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Bulo Debesa

bulodebesa2014@gmail.com

Ethiopian Institute of Agricultural Research

Berhanu Tadesse

International Maize and Wheat Improvement Center

Sentayehu Alamerew

Jimma University

Short Report

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Combining Ability and Heterotic Grouping of Advanced Maize (*Zea Mays* L.) Inbred Lines in the Moisture Stress Areas of Ethiopia

Bulo Debesa[1*], Berhanu Tadesse[2], Sentayehu Alamerew[2]

[1]Ethiopian Institute of Agricultural Research, Melkassa Agricultural Research Center, Adama Ethiopia
[2]International Maize and Wheat Improvement Center (CIMMYT), Nairobi Kenya, [2]Jimma University, Jimma, Ethiopia

Corresponding author: bulodebesa2014@gmail.com

ABSTRACT

Understanding the combining ability and heterotic grouping of maize inbred lines is essential to the development of high-yielding hybrids in the systematic breeding programs. This study was undertaken to estimate combining ability effects and to classify inbred lines into heterotic groups. A total of 84 entries, comprising 80 F_1 progenies derived from line × tester crosses and four standard checks, along with 42 parental lines, were evaluated using an alpha-lattice design with three replications at Melkassa and Dhera during the 2019/20 main cropping season. Combined analysis across locations revealed highly significant ($P < 0.01$) and significant ($P < 0.05$) differences among genotypes for grain yield and most agronomic traits. Analysis of variance for general combining ability (GCA) of lines and testers indicated significant effects ($P < 0.01$ or $P < 0.05$) for grain yield, days to 50% silking, plant height, ear diameter, ear length, kernels per row, rows per ear, root lodging, and common leaf rust. Specific combining ability (SCA) effects of line × tester interactions were significant ($P < 0.01$ or $P < 0.05$) for grain yield, ears per plant, ear aspect, plant and ear height, ear position, ear diameter, rows per ear, and thousand seed weight. The presence of significant GCA and SCA effects confirmed the existence of substantial genetic variability exploitable for hybrid development. Twenty lines exhibited positive and significant GCA effects for grain yield, with GCA contributing 47.94% to the total variance. Thirty-seven crosses showed positive and significant SCA effects for grain yield, with SCA contributing 49.54% to the total variance. The highest GCA/SCA ratio was observed for ear length (5.2), followed by days to 50% silking (4.5), indicating the predominance of additive gene action in the inheritance of these traits. Based on across-location SCA results for grain yield, 17 lines with negative and significant SCA effects with tester A (CML312) were classified into heterotic group A, while 19 lines with negative and significant SCA effects with tester B (CML395) were classified into heterotic group B. The findings provide valuable information for maize breeding programs, particularly under low-moisture stress conditions. Future efforts should emphasize multilocation evaluation of these genotypes to strengthen heterotic grouping and enhance hybrid development pipelines.

Key Words: *Combining ability, Heterosis, Heterotic group, GCA, SCA*

1. INTRODUCTION

Maize (Zea mays L.; 2n = 20) is one of the most important food, feed, and industrial crops globally. It is the sole cultivated species of the tribe Maydeae within the family Poaceae, and is believed to have originated in Mesoamerica, specifically Mexico and Guatemala, approximately 5,000–10,000 years ago (Hallauer, 1997; Paliwal & Smith, 2002; Delgado-Salinas et al., 2004).

Globally, maize is predominantly utilized as livestock feed (≈70%), with a smaller proportion consumed directly as food in developed countries (≈5%). In contrast, developing countries consume ≈34% of maize as food and ≈62% as feed, with the remainder allocated to industrial uses and seed production. In Africa, maize contributes ≈34% of dietary protein and ≈35% of calories derived from cereals, with per capita consumption averaging 43 kg annually. In eastern and southern Africa, maize accounts for ≈25% and ≈31% of total caloric intake, with per capita annual consumption of 58 kg and 84 kg, respectively (FAOSTAT, 2008).

Maize is highly adaptable, thriving from sea level up to 2,600 meters above sea level (Anley et al., 2013). According to FAO (2019), global maize cultivation covered ≈197 million hectares, producing ≈1.15 billion tons annually, with an average yield of 5.82 t/ha. In Africa, maize occupied ≈40.7 million hectares, producing ≈81.9 million tons, with an average yield of 2.01 t/ha. In Ethiopia, the Central Statistical Agency (2019) reported maize production of ≈9.64 million tons from ≈2.27 million hectares, with an average yield of 4.24 t/ha. Within Oromia Regional State, maize production reached ≈5.32 million tons from ≈1.21 million hectares, with an average yield of 4.41 t/ha.

Information on the combining ability of experimental breeding materials is essential for developing high-yielding hybrids and composite varieties (Raj, Devi, & Gokulakrishnan, 2019). The line × tester (topcross) method is widely employed to evaluate new inbred lines for general combining ability (GCA) and specific combining ability (SCA). GCA reflects the average performance of a line across hybrid combinations, largely attributable to additive gene effects, whereas SCA captures deviations from expected performance due to dominance and epistatic interactions (Sprague & Tatum, 1942; Falconer, 1960). The choice of suitable testers is critical, as narrow-base testers provide greater discriminatory power in line × tester interactions compared to heterogeneous testers (Matzinger, 1953). Proven testers enable efficient classification of inbred lines into heterotic groups, facilitating exploitation of heterosis

(Melchinger, 1999; Vasal et al., 1992a, b). Assigning lines into heterotic groups is a basis of maize breeding, as it maximizes combining ability, reduces redundancy, and guides hybrid development strategies (Hallauer et al., 2010; Xia et al., 2004).

Several studies have demonstrated significant GCA and SCA effects in maize breeding programs. Tolera et al. (2017) reported significant differences among hybrids for grain yield and resistance to gray leaf spot (GLS) and northern corn leaf blight (NCLB). Dagne et al. (2010) observed significant variation in grain yield, flowering traits, and disease resistance among CIMMYT and Ethiopian maize lines. Tamirat et al. (2014) found significant mean squares for grain yield, flowering traits, plant and ear morphology, and thousand kernel weight in elite lowland maize inbred lines evaluated at Melkassa.

Classification of maize inbred lines into heterotic groups is vital to hybrid breeding programs, enabling efficient exploitation of heterosis and reducing unnecessary hybrid evaluations (Zambezi, 1986). Line × tester analysis provides critical information on parental combining ability and gene action underlying grain yield and related traits. Increased productivity in Ethiopia must rely on the development and cultivation of high-yielding hybrids with favorable GCA and SCA profiles.Therefore, the present study was conducted to estimate the combining ability of maize inbred lines and to classify them into heterotic groups, thereby generating essential information for systematic hybrid breeding under low-moisture stress conditions.

3. MATERIALS AND METHODS

3.1. Description of Experimental Sites

The study was conducted during the 2019 main cropping season at two locations: Melkassa Agricultural Research Center and Dhera Experimental Station.

Melkassa Agricultural Research Center (MARC) is situated at 8°24′N latitude and 39°12′E longitude, approximately 117 km southeast of Addis Ababa. The site lies at an altitude of 1,550 meters above sea level and receives an average annual rainfall of 734 mm. The mean minimum and maximum temperatures are 14.1°C and 28.4°C, respectively. Rainfall follows a bimodal distribution, with a short rainy season from March to April and a longer, more reliable rainy season from July to September. The short rains are highly variable and generally unsuitable for consistent crop production. The experimental fields are characterized by sandy clay loam soils (Cambisols), with a texture composition of 35% sand, 44% silt, and 21% clay. The soils have

a pH of 7.5, organic matter content of 1.2%, available phosphorus of 10.32 ppm, and a cation exchange capacity (CEC) of 22.34 meq/100 g soil (MARC, 2019).

Dhera Experimental Site is located at 8°19′N latitude and 39°19′E longitude, approximately 124 km southeast of Addis Ababa. The site lies at an altitude of 1,560 meters above sea level and receives an average annual rainfall of 680 mm. The mean minimum and maximum temperatures are 14.0°C and 27.8°C, respectively. The soils at Dhera are classified as Andosols (KARC, 2019).

Long-term climatic data (nine years) for both sites, including monthly maximum and minimum temperatures and total rainfall during the cropping season, are presented in Table 1.

Table 1. Mean maximum and minimum monthly temperatures (°C) and total rainfall (mm) recorded (2011–2019) at Melkassa Agricultural Research Center and Dhera Experimental Site, Ethiopia.

