1.3	2.0	1.4	0.8	1.6	0.8	1.8	0.5	1.4	1.0

*=Significance level at 0.05, **=Significance level at 0.01   no asterisk of */**=non-significance at 0.05 and 0.01 levels, GCA=general combining ability SCA=specific combining ability, CLR=common leaf rusts, NKPR=number of kernels per row, EL=ear length, ED=ear diameter, TKW= thousand kernels weight, GLS=gray leaf spot, EPP=ear per plant, ER= ear rot, HC=husk cover, PLS= phaeosphaeria leaf spot, SL=stock lodging, RL= root lodging.

Darrigues *et al.*(2005) suggested that inbred lines indicating significant negative values for grain yield were unsuitable/poor combiner for developing high yielding maize.

Regarding plant height, across locations, L5, L6 and L7, L8 exhibited negative and positive significant GCA effects respectively whereas the others lines contributed either positive or negative non-significant GCA effects. In case of ear height; L5, L6 and L8 displayed negative and positive significant GCA effects, respectively, while the others showed either positive or negative non-significant GCA effects (Table-3).

The negative significant GCA effect has a tendency to reduce plant height whereas the positive significant has a trend to increase plant height in the crosses of offspring. These findings had resembled results with the preceding study of various authors (Matin *et al.*, 2016; Bitew *et al.*, 2017 and Melkamu *et al.*, 2020). In the same way, T1 (positive), T3 and T4 indicated positive and negative significant GCA effects for plant height whereas T1 and T3 showed significant GCA effects for EH to across locations (Table-3). Similarly, and Bitew (2016) reported that inbred lines with significant negative GCA effects were good combiners that had a tendency to decrease plant and ear height while those lines which had significant positive GCA effects were good combiners in increasing ear height. And, he suggested that short maize varieties are needed with reduced ear height to circumvent lodging under mid altitude agro-ecology. Shushay *et al.*(2011) reported that shorter plant height is desirable for lodging resistance. Similarly, the earlier investigators (Girma *et al.*, 2015 and Tolera *et al.*, 2017) observed significant positive and negative GCA effects for ear height.

For number of kernels per row across locations L9 was provided negative significant GCA effects for number of kernels per row traits and T2 revealed positive significant GCA effects for both number of kernels per row. Regarding the number of rows per ear only L9 showed positive and highly significant whereas the rest indicated positive and negative non-significant GCA effects. For ear per plant, combined across locations, L2 indicated positive and significant GCA effects whereas L6 displayed negative and significant GCA effects while T2 and T3 were given positive significant GCA effects for ear per plants(Table-3). Similar reports were forwarded by various academics (Tessema *et al.*, 2014; Alamerew *et al.*, 2015; Gemechu, 2019 and Tesfaye, 2019).

For ear rot, combined across locations, L2, L4 and L5 perceived negative and significant GCA effects whereas L8 and L9 displayed positive and significant GCA effects. Regarding to husk cover, L1, L2, L6 and L8 displayed negative and significant GCA effects whereas L4 and L9 perceived positive and significant GCA effects. For stock lodging, combined across locations, L4, L6 and L7 showed positive and negative significant GCA effects whereas for root lodging, L2, L4, L6 and L8 displayed positive and negative significant GCA effects (Table-3). Regarding the gray leaf spot, all lines indicated positive and negative non-significant GCA effects whereas for turcicum leaf blight, L4 and L9 displayed positive and significant GCA effects while L6 perceived negative and significant GCA effects. For common leaf rust, only L9 exhibited positive and significant GCA effects while the rest displayed negative and positive non-significant GCA effects (Table-3).

Table-3. Estimates of general combining ability (GCA) effects of lines and tester for grain yield and other agronomic traits combined across locations evaluated in 2019.