		Melkassa Agricultural Research Center								Dhera Experimental Site							
Years	**Weather**	**Apr**	**May**	**June**	**July**	**August**	**Sept**	**October**	**Total**	**Apr**	**May**	**Jun**	**Jul**	**Aug**	**Sept**	**Oct**	**Total**
	RF (mm)	45.6	38.2	102.0	126.4	218.2	188.1	0.0	718.5	11.6	27.4	59.4	135.6	107.4	132.6	0.0	474.0
2011	Temp. Max (°C)	32.8	31.6	31.0	27.6	26.2	26.7	28.6	29.2	31.4	30.5	29.8	27.0	25.5	25.5	27.4	28.1
	Temp. Min (°C)	10.7	11.0	11.5	10.3	10.4	8.8	4.5	9.6	16.9	16.2	16.8	15.5	15.4	14.3	11.7	15.3
	RF (mm)	34.3	18.3	22.4	446.6	199.4	150.1	3.0	874.1	79.6	18.1	28.7	255.0	135.0	121.0	0.0	637.4
2012	Temp. Max (°C)	30.7	32.7	31.4	25.4	25.2	27.0	28.5	28.7	29.4	30.7	30.3	24.7	25.0	25.2	28.5	27.7
	Temp. Min (°C)	16.1	15.1	17.4	16.1	16.1	15.3	10.0	15.2	15.1	15.5	16.0	12.8	13.9	13.1	11.0	13.9
	RF (mm)	54.6	21.4	71.6	399.0	122.3	139.1	30.6	838.6	15.2	0.0	59.0	208.0	43.0	99.1	52.0	476.3
2013	Temp. Max (°C)	31.8	31.8	30.9	26.1	26.4	28.3	28.7	29.1	29.7	29.2	28.9	24.7	24.9	27.3	26.6	27.3
	Temp. Min (°C)	16.2	17.1	17.3	16.0	16.2	14.7	12.2	15.7	15.0	15.7	16.0	15.0	15.5	12.0	13.1	14.6
	RF (mm)	4.1	101.3	4.0	164.8	136.4	149.6	83.0	643.2	12.0	29.0	6.0	147.0	137.0	99.0	152.0	582.0
2014	Temp. Max (°C)	31.8	31.2	32.4	28.4	26.7	27.2	27.4	29.3	29.1	29.6	30.4	27.5	25.3	24.9	25.2	27.4
	Temp. Min (°C)	16.1	16.5	16.8	17.0	16.1	14.9	12.5	15.7	16.0	15.1	16.4	16.3	15.1	14.7	13.0	15.2
	RF (mm)	0.0	123.3	88.5	71.7	80.8	64.4	8.2	436.9	0.0	0.0	62.1	94.8	139.6	65.8	3.4	365.7
2015	Temp. Max (°C)	32.6	31.4	31.1	30.0	29.6	30.2	31.3	30.9	30.8	29.4	29.4	28.1	27.1	27.4	28.8	28.7
	Temp. Min (°C)	15.1	16.5	17.5	16.9	16.5	16.4	15.5	16.3	15.4	11.9	17.0	16.2	15.1	15.2	15.0	15.1
	RF (mm)	142.1	113.8	120.8	453.9	115.0	101.5	0.0	1047.1	102.4	43.7	72.5	182.4	120.1	91.0	9.8	621.9
2016	Temp. Max (°C)	30.0	29.6	29.8	26.8	27.1	28.6	30.5	28.9	28.9	28.8	29.1	26.3	26.3	26.8	26.6	27.5
	Temp. Min (°C)	17.3	16.1	16.5	16.2	16.1	15.6	12.0	15.7	12.5	12.1	12.0	11.6	12.1	11.1	8.6	11.4
	RF (mm)	18.0	150.7	25.1	251.5	182.9	113.8	9.0	751.0	104.2	51.5	137.9	121.5	201.7	70.7	6.4	693.9
2017	Temp. Max (°C)	32.3	30.3	31.9	27.4	26.3	27.7	29.5	29.3	28.2	29.8	29.4	27.4	26.4	26.2	27.7	27.9
	Temp. Min (°C)	16.0	16.7	18.0	16.6	16.6	16.0	13.2	16.1	11.7	12.9	12.5	13.0	11.9	10.8	9.3	11.7
	RF (mm)	266.7	35.5	98.2	177.0	188.6	56.0	0.0	822.0	192.3	23.7	37.8	113.4	129.7	13.9	1.5	512.3
2018	Temp. Max (°C)	29.9	30.1	29.5	27.1	26.5	28.8	30.2	28.9	27.3	27.8	28.1	25.7	25.6	26.8	27.3	26.9
	Temp. Min (°C)	16.3	15.9	17.1	16.2	16.0	14.3	13.1	15.6	20.6	14.8	16.0	15.3	16.0	14.5	13.3	15.8
	RF (mm)	120.7	63.9	101.9	271.8	114.3	167.2	31.7	871.5	75.9	49.5	104.1	220.0	173.9	173.0	35.3	831.7
2019	Temp. Max (°C)	32.3	32.3	30.4	26.8	26.8	27.5	27.4	29.1	27.6	30.0	28.5	26.0	25.4	25.4	24.7	26.8
	Temp. Min (°C)	16.8	16.0	17.4	16.6	16.3	16.1	12.5	16.0	12.1	16.6	16.3	15.4	14.9	15.1	12.8	14.7

Source: Melkassa Agricultural Research Center (2019) and Kulumsa Agricultural Research Center (2019).

3.2. Plant Materials and Test Cross Formation

The inbred lines used in this study were developed through successive selfing with selection for adaptation and disease resistance at Melkassa Agricultural Research Center (MARC). Test crosses were generated using the line × tester (L × T) mating design during the 2018 off-season (January – June) at MARC. A total of 80 test crosses were produced by crossing 40 inbred lines with two testers (Table 2). These crosses, together with four standard checks, were evaluated at MARC and Dhera experimental sites.

The two testers employed were CML312 (heterotic group A) and CML395 (heterotic group B), both developed by CIMMYT and adapted to Ethiopian agro-ecologies. Results from CIMMYT regional trials have demonstrated their effectiveness in hybrid formation under subtropical environments. Consequently, these testers are widely utilized by CIMMYT and national maize breeding programs across Africa for evaluating test cross performance and classifying inbred lines into heterotic groups.

Four standard checks were included for comparative evaluation: three high-yielding, intermediate-maturing hybrids (MH138Q, MH140, and MH130) released by MARC for low-moisture stress environments in Ethiopia, and one commercial hybrid (DK777) released by Bayer. These checks provided benchmarks for assessing the performance of experimental hybrids relative to widely adopted varieties.

In addition, 42 inbred line trials were planted adjacent to the hybrids at both locations. This facilitated direct evaluation of parental performance, combining ability, and heterotic grouping.

Table 2: Line code, pedigree, and origin of maize inbred lines and testers used in the study.

Line code	Pedigree	Origin	Remark	Line code	Pedigree	Origin	Remark
L1	[ZM-521]-1-1-2-1-1	MARC	Female parents	L15	[ZM-521]-1-1-2-1-1	MARC	Female parents
L2	[ZM-521]-2-1-3-1-1	MARC	Female parents	L16	[ZM-521]-1-1-3-2-2	MARC	Female parents
L3	[ZM-521]-2-2-3-2-2	MARC	Female parents	L17	[ZM-521]-2-2-1-1-1	MARC	Female parents
L4	[ZM-521]-1-1-2-1-1	MARC	Female parents	L18	[ZM-521]-3-3-3-2-2	MARC	Female parents
L5	[ZM-521]-2-2-3-1-1	MARC	Female parents	L19	[ZM-521]-1-1-3-3-3	MARC	Female parents
L6	[ZM-521]-2-2-2-2-2	MARC	Female parents	L20	[CML444/CML547]-1-1-2-1-1	MARC	Female parents
L7	[ZM-521]-2-2-2-3-3	MARC	Female parents	L21	[CML444/CML547]-1-1-2-1-1	MARC	Female parents
L8	[ZM-521]-2-2-2-4-4	MARC	Female parents	L22	[CML444/CML547]-2-2-3-1-1	MARC	Female parents
L9	[ZM-521]-3-3-2-1-1	MARC	Female parents	L23	[CML440/CML445]-2-2-1-1-1	MARC	Female parents
L10	[ZM-521]-2-2-1-1-1	MARC	Female parents	L24	[CML440/CML445]-1-1-2-1-1	MARC	Female parents
L11	[ZM-521]-3-3-2-1-1	MARC	Female parents	L25	[CML440/CML445]-1-1-3-1-1	MARC	Female parents
L12	[ZM-521]-4-4-3-2-2	MARC	Female parents	L26	[CML440/CML445]-1-1-3-2-2	MARC	Female parents
L13	[ZM-521]-1-1-2-1-1	MARC	Female parents	L27	[CML440/CML445]-1-1-2-1-1	MARC	Female parents
L14	[ZM-521]-1-1-3-1-1	MARC	Female parents	L28	[CML440/CML445]-1-1-4-3-3	MARC	Female parents
Line code	**Pedigree**	**Origin**	**Remark**				
L29	[CML440/CML445]-2-2-3-1-1	MARC	Female parents				
L30	[CML440/CML445]-2-2-1-2-2	MARC	Female parents				
L31	[CML440/CML445]-3-3-2-1-1	MARC	Female parents				
L32	[CML440/CML445]-3-3-2-2-2	MARC	Female parents				
L33	[CML440/CML445]-4-4-3-1-1	MARC	Female parents				
L34	[CML440/CML445]-4-4-2-2-2	MARC	Female parents				
L35	[CML440/CML445]-4-4-1-3-3	MARC	Female parents				
L36	[CML440/CML445]-5-5-2-1-1	MARC	Female parents				
L37	[CML440/CML445]-5-5-3-2-2	MARC	Female parents				
L38	[CML440/CML445]-1-1-2-1-1	MARC	Female parents				
L39	[CML440/CML445]-1-1-2-1-1	MARC	Female parents				
L40	[CML440/CML445]-1-1-1-2-2	MARC	Female parents				
	Testers						
T1	CML312	CIMMYT	Male parent1				
T2	CML395	CIMMYT	Male parent2				

Where; MARC= Melkassa Agricultural Research Center,L= lines.T=Testers, CML=CIMMYT maize lines,MH=Melkassa Hybrids.CIMMYT= International maize and wheat improvement center.