Crosses	GY	DA	DS	DM	PH	EH	GLS	TLB	CLR	KPE	KPR	EL	EPP	ER	HC	SL	RL
L_1	0.23	0.8	1.1	0.08	4.2	2.30	0.02	0.09	-0.18	-0.4	-0.39	-0.21	0.02	-0.03	-0.7**	-0.10	0.11
L_2	-0.15	2**	2.3**	0.68	1.8	5.03	-0.15	-0.08	0.07	-0.01	-0.14	0.44	0.17**	-0.24*	-0.26*	-0.13	-0.26**
L_3	0.6*	-1	-1.18	0.31	-4.23	0.50	-0.06	-0.13	0.16	0.02	1.34	0.31	0.16	0.08	0.14	-0.13	-0.03
L_4	-0.07	-0.4	-0.38	-1.6	-1.68	0.43	0.09	0.19*	-0.09	-0.12	0.02	-0.06	-0.08	-0.3**	0.77**	0.4**	0.28**
L_5	0.5	-2.3**	-2.5**	-1.52	-8.5*	-9.54**	-0.05	0.00	0.13	-0.4	-1.21	0.08	-0.10	0.3**	-0.44*	0.04	0.08
L_6	-0.62*	0.5	0.3	0.03	-11**	-10.6**	0.06	-0.17*	-0.14	0.06	0.17	-0.04	-0.19**	-0.3**	-0.4**	0.4**	0.28**
L_7	-0.4	1.2	1.3	-0.4	8.42*	3.4	-0.04	-0.02	0.00	0.16	0.73	-0.19	0.02	-0.2	0.8**	0.08	-0.08
L_8	0.46	-0.72	-1.03	2.94*	11.2**	6*	-0.02	-0.06	-0.16	-0.01	1.25	0.19	0.04	0.5**	-0.43*	-0.5**	-0.25**
L_9	-0.59*	-0.1	-0.27	-0.52	0.01	2.41	0.15	0.18*	0.21*	0.7**	-1.8*	-0.51	-0.04	0.19*	0.52**	-0.04	-0.13
SE(lines)	**0.28**	**0.67**	**0.66**	1.30	**3.71**	**2.63**	**0.08**	**0.08**	**0.11**	**0.22**	**0.91**	**0.41**	**0.061**	**0.09**	**0.10**	**0.07**	**0.08**
SEd(lines)	**0.41**	**1.01**	**1.1**	2.39	**5.56**	**3.95**	**0.12**	**0.11**	**0.14**	**0.41**	**1.37**	**0.61**	**0.091**	**0.17**	**0.19**	**0.13**	**0.14**
T_1	0.60**	1.45**	1.6**	1.03	10.1**	5.58**	-0.08	-0.10*	-0.2**	0.01	0.16	-0.25	0.08	-0.06	-0.5**	0.10	0.06
T_2	0.6**	-0.83*	-0.93*	-0.14	2.9	1.93	-0.04	-0.13**	0.12*	-0.13	1.36*	0.5*	0.16**	0.28**	-0.11	0.10	-0.16**
T_3	-0.9**	-0.97*	-0.95*	-0.16	-5*	-7.17**	0.08	0.11*	0.38**	-0.55	-0.43	-0.19	-0.08	-0.14	0.37**	-0.3**	-0.01
T_4	-0.3*	0.35	0.20	-0.73	-8**	-0.34	0.04	0.12**	-0.3**	0.67	-1.09	-0.06	-0.16**	-0.08*	0.24	0.10*	0.11*
SE(Testers)	**0.17**	**0.41**	**0.41**	**0.80**	**2.27**	**1.61**	**0.05**	**0.05**	**0.06**	**0.13**	**0.56**	**0.25**	**0.053**	**0.06**	**0.06**	**0.04**	**0.05**
SEd(Testers)	**0.28**	**0.67**	**0.66**	**1.30**	**3.71**	**2.63**	**0.078**	**0.075**	**0.095**	**0.22**	**0.91**	**0.41**	**0.061**	**0.09**	**0.10**	**0.07**	**0.08**

GY=grain yield, DA= days to anthesis, DS=days to silking, PH=plant height, GLS=gray leaf spot, turcicum leaf blight, CLR=common leaf rusts, KPR=number of kernels per rows, EL=ear length, EPP=ear per plant, SE(lines)=standard error of general combining ability effect for lines, SE(testers)= standard error of general combining ability effect for testers, SEd(lines)=Standard error of the difference of general combining ability effects of lines, SEd(testers)=Standard error of difference of general combining ability effects of testers.

In general, many researchers have reported similar results with respect to the GCA effect of maize traits. For instance; Keimeso *et al*. (2020) combining ability of highland adapted maize DH lines for desirable agronomic traits and reported that positive and negative significant GCA effects for the traits of grain yield, days to silking, days to anthesis, plant height, ear per plant height, ear diameter and thousand kernel weights. Bitew *et al*. (2017) studied combining ability analysis of quality protein maize inbred lines for grain yield, agronomic traits, and reaction to grey leaf spot in mid-altitude and reported that positive and negative significant GCA effect for the traits grain yield, days to anthesis, days to silking, anthesis silking interval, plant and ear height, gray leaf spot and ear per plants.