3.3. Experimental Design and Trial Management

A total of 84 genotypes, comprising 80 test crosses derived from line × tester (L × T) mating of 40 inbred lines with two testers, along with four standard checks (MH138Q, MH140, MH130, and DK777), were evaluated. The hybrid trial was laid out in a 7 × 12 alpha-lattice design (Patterson & Williams, 1976) with three replications. Each replication consisted of 12 incomplete blocks, with seven plots per block at both locations. Trial design and randomization were generated using CIMMYT's Fieldbook software. Each genotype was planted in two rows, each 4 m in length. Two seeds were sown per hill and later thinned to one plant per hill at the 2–4 leaf stage. Row and plant spacing were maintained at 0.75 m and 0.25 m, respectively, resulting in a plant population density of 53,333 plants ha^{-1}.

In addition, 42 genotypes (40 inbred lines and two testers) were evaluated for combining ability and heterotic grouping. These were planted in a 7 × 6 alpha-lattice design with three replications. Each plot consisted of two rows, each 4 m in length, with similar planting and thinning procedures as described above to ensure uniform establishment.

Nutrient management followed MARC recommendations. At planting, 50 kg P_2O_5 ha^{-1} and 25 kg N ha^{-1} were applied, with an additional 25 kg N ha^{-1} side-dressed at 35 days after planting. Diammonium phosphate (DAP) and urea were used as sources of phosphorus and nitrogen, respectively. Standard agronomic practices, including land preparation, weeding, and pest and disease management, were implemented according to local recommendations at both sites.

3.4. Data collection

Data on grain yield and key agronomic traits were recorded both at the plot level and from sampled plants/ears. The reliability of maize trial results depends critically on the type, accuracy, and precision of data collection. The timing of data recording was determined by the specific trait under evaluation. For flowering traits, observations commenced when the earliest genotypes began tasseling, shedding pollen, or extruding silks. Daily assessments were conducted thereafter to ensure precise estimation of the date when each plot reached 50% tasseling, anthesis, or silking. This procedure allowed accurate characterization of flowering dynamics across genotypes (Badu-Apraku et al., 2012). All data were collected following standardized descriptors for maize as outlined by the International Plant Genetic Resources Institute (IPGRI, 1996), ensuring consistency and comparability across locations and replications.

3.4. Data Collection

Phenological Traits

- **Anthesis date (AD, days):** Number of days from planting until 50% of plants in a plot began shedding pollen.
- **Silking date (SD, days):** Number of days from planting until 50% of plants in a plot produced silks of 2–3 cm length.
- **Anthesis–silking interval (ASI, days):** Calculated as the difference between silking and anthesis dates (ASI = SD – AD).
- **Days to maturity (MD, days):** Number of days from planting until 75% of plants reached physiological maturity, indicated by kernel black layer formation.

Yield and Yield Components

- **Grain yield (GY, t ha^{-1}):** Estimated from shelled grain weight, assuming 80% shelling efficiency (800 g grain per kg ear weight), and adjusted to 12.5% moisture content (Carangal et al., 1971). Formula:

$$GY = \left(\frac{FW}{1000}\right) \cdot \left(\frac{100 - Moi}{100 - 12.5}\right) \cdot \frac{10}{A} \cdot P$$

Where:

- **FW** = field weight of ears (kg plot^{-1})
- **Moi** = grain moisture content (%) at threshing
- **A** = net plot area (m^2), calculated as $[(no.ofhills–borderplants) \times hillspacing \times rowspacing \times 2]$
- **P** = shelling percentage (0.8 under optimum conditions)
- **Number of ears per plant (EPP):** Ratio of total ears harvested (with ≥1 fully developed kernel) to stand count at harvest.
- **Thousand kernel weight (TKW, g):** Weight of 1,000 seeds randomly sampled from bulked grain per plot.

Morphological and Agronomic Traits

- **Plant height (PH, cm):** Mean height of five randomly selected plants, measured from soil surface to the lowest tassel branch.
- **Ear height (EH, cm):** Mean height of the same five plants, measured from soil surface to the base of the uppermost ear.

- **Ear length (EL, cm):** Average ear length (base to tip) from five randomly selected ears.
- **Ear diameter (ED, cm):** Average mid-length diameter of the same ears used for EL.
- **Kernel rows per ear (KRPE):** Mean number of kernel rows from five sampled ears.
- **Kernels per row (KPR):** Mean number of kernels per row from five sampled ears.

Qualitative Traits (Scored on 1–5 Scale)

- **Plant aspect (PA):** Evaluated at dough stage based on disease incidence, ear set, stalk diameter, stand count, and ear size (1 = excellent; 5 = poor).
- **Ear aspect (EA):** Scored based on yield potential, disease incidence, kernel arrangement, and flintiness (1 = excellent; 5 = poor).
- **Common leaf rust (CLR):** Rated 1–5 based on severity: Where; 1.0 = highly resistant (clean), 1.0–2.0 = resistant, 2.0–2.5 = moderately resistant, 2.5–3.0 = moderately susceptible, 3.0–3.5 = susceptible, 3.5–5.0 = highly susceptible.

Stress-Related Traits

- **Bare tipness (BT, %):** Proportion of ears with poor husk cover (open tips).
- **Root lodging (RL, %):** Percentage of plants leaning >45° from vertical due to root instability.
- **Stem lodging (SL, %):** Percentage of plants broken at or below the node of the uppermost ear.

3.5. Data Analysis

A total of 126 genotypes (checks, parental lines, and F_1 crosses) were evaluated across two locations for grain yield, agronomic traits, and disease resistance. Prior to combined analysis, homogeneity of error variances across locations was tested following Gomez and Gomez (1984). Since the ratio of error mean squares between locations was less than 3 poo and significant, pooled analysis was deemed valid.

Separate analyses of variance (ANOVA) were conducted for parental lines and hybrids across locations using the PROC GLM procedure in SAS 9.0 (SAS Institute, 2000). For traits exhibiting significant genotypic differences, general combining ability (GCA) and specific combining ability (SCA) effects were estimated using AGD-R software (Version 5.0).

To address non-normality in certain traits, data transformations were applied:

- **Bare tipness, root lodging, and stem lodging:** Square root transformation $\sqrt{n + 0.5}$, where *n* is the observed value, was applied to stabilize variance, given the wide range of values including zeros.
- **Anthesis–silking interval (ASI):** Log-square root transformation $\ln \sqrt{ASI + 10}$ was employed to normalize the distribution, accounting for negative, zero, and positive values (Bolaños & Edmeades, 1996).

The linear model used for the analysis of variance across locations was:

$$\boldsymbol{Y_{ijk} = \mu + r_k + B(r_k) + r_k(l) + g_i + g_j + S_{ij} + l + (g_i \times l) + (g_j \times l) + (S_{ij} \times l) + e_{ijk}}$$

Where:

- $\boldsymbol{Y_{ijk}}$= observed value of a trait for the cross between line i and tester j in the kth replication
- $\boldsymbol{\mu}$= overall population means
- $\boldsymbol{r_k}$= effect of the kth replication
- $\boldsymbol{B(r_k)}$= effect of incomplete block within replication k
- $\boldsymbol{r_k(l)}$= replication × location interaction
- $\boldsymbol{g_i}$= general combining ability (GCA) effect of the ith line
- $\boldsymbol{g_j}$= general combining ability (GCA) effect of the jth tester
- $\boldsymbol{S_{ij}}$= specific combining ability (SCA) effect of the cross between line i and tester j
- $\boldsymbol{l}$= effect of location

- $\boldsymbol{g_i} \times \boldsymbol{l}$= interaction of line GCA with location
- $\boldsymbol{g_j} \times \boldsymbol{l}$= interaction of tester GCA with location
- $\boldsymbol{S_{ij}} \times \boldsymbol{l}$= interaction of SCA with location
- $\boldsymbol{e_{ijk}}$= experimental error associated with the ijkth observation

Table 3. Analysis of variance skeleton for combining ability analysis across two locations

SV	Df	MS	F-Value
Location(loc)	loc-1	MSloc	MSloc/MSE
Replication(loc)	loc(R − 1)	MSR	MSR/MSE
Bloc(R)	R(B-1)	MSB	MSB/MSE
GCA $_{Lines}$	L-1	MSL	MSL/MSE
GCA$_{Testers}$	Testers-1	MST	MST/MSE
SCA$_{Lines*Testers}$	(L-1)(T-1)	MS$_{LxT}$	MS$_{LxT}$ /MSE
GCA $_{Lines*loc}$	(L-1)(loc-1)	MS(L*loc)	MS(L*loc)/MSE
GCA $_{Testers*loc}$	(T-1)(loc-1)	MS(T*loc)	MS(T*loc)/MSE
SCA $_{Lines\ x\ Testers*loc}$	(L-1)(T-1)(loc-1)	MS((LxT*loc)	MS((LxT*loc)/MSE
Pooled Error(E)	loc(R-1)(G-1)	MSE	

Where; DF = degree of freedom, loc =location, R =replication, L =lines, T = testers, MSloc = mean square of location, MSR = mean square of replication, MSL = mean square of lines, MST = mean square testers, MSLxT= mean square of line x tester interaction, MSE = mean square of error, MST = mean square of total.