Specific combining ability effect estimates

Specific combining ability effects for grain yield and yield related traits for combined across locations is presented in Table-4. For grain yield, the crosses; L2xT4, L3xT3, L3xT4, L4xT4, L5xT2, L7xT2, L9xT1 and L9xT4 showed positive significant SCA effects which indicates that these were best combinations with favorable SCA estimates for grain yield. Promising lines from these genotypes can efficiently be utilized to advance high performing hybrids for grain yields. These crosses exhibited positive and significant SCA estimates may be used in the future as a source of breeding material or as a new variety after this result will be confirmed by further testing. The crosses, L1xT4, T3xT1, L5xT3, L6xT1, L7xT4, L8xT4, L9xT2 and L9xT3 displayed a negative significant SCA effects which indicates that these were poor combinations with unfavorable SCA estimates for grain yield (Table-4). Similar findings were reported by other researchers (Mohamed *et al*., 2014; Tessema *et al*., 2014; Gideon *et al*., 2017 and Tesfaye *et al*., 2019). According to Melkamu *et al*. (2020) SCA effects relate to

dominance and epistatic components of variations. Significant SCA showed comparative importance of interactions in determining the performance of produced hybrids. And, he suggested that positive significant SCA effects indicated that produced hybrids were good specific combiners for developing high-yielding hybrids. Tolera *et al.* (2017) suggested that the crosses had significantly positive SCA effects for grain yield indicating the importance of non-additive gene action in cross combinations and there was significant positive interaction of genes between the two parents for grain yield traits.

For days to silking, across locations, the crosses such as; L2xT3, L4xT3, L5xT5, L6xT1, L7xT3, L8xT4 and L9xT2 were indicated positive significant SCA effects which indicates that these were best combinations with disapproving SCA estimates for days to ,silking, whereas L1xT3, L4xT1, L3xT4, L4xT2, L6xT3, L7xT1, L8xT3 and L9xT4 crosses exhibited negative significant SCA effects which indicates that these were best combinations with favorable SCA estimates for days to silking. The crosses displayed negative and significant SCA effects, which are considered desirable as those were related with earliness. In contrast, the cross exhibited positive and highly significant SCA effect towards undesirable direction of lateness. As a result, those crosses with high SCA effects had a tendency to enhance late maturity, while crosses that had lower SCA effect regarded as a propensity to enhance early maturity (Table-4).The results were well supported by the findings of former investigators (Dufera, 2017; Tolera *et al*.,2017 and Woldu *et al*.,2020).

For number of kernels per row, across locations, about 7 crosses revealed negative significant SCA effects which was indicating undesirable directions whereas the crosses, L2xT4, L4xT1, L8xT2 and L9xT4 displayed positive and significant SCA effect which

indicates that these were best combinations with desirable SCA estimates for number of kernels per row. For ear per plant, about 7 crosses displayed significant SCA effects in undesirable directions whereas about five crosses exhibited significant SCA effects in desirable directions (Table-4). The crosses showed positive and significant SCA effect for the number of kernels per row, indicating the tendency of the crosses to enhance grain yield. On the other hand, the crosses showed negative and significant SCA effects, indicating the propensity of the hybrid combinations to decrease the trait.

The crosses indicated significant positive SCA effects for ear per plant towards the desirable direction contribute to grain yields improvement. On the contrary the crosses displayed significant negative SCA effects indicating that these crosses had poor specific combination for ear per plant. This finding authorizes the finding of the scholars (Alamerew *et al*., 2015 and Woldu *et al.,* 2020). Therefore, the positive significant SCA effect crosses are desirable to enhance grain yield since that is straightly related with grain yield. On the other hand, negative and significant SCA effects were indicative of poor specific combiner for number of ears per plant. Dagne *et al.(*2014), significant positive or negative SCA effects indicated that the crosses performed better or poorer than what would be expected from the GCA effects of their respective parents. As Arsode *et al*.(2017) suggested in the development of improved cultivar, the estimation of SCA effects serves as supportive information on both parental forms (maternal and paternal) used in the individual cross combination. As Begum *et al. (*2018) suggested that the SCA effects of the crosses exhibited no specific trends in cross combinations between parents having high, medium, and low GCA effects.

Plant height across locations, the crosses L2xT4, L3xT1, L3xT3, L4xT1, L5xT2, L6xT3, L7xT1, L8xT4, L9xT2, and L9xT3

displayed positive and significant SCA effects whereas about 10 crosses exhibited negative and significant SCA effects for ear height (Table-4). The crosses displayed positive and significant SCA effects for plant and ear height towards undesirable direction of tallness as this contributes to susceptibility to lodging. On the other hand, the crosses exhibited negative and highly significant SCA effects for plant and ear height towards the desirable direction of shortness, indicated that this hybrid was a good specific combiner for plant height. These results were in line with the findings of various researchers (Kamara *et al*., 2014; Tolera *et al*.,2017 and Tesfaye *et al*.,2019).

For gray leaf spot, across locations, the crosses L1xT3, L2xT3, L5xT2, L8xT1 and L9xT4 displayed negative and significant SCA effects whereas the cross L1xT4, L2xT2, L4xT1, L5xT3 and L8xT2 showed positive and significant SCA effect. Regarding turcicum leaf blight, about 16.67% crosses exhibited negative and significant SCA effect whereas 11.11% displayed positive and significant SCA effect. For ear rot about 44.44% and 30.56% crosses displayed negative and positive significant SCA effect, respectively whereas about 13.89% and 8.33% crosses displayed negative and positive significant SCA effects for phaeosphaeria leaf spot, respectively. For husk cover, across locations, about 41.67% and 30.56% crosses exhibited negative and positive significant SCA effects, respectively (Table-4). Regarding to common leaf rust across locations, crosses as assessed SCA effects, about 22.22% and 11.11% of crosses displayed negative and positive from significant to highly significant SCA effects whereas for husk cover about 41.67% and 27.78% of crosses exhibited negative and positive SCA effect, respectively (Table-4). Similar results reported by others scholars by different time, place, and designs (Berhanu, 2009; Girma *et al.,* 2015 and Beyene, 2016).

Table-4. Estimates of specific combining abilities of Line x tester across locations for yield and yield related characters