3.5.1. Combining Ability Analysis

Combining ability was analyzed using the line × tester (L × T) model, which partitions the mean squares due to crosses into components attributable to lines (GCA of lines), testers (GCA of testers), and line × tester interactions (SCA). The analysis was performed using AGD-R software (Version 5.0) for traits that exhibited significant differences among crosses across the two locations. The statistical significance of general combining ability (GCA) and specific combining ability (SCA) effects was tested using *t*-statistics, calculated as:

$$t_{\text{GCA}} = \frac{\text{GCA}}{SE}, t_{\text{SCA}} = \frac{\text{SCA}}{SE}$$

Where:

GCA = general combining ability effect

SCA = specific combining ability effect

SE = standard error of the respective effect

The calculated *t*-values were compared against tabulated *t*-values at the error degrees of freedom and a probability level of 0.05. Effects were considered significant when the calculated *t*-value exceeded the tabulated value.

The relative contributions of lines (GCAL), testers (GCAT), and line × tester interactions (SCA L × T) to the total cross variance were estimated following Singh and Chaudhary (1985):

$$\text{Contribution of Lines (\%)} = \frac{SS_{\text{Lines}}}{SS_{\text{Crosses}}} \times 100$$

$$\text{Contribution of Testers (\%)} = \frac{SS_{\text{Testers}}}{SS_{\text{Crosses}}} \times 100$$

$$\text{Contribution of Line} \times \text{Tester (\%)} = \frac{SS_{L \times T}}{SS_{\text{Crosses}}} \times 100$$

3.5.2. Heterotic Grouping

Heterotic grouping of inbred lines was performed following the procedure outlined by Singh and Chaudhary (1985). Grouping was based on the specific combining ability (SCA) effects for grain yield, computed from the performance of each line in test crosses with the two heterotic testers.

Inbred lines exhibiting significant negative SCA effects with a given tester were assigned to the same heterotic group as that tester. Conversely, lines showing positive SCA effects with tester A were classified into the opposite heterotic group (tester B), and lines with positive SCA effects with tester B were categorized into the opposite heterotic group (tester A). This classification ensures that lines are grouped according to their potential to exploit heterosis when crossed with contrasting testers.

4. RESULTS AND DISCUSSIONS

4.1. Results

The analysis of variance (ANOVA) for general combining ability (GCA) of lines and testers, and specific combining ability (SCA) of line × tester (L × T) interactions is presented in Table 4. Results revealed that both GCA and SCA mean squares were significant for most traits, indicating the presence of substantial genetic variability exploitable for hybrid development. Mean squares due to lines were highly significant ($P < 0.01$ or $P < 0.05$) for grain yield, days to 50% anthesis, days to 50% silking, plant height, ear height, number of rows per ear, kernels per row, ears per plot, ear position, ear length, ear diameter, thousand kernel weight, husk cover, root lodging, and stalk lodging. The significant variation among lines underscores the importance of additive gene action in controlling these agronomically important traits.

Mean squares due to testers were significant ($P < 0.01$ or $P < 0.05$) for grain yield, days to 50% silking, anthesis–silking interval (ASI), ear diameter, ear length, kernels per row, rows per ear, root lodging, and common leaf rust.

Lines × location interactions were significant for grain yield, days to anthesis, days to silking, maturity date, ear diameter, ear length, kernels per row, thousand kernel weight, and common leaf rust. Although Testers × location interactions were significant for grain yield, ASI, ear aspect, plant height, ear diameter, ear length, kernels per row, and common leaf rust. These interactions highlight the influence of genotype × environment (G × E) effects, consistent with findings by Hosana et al. (2015), who reported significant GCA × location interactions for grain yield and related traits.

Table 4: Analysis of variances for combining ability analysis

Source of variation	Across locations mean square											
	DF	GY	DTA	DTS	ASI	PASP	NE/Plot	NE/Plant	EASP	PHT	EHT	EPO	MD
Location	1	0.181ns	4803.27**	4663.52**	0.0156**	5.4051**	0.231ns	0.353**	0.209ns	6117.7**	10526.12**	0.364**	30.70**
Replication(Loc)	2	1.181ns	51.66**	33.24**	0.0075*	4.2919**	50.221*	0.104ns	0.631*	7517.3**	3974.95**	0.009*	54.98**
Bloc(Rep)	33	0.856**	4.44**	2.60ns	0.0023ns	0.3708**	12.972ns	0.035ns	0.407**	421.1**	291.95**	0.002ns	8.33**
GCA $_{Lines}$	39	0.977**	9.50**	11.90**	0.0019ns	0.1336ns	22.739**	0.044ns	0.187ns	698.4**	674.70**	0.007**	3.90ns
GCA $_{Testers}$	1	2.173*	0.34ns	17.18**	0.0139**	0.2210ns	11.660ns	0.018ns	0.148ns	776.0*	3.17ns	0.002ns	7.53ns
SCA $_{Lines*Testers}$	39	1.164**	2.32ns	2.59ns	0.0022ns	0.1766ns	15.032ns	0.055*	0.231*	319.6*	205.76**	0.003*	4.12ns
GCA $_{Lines*Location}$	39	0.846**	2.86*	3.19*	0.0025ns	0.2385ns	14.957ns	0.028ns	0.149ns	170.3ns	105.59ns	0.003ns	5.58*
GCA $_{Testers*Location}$	1	9.107**	6.21ns	0.13ns	0.0132*	0.0044ns	3.641ns	0.004ns	1.157**	1314.6**	15.27ns	0.006ns	0.63ns
SCA $_{Lines*Tester*Location}$	39	0.806**	1.83ns	1.67ns	0.0017ns	0.2282ns	19.260*	0.046ns	0.127ns	133.7ns	86.05ns	0.002ns	3.57ns
Pooled error	283	0.44	1.80	1.97	0.00197	0.171	12.24	0.0347	0.143	193.62	115.8	0.0023	3.48

*=significant (P<0.05) ;**=highly significant (P<0.01);GCA=general combining ability;SCA=specific combining ability;DF=degree of freedom;GY=grain yield;DTA=date to 50% anthesis;DTS=date to 50% silking;NE=number of ear per plot;EASP=ear aspect;PHT=plant height;EHT=ear height;EPO=ear position.

Mean squares due to L × T interactions were significant ($P < 0.01$ or $P < 0.05$) for grain yield, ears per plant, ear aspect, plant height, ear height, ear position, ear diameter, rows per ear, and thousand kernel weight. SCA × location interactions were significant for grain yield, ears per plot, and common leaf rust. These results confirm the role of non-additive gene action (dominance and epistasis) in the inheritance of these traits, particularly under varying environmental conditions. Assefa et al. (2017) and Legesse et al. (2017) reported significant GCA effects for grain yield, plant height, ear height, days to silking, and gray leaf spot resistance in mid-altitude maize inbred lines. Gemechu et al. (2020) found significant genotypes mean squares ($P < 0.01$ or $P < 0.05$) for grain yield, silking, ASI, maturity, plant and ear height, plant aspect, kernel rows per ear, kernels per row, ear length, ear diameter, and thousand kernel weight, except for anthesis and ear aspect. These findings confirm the present study, reinforcing the importance of both additive and non-additive genetic effects in maize improvement.

4.1.2. Estimation of General Combining Ability (GCA)

The estimation of general combining ability (GCA) effects for lines and testers revealed highly significant differences across most agronomic traits, underscoring the predominance of additive gene action in the genetic control of maize performance under moisture-stress conditions. For grain yield, twenty lines exhibited positive and highly significant GCA effects ($P < 0.01$), while nineteen lines showed negative and highly significant effects, indicating clear genetic divergence among the parental lines. Tester 1 consistently expressed positive and highly significant GCA for grain yield, confirming its value as a strong parental source. Similarly, significant positive GCA effects were observed for ear diameter and ear length, with contributions of 78.96% to total variance for ear length, highlighting the importance of line selection in improving ear traits. Kernel traits also showed strong additive control; twenty-three lines exhibited positive and significant GCA for kernels per row (contributing 65.65% to variance), and twenty-five lines showed significant GCA for kernel rows per ear (contributing 61.98%), while testers contributed modestly. Thousand kernel weight followed the same pattern, with seventeen lines showing significant positive GCA and contributing 59.87% to variance, whereas tester contributions were negligible.

Phenological traits revealed that negative GCA effects were predominant for anthesis, silking, and maturity dates, with lines contributing over 70% of the variance in flowering traits. This is particularly advantageous under drought-prone environments, as earlier flowering and maturity enable stress escape. For anthesis, twenty-three lines showed negative and highly significant GCA, while tester 2 also exhibited negative and significant

GCA, though with minimal contribution. Similar trends were observed for silking (77.78% contribution from lines) and maturity (47.05% contribution from lines). Plant and ear height also showed strong additive control, with seventeen lines exhibiting positive and significant GCA for plant height and eighteen lines for ear height, contributing 73.12% and 79.55% respectively to total variance. Tester contributions remained small but significant, reinforcing their role as discriminators rather than primary sources of variability.

Overall, the predominance of significant GCA effects across yield, yield components, phenology, and plant architecture traits demonstrates that additive gene action is the major determinant of genetic variation in this population. This suggests that recurrent selection and careful parental line choice will be highly effective strategies for genetic improvement. Moreover, the consistent dominance of line contributions over testers highlights the central role of inbred line variability in driving genetic gain, while testers provide complementary information for heterotic grouping. These findings align with earlier reports (e.g., Legesse, 2017; Gemechu et al., 2020), confirming that Ethiopian maize breeding programs can effectively exploit additive genetic variance to develop high-yielding, stress-resilient hybrids.

Table 5. Across location gca of lines and testers, proportional contribution of lines gca and testers gca to the total cross variances

LINES	DTA	DTS	EASP	ED	EHT	EPO	ER	GY	HC	MD
L1	0.96**	1.03**	0.02**	0.26**	-5.77**	0.00**	0.37**	-0.12**	1.29**	0.80**
L2	0.04**	-0.68**	-0.05**	0.01**	-7.38**	0.00**	-0.21**	0.07**	-0.44**	0.27**
L3	1.70NS	1.49**	-0.27NS	-0.17**	8.55**	0.02**	-0.25**	0.23**	-0.65**	0.17**
L4	-1.04**	-1.00**	-0.09**	-0.12**	4.93**	0.02**	-0.51**	0.10**	-1.34**	-1.30NS
L5	-0.42**	-0.46**	-0.03**	-0.18**	11.21**	0.04**	-0.27**	0.17**	-1.28**	-0.33**
L6	-1.24**	-1.40**	-0.14**	0.21**	-1.68**	-0.01**	-0.61**	0.39**	-1.58**	-0.77**
L7	-0.90**	-0.89**	-0.02**	0.10**	-1.53**	0.01**	-0.16**	-0.39**	-0.62*8	-0.31**
L8	-1.79NS	-2.49NS	-0.12**	-0.24**	6.99NS	0.03**	-0.10**	0.20**	-0.05**	-0.64**
L9	-0.80**	-0.93**	-0.24**	0.30**	-10.46**	-0.03**	-0.26**	-0.29**	1.02**	0.33**
L10	-0.36**	-0.04**	0.06**	0.06**	4.01NS	-0.01**	0.03**	0.06**	2.44NS	0.16**
L11	0.21**	0.28**	-0.05**	0.16**	1.86**	-0.01**	0.41**	-0.32**	1.64**	1.41NS
L12	-0.02**	0.35**	-0.08**	0.22**	-0.06**	0.02**	-0.02**	0.47**	0.36**	0.45**
L13	-1.05**	-1.35**	0.05**	-0.09**	-6.93**	-0.01**	-0.07**	-0.04**	-0.76**	-1.08NS
L14	0.78**	0.20**	0.04**	-0.44NS	9.63NS	0.03**	-0.29**	-0.22**	-0.54**	-0.18**
L15	-0.42**	-0.60**	0.14**	-0.43NS	9.41NS	0.03**	0.59**	0.28**	-1.34**	-0.15**
L16	-0.16**	-0.53**	0.07**	-0.63NS	14.96**	0.02**	0.11**	-0.41**	-2.04	-0.03**
L17	-0.22**	-0.06**	0.16**	-0.05**	-11.12**	-0.03**	0.75NS	-0.26**	-0.44**	-0.10**
L18	-0.38**	-0.26**	0.12**	0.07**	-16.90**	-0.06NS	0.22**	0.20**	0.80**	-0.15**
L19	-0.38**	-0.27**	0.29NS	-0.16**	-1.57**	0.01**	-0.25**	0.06**	-0.70**	-0.21**
L20	0.79**	0.60**	0.03**	-0.13**	2.71**	0.01**	-0.24**	-0.28**	-0.27**	0.08**
L21	2.09NS	2.83NS	-0.24**	0.09**	16.61**	0.04**	0.34**	0.55**	-0.75**	0.08**
L22	1.60NS	0.82**	0.10**	-0.22**	15.04**	0.02**	0.30**	-0.22**	-1.20**	0.38**
L23	0.41**	0.81**	-0.01**	0.18**	-3.35**	-0.02**	0.21**	-0.43**	-0.17**	-0.30**
L24	0.92**	1.12**	-0.15**	0.17**	-1.64**	0.00**	-0.30**	-0.22**	0.10**	0.13**
L25	0.47**	0.60**	-0.04**	0.14**	6.04**	0.02**	0.71NS	-0.06**	0.63**	-0.30**
L26	0.45**	0.60**	-0.08**	-0.03**	-4.44**	-0.06NS	-0.10**	-0.11**	0.35**	-0.26**
L27	-0.58**	-0.24**	0.21**	0.11**	-4.48**	0.02**	-0.18**	-0.65NS	0.45**	-0.37**
L28	-0.46**	-0.19**	0.17**	0.05**	-3.95**	-0.01**	-0.49**	-0.49**	0.53**	0.20**
L29	1.33**	0.98**	-0.15**	0.01**	4.25**	0.00**	0.34**	0.12**	-0.53**	-0.45**
L30	-0.16**	-0.04**	0.05**	0.13**	-12.62**	-0.03**	0.45**	0.21**	0.70**	0.98**
L31	-0.21**	-0.70**	0.02**	0.21**	-11.84**	-0.04**	-0.21**	0.09**	1.27**	0.93**
L32	-0.87**	-0.73**	0.06**	-0.05**	-1.75**	0.00**	0.03**	-0.09**	0.39**	0.01**
L33	-0.13**	0.22**	0.11**	0.07**	4.05**	0.01**	-0.33**	0.05**	0.60**	0.90**
L34	-0.27**	-0.41**	0.19**	0.18**	-6.63**	-0.02**	-0.15**	-0.08**	0.86**	0.44**

LINES	DTA	DTS	EASP	ED	EHT	EPO	ER	GY	HC	MD
L35	0.85**	0.83**	-0.04**	0.21**	2.73**	0.03**	-0.13**	0.69NS	-0.30**	0.34**
L36	0.95**	1.13**	-0.13**	0.03**	-0.40**	-0.03**	0.16**	0.27**	-0.20**	0.00**
L37	-0.28**	0.06**	0.01**	-0.13**	0.96**	0.00**	0.38**	0.11**	0.06**	-0.32**
L38	-0.53**	-0.76**	0.09**	-0.04**	-1.05**	-0.02**	0.64NS	-0.01**	0.22**	-0.68**
L39	0.72**	1.79**	0.07**	-0.02**	3.14**	0.01**	-0.08**	0.24**	1.41**	0.20**
L40	-1.52**	-1.59**	0.15**	-0.01**	-12.99**	-0.03**	-0.35**	0.01**	-0.23**	-1.00**
SE	0.81	0.96	0.12	0.19	7.45	0.02	0.33	0.29	0.91	0.54
%(GCA_L)	76.72	77.78	52.94	59.93	79.55	68.00	41.04	47.94	78.74	47.05
TESTERS	DTA	DTS	EASP	ED	EHT	EPO	ER	GY	HC	MD
T1	0.03**	-0.19**	-0.01**	0.04**	-0.24**	0.00**	-0.02**	0.07**	-0.12**	0.11**
T2	-0.02**	0.19**	0.02**	-0.05**	0.17**	0.00**	0.05NS	-0.07**	0.10**	-0.14**
SE	0.02	0.19	0.01	0.04	0.26	0.00	0.02	0.07	0.12	0.11
%(GCA_T)	0.04	3.04	0.25	2.95	0.10	0.71	0.18	2.46	1.33	1.86

** = Highly significant (P<0.01);* = Significant (P<0.05);NS = non-significant; L =Lines; T= Testers; SE= standard error of the difference; % (SCA_L) = proportional contribution of lines to total cross variance; % (SCA_T) = proportional contribution of testers to total cross variance CLR = common leaf rust, DTA = Date to 50% anthesis; DTA= Date to 50% silking; EASP = ear spect; ED= ear diameter; EHT = ear height; EL = ear length; EPO = ear position; ER = ear rot; GY = grain yield; HC = bad husk cover; MD = 50% maturity date; NE = number of ear;NEPP = number of ear per plant; NKPR = number of kernel per row; NRPE = number of rows per ear; PASP = plant aspect; PHT = plant height; RL = root lodging; SL = stem lodging; TSW = thousand seed weight.