Crosses	GY	DA	DS	DM	PH	EH	GLS	TLB	CLR	KPR	RPE	EPP	ER	PLS	HC	ED	TKW
L1 xT1	0.32	-0.24	-0.34	-0.2	-0.31	2.12	0.098	0.18**	-0.02	1.11	-0.51**	-0.045	-0.23**	0.14	0.48**	0.15	3.42**
L1xT2	0.23	0.85	0.26	-3.3*	-2.56	0.27	-0.06	0.17*	0.21	-0.61	0.37	0.091	0.36**	-0.09	0.05	-0.14	-3.7**
L1xT3	-0.0012	-0.89	-1.6**	0.8	-8.3*	-6.9**	-0.26**	-0.25**	-0.10	-0.21	0.35	0.08	-0.06	0.08	-0.44**	-0.22	0.86**
L1xT4	-1.46**	-0.55	0.31	2.6	7.79	-3.13	0.21**	-0.17**	0.11	-1.55	0.30	-0.16**	0.21*	-0.17	-0.19*	0.10	-3.3**
L2xT1	-0.67**	-0.62	-0.70	-1.6	-11.7**	-12**	-0.11	0.052	0.03	-0.23	0.10	0.004	-0.64**	-0.25*	0.08	0.10	0.59**
L2xT2	-0.41	-0.09	-0.35	-1.5	-0.86	-3.63	0.15*	0.13	0.12	-1.2	0.18	-0.008	0.53**	0.15	0.23*	-0.06	-1.2**
L2xT3	-0.37	-0.19	1.25*	4.7**	2.71	8.97**	-0.18*	0.002	-0.17*	-1.8*	-0.19	-0.09	-0.56**	0.11	0.00	0.07	2.53**
L2xT4	1.25**	1.8**	1.11	0.2	7.8*	8.47**	0.03	-0.17**	-0.22**	3.1**	-0.14	-0.050	-0.13	-0.14**	-0.42**	0.00	0.04
L3xT1	-1.01**	0.48	0.91	-0.4	10.9**	2.42	-0.11	-0.23**	-0.22**	-1.24	0.03	-0.28**	-0.58**	0.04	-0.49**	-0.05	1.05**
L3xT2	0.14	-0.90	-0.84	-1.2	-12.8**	-4.93*	-0.06	-0.03	0.077	0.03	0.00	0.07	0.26**	-0.02	-0.09	0.03	-5.4**
L3xT3	0.50*	1.16*	1.01	2.4	11.6**	8.50**	0.03	0.010	0.002	2.62*	0.13	0.12*	0.01	-0.19	-0.32**	0.08	1.41**
L3xT4	0.73**	-0.92	-1.14*	-2.9	-16.4**	-7.3**	0.03	0.19	-0.14	-1.7*	0.26	0.05	0.44**	0.31	0.85**	-0.09	1.01**
L4xT1	-0.21	-1.9**	-2.4**	-7**	-13.5**	-9.2**	0.16*	-0.47**	0.03	2.6**	-0.41*	0.05	-0.34**	-0.10	-0.29**	-0.09	-1.3**
L4xT2	-0.091	-1.34*	-1.30*	-6**	8.01*	3.47	-0.21**	-0.02	0.24**	0.98	-0.10	0.09	-0.18*	0.09	-0.55**	-0.04	-1.3**
L4xT3	-0.43	3.5**	3.71**	3.5	-0.42	-3.09	0.09	-0.02	-0.17*	-4**	0.28	0.02	0.41**	-0.16	1.63**	-0.13	-0.8**
L4xT4	0.53*	-0.27	-0.10	4.6	6.97*	4.57*	-0.035	0.19**	0.13	0.67	-0.22	0.0008	0.09	0.85	-0.45**	0.07	1.4**
L5xT1	0.17	1.25*	1.37*	-2.4	-0.67	-0.51	-0.073	0.06	-0.11	1.21	-0.01	0.073	1.38**	-0.12	0.25**	-0.07	-1.5**
L5xT2	0.51*	0.04	0.14	6.3**	17.2**	11.2**	-0.19**	-0.07	-0.06	-0.32	0.07	-0.04	-0.32**	-0.10	-0.18*	0.14	3.2**
L5xT3	-0.69**	-0.65	-0.68	-6**	-14.6**	-7.7**	0.53**	0.09	0.28**	-1.36	-0.19	-0.18**	-0.23**	0.07	0.17	-0.05	-2.76
L5xT4	0.041	-0.65	-0.83	2.5	-1.88	-2.91	-0.02	-0.08	-0.11	0.47	0.13	0.14**	-0.63**	0.15	-0.25**	-0.02	1.1**
L6xT1	-0.57*	2.13**	2.62**	2.1	-3.17	-1.75	-0.073	0.06	-0.01	0.72	0.60**	-0.06	-0.03	-0.21*	-0.12	-0.14	-2.2**