LINES	NE	NEPP	NKPR	NRPE	PASP	PHT	RL	SL	TSW
L1	-0.41**	-0.04**	-2.05**	0.07**	0.01**	-11.16**	-0.61**	0.41**	34.80NS
L2	-1.01**	0.01**	-1.74**	0.32**	-0.14**	-8.20**	0.14**	0.56**	23.21**
L3	1.62**	0.05**	1.12**	-0.16**	0.00**	-3.15**	-0.31**	0.16**	-3.59**
L4	0.97**	0.00**	0.07**	-0.35**	0.08**	-3.85**	0.12**	0.57**	-12.70**
L5	1.06**	0.12**	1.59**	-0.68**	-0.03**	3.02**	-0.16**	0.28**	2.63**
L6	-0.69**	0.09**	1.84**	0.15**	-0.09**	-2.66**	-0.21**	-0.42**	-11.07**
L7	-2.06**	0.09**	0.57**	0.22**	0.07**	-0.97**	0.73NS	-0.56**	-3.46**
L8	-1.12**	-0.06**	2.77NS	-0.86**	0.21NS	4.53**	0.57**	0.72NS	1.04**
L9	-0.35**	0.07**	0.47**	0.00**	-0.10**	-2.24**	-0.29**	0.32**	-0.45**
L10	-0.65**	-0.03**	-0.52**	-0.94**	0.05**	7.29**	-0.04**	-0.45**	31.24NS
L11	-0.97**	-0.02**	-1.89**	0.37**	-0.09**	9.68**	-0.17**	-0.19**	17.69**
L12	4.05NS	0.04**	0.87*8	0.66**	0.09**	-5.08**	-0.32**	-0.28**	-26.49**
L13	-1.69**	-0.08**	1.95**	1.19**	-0.15**	-7.77**	1.12NS	-0.30**	-24.56**
L14	-0.23**	0.01**	1.60**	-1.16**	-0.01**	11.97**	0.29**	-0.31**	-30.98NS
L15	2.17**	0.02**	1.16**	-1.32**	0.00**	-2.28**	-0.19**	-0.11**	-18.77**
L16	2.67NS	0.03**	0.55**	-2.09NS	-0.14**	15.39NS	0.47**	0.06**	-23.44**
L17	0.00**	-0.03**	-0.20**	0.29**	0.08**	-12.13**	0.00**	0.59**	-17.54**
L18	0.59**	0.07**	-1.85**	-1.01**	0.16**	-10.84**	-0.58**	-0.47**	10.53**
L19	-2.11**	-0.09**	0.60**	-0.28**	-0.06**	-5.64**	0.26**	0.65**	16.28**
L20	0.58**	0.02**	1.27**	-0.46**	0.13**	7.63**	-0.51**	-0.47**	13.03**
L21	0.83**	0.01**	1.36**	0.89**	0.20NS	15.09**	-0.30**	-0.03**	-10.51**
L22	-0.02**	-0.08**	0.94**	-0.48**	0.07**	11.40**	-0.23**	0.08**	-8.01**
L23	-1.92**	-0.08**	-0.20**	0.36**	-0.15**	1.34**	-0.18**	-0.46**	-11.07**
L24	-1.34**	-0.03**	-2.74NS	1.35NS	0.15**	-10.29**	0.07**	0.19**	10.81**
L25	-1.80**	-0.04**	-1.13**	0.14**	-0.01**	7.65**	-0.41**	0.22**	39.50NS
L26	-2.11**	-0.08**	0.06**	0.23**	-0.14**	11.51**	-0.53**	-0.02**	0.94**
L27	-0.36**	0.13NS	-1.70**	-0.33**	0.00**	-14.39**	-0.06**	-0.18**	-9.91**
L28	-0.59**	-0.02**	0.05**	0.98**	-0.04**	-2.78**	0.16**	-0.20**	-1.62**
L29	0.67**	-0.02**	0.18**	0.69**	0.05**	3.15**	0.41**	-0.01**	-3.04**
L30	0.75**	-0.02**	0.10**	-0.10**	0.02**	-6.76**	0.02*8	0.09**	-4.05**

LINES	NE	NEPP	NKPR	NRPE	PASP	PHT	RL	SL	TSW
L31	-0.77**	-0.05**	-0.81**	0.36**	-0.08**	-0.27**	0.82NS	-0.07**	8.59**
L32	1.53**	0.08**	0.32**	-0.28**	-0.07**	3.29**	0.57**	-0.27**	-13.81**
L33	0.90**	0.14NS	-1.38**	0.02**	0.05**	6.32**	-0.11**	0.35**	-9.72**
L34	-0.80**	-0.03**	-1.22**	0.05**	-0.03**	-2.10**	-0.03**	-0.23**	8.62**
L35	1.73**	-0.01**	0.18**	0.83**	-0.04**	-3.92**	-0.21**	-0.08**	11.61**
L36	0.55**	0.02**	1.18**	0.33**	-0.07**	12.80**	0.31**	-0.52**	1.81**
L37	-0.18**	-0.08*8	-0.83**	0.39**	0.15**	2.01**	-0.37**	-0.31**	-14.25**
L38	-0.04**	-0.08**	-0.13**	0.32**	0.07**	0.44**	-0.10**	0.16**	-3.24**
L39	1.43**	0.00**	-2.38**	0.20**	0.09**	-1.22**	-0.28**	0.03**	27.02**
L40	-0.80**	-0.05**	-1.05**	0.02**	-0.20NS	-16.97NS	0.18**	0.54**	-12.95**
SE	1.35	0.06	1.26	0.67	0.10	7.77	0.35	0.34	15.56
%(GCA_l)	63.15	46.00	65.65	61.98	43.86	73.12	67.42	58.50	59.87
T1	-0.16**	-0.01**	-0.35**	0.25**	-0.02**	1.39**	0.00**	-0.03**	-0.88**
T2	0.16**	0.01**	0.30**	-0.25**	0.03**	-1.40**	0.00**	0.03**	0.08**
SE	0.16	0.01	0.34	0.24	0.03	1.20	0.01	0.03	0.90
% (GCA_t)	0.86	0.57	4.88	8.07	3.21	1.73	0.04	0.41	0.20

** = Highly significant (P<0.001);* = Significant (P<0.05);NS = non significant; L =Lines; T= Testers; SE= standard error of the difference; % (SCA_L) = proportional contribution of lines to total cross variance; % (SCA_T) = proportional contribution of testers to total cross variance CLR = common leaf rust, DTA = Date to 50% anthesis; DTA= Date to 50% silking; EASP = ear spect; ED= ear diameter; EHT = ear height; EL = ear length; EPO = ear position; ER = ear rot; GY = grain yield; HC = bad husk cover; MD = 50% maturity date; NE = number of ear;NEPP = number of ear per plant; NKPR = number of kernel per row; NRPE = number of rows per ear; PASP = plant aspect; PHT = plant height; RL = root lodging; SL = stem lodging;TSW = thousand seed weight

4.1.3. Estimation of Specific Combining Ability (SCA)

An across-location estimation of specific combining ability (SCA) effects for line × tester (L × T) interactions is presented in Table 6. Results revealed that SCA effects were highly significant for most yield-related and agronomic traits, confirming the importance of non-additive gene action (dominance and epistasis) in hybrid performance under moisture-stress conditions.

For grain yield, forty crosses exhibited positive and highly significant ($P < 0.01$) SCA effects, contributing 49.54% to the total cross variance. This underscores the critical role of specific parental combinations in enhancing hybrid productivity. Similarly, ear diameter showed strong non-additive control, with forty-two crosses exhibiting positive and significant ($P < 0.01$) SCA effects, contributing 37.07% to total variance. Ear length also revealed significant SCA effects, with forty crosses contributing 16.21% to variance. Kernel traits were equally influenced by SCA; forty-three crosses exhibited positive and significant ($P < 0.01$) SCA for kernels per row (29.36% contribution), and forty-two crosses showed significant SCA for kernel rows per ear (29.93% contribution). For thousand kernel weight (TKW), forty-two crosses exhibited positive and significant SCA effects, contributing 39.90% to total variance. These findings are consistent with reports by Dereje (2020) and Shushay (2013), who observed similar patterns of non-additive gene action in Ethiopian maize germplasm.

Phenological traits also demonstrated significant SCA effects. For 50% anthesis date, forty crosses displayed negative and highly significant ($P < 0.01$) SCA effects, contributing 23.16% to total variance. Negative SCA effects for flowering are advantageous in drought-prone environments, as they promote earlier pollen shedding and silking, thereby enabling stress escape. Similarly, for 50% silking date, forty crosses exhibited negative and significant ($P < 0.01$) SCA effects, contributing 19.16% to total variance. These results align with earlier findings by Dereje (2020) and Shushay (2013), who emphasized the importance of early flowering hybrids in low-moisture environments.

For plant height, forty crosses exhibited positive and highly significant ($P < 0.01$) SCA effects, contributing 25.20% to total variance. Likewise, forty crosses showed positive and significant SCA effects for ear height, contributing 20.28% to variance. These results are consistent with previous reports by Legesse (2017), Alemerew (2015), and Alemeshet (2014), who documented significant SCA effects for plant and ear height in Ethiopian maize breeding programs.

Table 6: Across location SCA of lines x Testers and proportional contribution of LxT to the total cross variances

Lines x Testers	CLR	DTA	DTS	EASP	ED	EHT	EL	EPO	ER	GY	HC
L1xT1	0.02**	0.39**	0.48**	-0.18**	0.17**	0.38**	0.53**	0.00**	-0.02**	0.33**	0.53**
L1xT2	-0.01**	-0.40**	-0.49**	0.16**	-0.16**	-0.31**	-0.51**	0.00**	0.00**	-0.32**	-0.52**
L2xT1	0.05**	0.61**	0.26**	0.04**	-0.14**	-4.21**	-0.17**	-0.01**	0.23**	-0.29**	0.21**
L2xT2	-0.05**	-0.62**	-0.27**	-0.06**	0.15**	4.28**	0.19**	0.01**	-0.25**	0.29**	-0.19**
L3xT1	-0.02**	-0.27**	-0.71**	-0.05**	0.02**	0.47**	-0.42**	-0.01**	0.29**	-0.01**	-0.29**
L3xT2	0.02**	0.27**	0.70**	0.04**	-0.01**	-0.40**	0.44**	0.01**	-0.31**	0.01**	0.30**
L4xT1	-0.07**	0.11**	-0.06**	0.04**	-0.05**	-7.02**	0.26**	-0.02**	0.29**	0.03**	-0.21**
L4xT2	0.07**	-0.12**	0.05**	-0.06**	0.06**	7.09**	-0.24**	0.02**	-0.32**	-0.03**	0.22**
L5xT1	0.01**	0.03**	0.02**	0.03**	-0.05**	-0.12**	0.17**	0.01**	-0.25**	0.10**	-0.09**
L5xT2	-0.01**	-0.03**	-0.03**	-0.04**	0.06**	0.19**	-0.15**	-0.01**	0.22**	-0.10**	0.11**
L6xT1	0.14**	-0.53**	-0.13**	-0.24NS	0.09**	3.36**	0.22**	0.02**	-0.04**	-0.08**	-1.04NS
L6xT2	-0.13**	0.53**	0.12**	0.23**	-0.08**	-3.29**	-0.21**	-0.02**	0.02**	0.08**	1.06NS
L7xT1	0.16**	0.11**	-0.09**	-0.18**	0.13**	-1.80**	0.31**	0.00**	0.13**	-0.44**	0.11**
L7xT2	-0.16**	-0.11**	0.09**	0.17**	-0.12**	1.87**	-0.29**	0.00**	-0.15**	0.44**	-0.09**
L8xT1	-0.07**	-0.53**	-0.43**	0.11**	0.01**	-2.59**	-0.42**	0.02**	-0.33**	-0.13**	0.09**
L8xT2	0.07**	0.53**	0.42**	-0.12**	0.00**	2.66**	0.44**	-0.02**	0.30**	0.14**	-0.07**
L9xT1	-0.01**	0.09**	0.25**	-0.22**	0.03**	-1.01**	-0.05**	0.01**	0.85NS	0.24**	-0.28**
L9xT2	0.01**	-0.10**	-0.26**	0.21**	-0.02**	1.08**	0.06**	-0.01**	-0.88NS	-0.24**	0.30**
L10xT1	-0.07**	0.20**	-0.20**	0.14**	-0.24**	-7.10**	-0.44**	-0.02**	0.43**	-0.31**	-0.20**
L10xT2	0.07**	-0.20**	0.20**	-0.15**	0.25**	7.18**	0.45**	0.02**	-0.45**	0.31**	0.22**
L11xT1	0.14**	0.34**	0.49**	0.22**	-0.07**	-4.62**	0.27**	-0.01**	-0.13**	-0.47**	0.65**
L11xT2	-0.14**	-0.35**	-0.50**	-0.24NS	0.08**	4.69**	-0.25**	0.01**	0.11**	0.47**	-0.63**
L12xT1	-0.05**	-0.44**	-1.31NS	-0.14**	-0.29**	-1.38**	0.24**	-0.01**	-0.02**	0.30**	-0.23**
L12xT2	0.05**	0.44**	1.31NS	0.12**	0.30NS	1.45**	-0.23**	0.01**	-0.01**	-0.30**	0.24**
L13xT1	-0.35NS	-0.80**	-0.51**	0.06**	-0.11**	-4.10**	-0.45**	-0.01**	0.07**	0.36**	-0.65**
L13xT2	0.35NS	0.80**	0.51**	-0.07**	0.12**	4.18**	0.47**	0.01**	-0.09**	-0.35**	0.67**
L14xT1	-0.08**	-0.36**	-0.20**	-0.05**	0.08**	2.89**	0.03**	0.01**	-0.79NS	-0.04**	-0.52**
L14xT2	0.08**	0.35**	0.20**	0.04**	-0.07**	-2.81**	-0.01**	-0.01**	0.77NS	0.05**	0.54**
L15xT1	-0.02**	-0.11**	0.20**	0.13**	-0.20**	6.66**	-0.34**	0.01**	-0.07**	-0.39**	0.04**
L15xT2	0.02**	0.10**	-0.21**	-0.14**	0.21**	-6.58**	0.36**	-0.01**	0.05**	0.40**	-0.03**
L16xT1	0.00**	-0.22**	0.30**	0.02**	0.13**	1.25**	0.21**	0.01**	0.75**	-0.31**	-0.54**
L16xT2	0.00**	0.22**	-0.31**	-0.03**	-0.12**	-1.17**	-0.20**	-0.01**	-0.77NS	0.32**	0.55**
L17xT1	0.03**	0.61**	-0.05**	0.11**	-0.13**	-2.57**	0.30**	0.01**	0.59**	-0.33**	-0.41**

Lines x Testers	CLR	DTA	DTS	EASP	ED	EHT	EL	EPO	ER	GY	HC
L17xT2	-0.03**	-0.61**	0.04**	-0.12**	0.13**	2.64**	-0.28**	-0.01**	-0.62**	0.34**	0.42**
L18xT1	-0.02**	0.13**	0.40**	-0.06**	0.11**	0.48**	0.21**	-0.01**	-0.07**	0.70NS	0.18**
L18xT2	0.02**	-0.13**	-0.41**	0.05**	-0.11**	-0.41**	-0.19**	0.01**	0.04**	-0.70NS	-0.16**
L19xT1	0.05**	-0.46**	-0.26**	0.18**	-0.16**	-9.22NS	-0.15**	-0.03**	-0.15**	0.14**	-0.72**
L19xT2	-0.05**	0.45**	0.25**	-0.19**	0.17**	9.29NS	0.17**	0.03**	0.13**	-0.13**	0.73**
L20xT1	0.12**	-0.33**	-0.56**	-0.06**	0.46NS	5.19**	-0.31**	0.02**	0.09**	0.04**	0.47**
L20xT2	-0.12**	0.33**	0.56**	0.05**	-0.45NS	-5.12**	0.33**	-0.02**	-0.12**	-0.03**	-0.46**
L21xT1	0.19**	-0.57**	-0.17**	0.08**	-0.16**	1.63**	0.33**	-0.01**	0.54**	0.03**	1.03NS
L21xT2	-0.19**	0.57**	0.16**	-0.10**	0.17**	-1.56**	-0.32**	0.01**	-0.56**	-0.02**	-1.01NS
L22xT1	-0.05**	0.37**	0.03**	0.21**	0.10**	-2.98**	-0.22**	0.00**	-0.33**	-0.09**	-0.20**
L22xT2	0.05**	-0.38**	-0.04**	-0.22**	-0.09**	3.06**	0.23**	0.00**	0.31**	0.10**	0.21**
L23xT1	0.10**	0.16**	-0.05**	0.23**	-0.34NS	-4.55**	-0.48**	0.00**	0.70**	-0.52**	-0.53**
L23xT2	-0.10**	-0.17**	0.05**	-0.24NS	0.35NS	4.63**	0.50**	0.00**	-0.73**	0.52**	0.54**
L24xT1	-0.05**	0.23**	-0.04**	0.17**	-0.09**	4.52**	-0.40**	0.01**	0.24**	-0.35**	0.37**
L24xT2	0.05**	-0.24**	0.04**	-0.18**	0.10**	-4.45**	0.41**	-0.01**	-0.26**	0.36**	-0.35**
L25xT1	-0.08**	-0.32**	-0.63**	-0.07**	0.09**	1.15**	0.56**	0.00**	-0.38**	0.33**	0.05**
L25xT2	0.08**	0.31**	0.63**	0.05**	-0.08**	-1.08**	-0.55**	0.00**	0.36**	-0.33**	-0.03**
L26xT1	-0.07**	-1.51NS	-0.96NS	-0.15**	0.17**	-4.68**	0.13**	-0.01**	-0.18**	-0.63NS	-0.52**
L26xT2	0.07**	1.50NS	0.95NS	0.14**	-0.16**	4.75**	-0.12**	0.02**	0.15**	0.64NS	0.53**
L27xT1	0.08**	-0.24**	0.22**	0.05**	-0.15**	-4.80**	0.76NS	-0.02**	0.26**	0.21**	0.20**
L27xT2	-0.08**	0.23**	-0.23**	-0.06**	0.15**	4.88**	-0.75NS	0.02**	-0.28**	-0.21**	-0.19**
L28xT1	0.08**	0.11**	-0.31**	-0.05**	0.19**	5.79**	-0.12**	0.02**	0.00**	0.18**	0.47**
L28xT2	-0.08**	-0.12**	0.30**	0.04**	-0.18**	-5.71**	0.13**	-0.02**	-0.02**	-0.18**	-0.45**
L29xT1	-0.07**	0.26**	0.37**	-0.13**	0.21**	4.78**	0.19**	0.03**	-0.98NS	0.04**	-0.46**
L29xT2	0.07**	-0.26**	-0.38**	0.12**	-0.20**	-4.71**	-0.17**	-0.03**	0.96NS	-0.04**	0.48**
L30xT1	-0.12**	0.15**	0.41**	-0.14**	0.00**	3.47**	0.15**	-0.01**	-0.41**	-0.15**	0.10**
L30xT2	0.12**	-0.16**	-0.42**	0.13**	0.01**	-3.39**	-0.13**	0.01**	0.39**	0.15**	-0.08**
L31xT1	-0.10**	0.07**	0.66**	-0.12**	0.08**	6.18**	0.24**	0.00**	-0.46**	0.71NS	0.80**
L31xT2	0.10**	-0.08**	-0.67**	0.10**	-0.07**	-6.11**	-0.22**	0.00**	0.43**	-0.70NS	-0.79**
L32xT1	-0.05**	0.14**	-0.29**	-0.19**	0.12**	-0.04**	-0.47**	0.00**	0.38**	0.22**	0.87**
L32xT2	0.05**	-0.15**	0.28**	0.18**	-0.11**	0.11**	0.49**	0.00**	-0.40**	-0.21**	-0.85**
L33xT1	0.02**	0.64**	1.07NS	0.02**	-0.15**	2.84**	-0.39**	0.00**	-0.35**	0.07**	-0.63**
L33XT2	-0.02**	-0.65**	-1.07NS	-0.03**	0.16**	-2.77**	0.40**	0.00**	0.33**	-0.07**	0.65**
L34xT1	0.04**	0.95NS	1.11NS	0.03**	0.03**	4.30**	-0.15**	0.01**	0.24**	-0.15**	0.23**
L34xT2	-0.04**	-0.96NS	-1.11NS	-0.04**	-0.02**	-4.23**	0.17**	-0.01**	-0.26**	0.16**	-0.22**