Table-4. continued

L6xT2	-0.31	0.58	0.36	1.8	-6.01	-2.11	-0.023	-0.24**	-0.37**	1.13	-0.87**	-0.21**	-0.19*	0.07	0.11	-0.02	3.5**
L6xT3	1.92**	-2.9**	-3.26**	-1.0	18.6**	7.67**	0.11	0.61**	0.36**	0.49	0.65**	0.11*	0.27	0.07	-0.78**	0.23	-1.3**
L6xT4	-0.14	0.23	0.42	-2.9	-9.38**	-3.83	-0.015	0.002	0.16	-1.8*	-0.37	0.15**	0.16	0.07	0.71**	-0.08	-0.1**
L7xT1	0.10	-1.20*	-1.42*	2.4	6.74*	10**	0.03	0.08	0.52**	-0.76	0.66**	-0.03	0.27**	-0.66	-0.29**	0.03	-3.2**
L7xT2	1.27**	-0.75	-0.82	3.7	-5.42	-4.68*	0.081	-0.05	-0.27**	1.25	-0.37	0.0081	-0.40**	0.26*	-0.05	-0.08	3.9**
L7xT3	-0.34	2.77**	2.53**	3.2	3.14	10.9	-0.04	0.031	-0.26**	0.592	-0.69**	-0.12*	0.35**	-0.24*	-0.54**	0.01	-1.4**
L7xT4	-1.03**	-0.77	-0.29	-9**	-4.46	-4.75*	-0.08	-0.06	0.015	-0.53	0.40*	0.14*	-0.22**	0.01	0.88**	0.04	0.63**
L8xT1	0.41	-0.33	-0.42	7.4**	5.66	3.54	-0.16*	0.04	-0.17*	-2**	0.15	0.102	0.02	-0.06	0.21*	-0.09	-0.1**
L8xT2	0.38	-0.71	-0.82	-5.4*	-0.17	1.28	0.23**	-0.01	-0.04	2.7**	0.19	-0.04	-0.32*	-0.37**	0.11	0.09	-0.1**
L8xT3	0.13	-1.7**	-1.64**	-5.8*	-9.27**	-6.3**	-0.06	0.073	0.05	1.02	-0.43*	0.14**	-0.07	0.46**	-0.20*	0.06	0.83**
L8xT4	-0.91**	2.77**	2.9**	3.7*	14.79	1.55	-0.02	-0.10	0.16	-1.32	0.09	-0.13*	0.37**	-0.04	-0.12	-0.06	-0.7**
L9xT1	1.12**	0.25	0.12	-2.6	2.16	4.84*	0.09	-0.023	0.14	-1.06	0.16	0.34**	0.48**	0.52**	0.30**	-0.04	-2.1**
L9xT2	-0.97**	1.22*	2.05**	5.6*	1.66	-0.18	0.06	0.094	-0.06	-2.4*	0.27	-0.08	-0.19*	-0.12	0.36**	0.10	0.19**
L9xT3	-0.80**	-0.81	-0.76	-4.7*	-10.8**	-9.1**	0.03	0.010	-0.05	1.31	-0.16	-0.25**	-0.11	-0.04	0.55**	-0.06	1.24**
L9xT4	0.67**	-0.65	-1.41*	1.7	6.95*	4.42	-0.18**	-0.081	-0.084	2.2**	-0.27	-0.005	-0.18*	-0.37**	-1.20**	-0.003	0.59**
SE(LxT)	**0.24**	**0.58**	**0.58**	0.80	**3.21**	**2.28**	**0.07**	**0.07**	**0.08**	**0.79**	0.13	**0.053**	**0.06**	**0.07**	**0.06**	0.06	0.01
SE(Sji-Skl)	**0.83**	**2.02**	**1.99**	3.91	**11.12**	**7.89**	**0.24**	**0.23**	**0.29**	**2.73**	0.65	**0.18**	**0.28**	**0.34**	**0.31**	0.20	0.04

GY=grain yield, DA= days to anthesis, DS=days to silking, PH=plant height, EH= ear height, GLS=gray leaf spot, TLB=turcicum leaf blight, CLR=common leaf rusts, NKPR=number of kernels per rows, KRE= number of rows per ear EL=ear length, EPP=ear per plant, ED= ear diameter=thousand kernel weight, SE (LxT) =standard error of specific combining ability of lines by testers, SE (Sji-Skl) =standard error differences of specific combining ability effects of lines by testers.

CONCLUSION

Analysis of variance showed that both additive and non-additive gene effects were most elaborate in the control of traits. Though, the proportion of GCA sum of squares was higher than that of SCA for most of the traits. This showed the higher contribution of additive gene effects to genetic inconsistency of the traits than the non-additive genetic variance in the crosses for most of traits. Additive and non-additive gene actions are imperative in governing grain yield and yield contributor traits which is approved by the existence of vastly significant GCA and SCA mean squares. In this study, for grain yield, combined across locations estimated GCA effect of line only L3 exhibited positive and significant that is reflected as anticipated good combiner; whereas L6 and L9 displayed negative significant GCA effects and this indicates that it is a poor combiner while the other lines had positive and negative non-significant GCA effects for grain yield where identified. For grain yield, the crosses; L2xT4, L3xT3, L3xT4, L4xT4, L5xT2, L7xT2, L9xT1, and L9xT4 had positive significant SCA effects. These crosses that exhibited positive and significant SCA estimates may be used in the future as a source of breeding material or as a new variety after this result will be confirmed by further testing.

From the study it can be decided that better performing hybrids, inbred lines with desirable GCA and cross combinations with desirable SCA effects for grain yield and other grain yield related traits were successfully identified. Inbred lines with a high GCA effect for grain yield and yield related traits are desirable for crosses and open pollinated varieties development in QPM breeding program. Finally, these genotypes help as a basis of promising alleles that could be used for future breeding work in the development of quality protein maize cultivars with desirable traits composition for mid altitude agroecology of Ethiopia.

CONFLICT OF INTERESTS

The authors have not acknowledged any conflict of interests.

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