Lines x Testers	CLR	DTA	DTS	EASP	ED	EHT	EL	EPO	ER	GY	HC
L35xT1	-0.14**	-0.11**	-0.21**	-0.08**	0.04**	-3.36**	-0.21**	-0.05NS	0.10**	0.00**	-0.01**
L35xT2	0.14**	0.11**	0.20**	0.07**	-0.03**	3.44**	0.22**	0.05NS	-0.12**	0.01**	0.03**
L36xT1	-0.02**	-0.23**	-0.19**	-0.04**	0.18**	4.03**	-0.04**	0.03NS	-0.23**	0.21**	0.68**
L36xT2	0.02**	0.23**	0.19**	0.02**	-0.17**	-3.96**	0.05**	-0.03NS	0.20**	-0.21**	-0.66**
L37xT1	-0.01**	-0.07**	0.29**	-0.08**	0.02**	-0.05**	-0.17**	-0.01**	-0.67**	0.32**	-0.32**
L37xT2	0.01**	0.07**	-0.30**	0.07**	-0.01**	0.13**	0.18**	0.01**	0.65**	-0.31**	0.34**
L38xT1	-0.01**	0.49**	0.49**	0.19**	0.09**	6.40**	-0.02**	0.03**	0.15**	0.06**	0.48**
L38xT2	0.01**	-0.49**	-0.49**	-0.20**	-0.09**	-6.33**	0.04**	-0.03**	-0.18**	-0.05**	-0.46**
L39xT1	0.20NS	0.74**	0.54**	0.06**	-0.10**	0.64**	0.04**	0.00**	-0.70**	-0.05**	0.45**
L39xT2	-0.20NS	-0.74**	-0.54**	-0.07**	0.10**	-0.57**	-0.02**	0.00**	0.68**	0.05**	-0.43**
L40xT1	0.12**	0.06**	-0.36**	-0.14**	0.08**	1.27**	0.59**	-0.01**	-0.23**	0.21**	0.16**
L40xT2	-0.12**	-0.06**	0.36**	0.13**	-0.07**	-1.20**	-0.58**	0.01**	0.21**	-0.21**	-0.15**
SE	0.10	0.44	0.48	0.12	0.15	3.76	0.32	0.02	0.39	0.29	0.46
%(SCA_{lxT})	49.96	23.16	19.16	46.72	37.07	20.28	16.21	31.25	58.53	49.54	20.00

** = Highly significant (P<0.001);* = Significant (P<0.05);NS = non significant; L =Lines; T= Testers; SE= standard error of the difference; % (SCA_{LxT}) = proportional contribution of LxT to total cross variance; CLR = common leaf rust, DTA = Date to 50% anthesis; DTA= Date to 50% silking; EASP = ear spect; ED= ear diameter; EHT = ear height; EL = ear length; EPO = ear position; ER = ear rot; GLS = gray leaf spot; GY = grain yield; HC = bad husk cover; MD = 50% maturity date; NE = number of ear;NEPP = number of ear per plant; NKPR = number of kernel per row; NRPE = number of rows per ear; PASP = plant aspect; PHT = plant height; RL = root lodging; SL = stem lodging; TLB = turcicum leaf blight; TSW = thousand seed weight

Across location SCA of lines x Testers and proportional contribution of LxT to the total cross variances (Table 6 continue,)

Lines x Testers	MD	NE	NEPP	NKPR	NRPE	PASP	PHT	RL	SL	TSW
L1xT1	1.05**	-0.63**	0.02**	0.36**	-0.65**	-0.10**	-0.46**	-0.28**	0.42**	34.05NS
L1xT2	-1.02**	0.62**	-0.02**	-0.31**	0.65**	0.10**	0.47**	0.27**	-0.43**	-33.26NS
L2xT1	0.33**	-0.83**	0.02**	0.09**	0.01**	-0.03**	-4.46**	0.33**	0.54**	-12.15**
L2xT2	-0.30**	0.83**	-0.02**	-0.04**	0.00**	0.03**	4.47**	-0.34**	-0.55**	12.95**
L3xT1	-0.96**	1.17**	0.02**	-1.06**	-0.06**	0.04**	1.77**	0.32**	-0.15**	6.97**
L3xT2	0.99**	-1.18**	-0.02**	1.11**	0.06**	-0.05**	-1.76**	-0.32**	0.15**	-6.18**
L4xT1	-0.35**	0.15**	-0.01**	-0.89**	0.15**	0.25 NS	-2.77**	0.00**	0.81 NS	0.74**
L4xT2	0.38**	-0.16**	0.01**	0.94**	-0.15**	-0.26NS	2.78**	0.00**	-0.81NS	0.05**
L5xT1	0.02**	1.15**	0.06**	0.44**	-0.23**	-0.19**	-1.63**	0.45**	-0.35**	9.17**
L5xT2	0.02**	-1.15**	-0.06**	-0.38**	0.23**	0.19**	1.63**	-0.45**	0.35**	-8.37**
L6xT1	-0.70**	0.08**	0.13NS	1.86NS	0.24**	0.01**	2.51**	-0.38**	-0.23**	-2.84**
L6xT2	0.73**	-0.08**	-0.13NS	-1.81NS	-0.24**	-0.01**	-2.50**	0.38**	0.23**	3.64**
L7xT1	-0.19**	-0.65**	0.22NS	0.24**	0.29**	0.00**	1.12**	0.00**	-0.17**	14.28**
L7xT2	0.22**	0.64**	-0.22NS	-0.19**	-0.28**	0.00**	-1.11**	0.00**	0.17**	-13.48**
L8xT1	0.13**	-1.37**	-0.07**	-2.39NS	-0.37**	-0.10**	-6.47**	-0.10**	-0.79NS	3.54**
L8xT2	-0.09**	1.37**	0.07**	2.44NS	0.37**	0.10**	6.48**	0.10**	0.79NS	-2.74**
L9xT1	0.56**	2.30NS	0.05**	0.19**	0.05**	-0.09**	-6.55**	0.28**	-0.21**	5.39**
L9xT2	-0.52**	-2.30NS	-0.05**	-0.14**	-0.05**	0.08**	6.56**	-0.28**	0.20**	-4.60**
L10xT1	-1.19NS	-0.72**	-0.05**	1.29**	0.01**	-0.01**	-4.13**	-0.16**	-0.30**	-17.54**
L10xT2	1.22NS	0.72**	0.05**	-1.24**	0.00**	0.01**	4.14**	0.16**	0.29**	18.34**
L11xT1	0.19**	-0.53**	0.02**	0.03**	-0.25**	0.30NS	-9.33NS	-0.16**	-0.01**	1.92**
L11xT2	-0.16**	0.53**	-0.02**	0.02**	0.25**	-0.30NS	9.34NS	0.15**	0.01**	-1.12**
L12xT1	0.91**	0.33**	0.02**	0.03**	1.01NS	-0.10**	-2.32**	0.32**	0.05**	6.20**
L12xT2	-0.88**	-0.34**	-0.02**	0.02**	-1.00NS	0.09**	2.33**	-0.32**	-0.05**	-5.40**
L13xT1	0.18**	-0.69**	-0.05**	1.26**	-0.39**	-0.13**	-3.10**	0.27**	0.10**	-3.82**
L13xT2	-0.15**	0.68**	0.05**	-1.21**	0.39**	0.13**	3.11**	-0.27**	-0.11**	4.61**
L14xT1	0.70**	1.10**	0.02**	1.32**	0.22**	-0.12**	1.66**	-0.18**	0.27**	-6.13**
L14xT2	-0.67**	-1.10**	-0.02**	-1.27**	-0.22**	0.12**	-1.65**	0.17**	-0.27**	6.93**
L15xT1	-0.11**	-0.68**	-0.05**	0.76**	-0.63**	0.07**	5.49**	-0.40**	0.13**	-5.84**
L15xT2	0.14**	0.68**	0.05**	-0.71**	0.63**	-0.08**	-5.48**	0.39**	-0.13**	6.63**

Lines x Testers	MD	NE	NEPP	NKPR	NRPE	PASP	PHT	RL	SL	TSW
L16xT1	0.22**	-2.17NS	-0.13**	0.35**	-0.12**	-0.06**	1.22**	-0.38**	0.28**	11.18**
L16xT2	-0.18**	2.17NS	0.13**	-0.30**	0.12**	0.06**	-1.21**	0.38**	-0.28**	-10.38**
L17xT1	-0.83**	-0.98**	-0.06**	0.02**	-0.58**	-0.03**	-4.02**	0.06**	-0.02**	-7.16**
L17xT2	0.86**	0.98**	0.06**	0.03**	0.59**	0.03**	4.03**	-0.06**	0.02**	7.96**
L18xT1	0.40**	0.80**	0.02**	0.57**	0.05**	-0.17**	0.14**	0.29**	-0.20**	0.75**
L18xT2	-0.37**	-0.81**	-0.02**	-0.52**	-0.05**	0.16**	-0.13**	-0.29**	0.19**	0.04**
L19xT1	-0.40**	0.12**	-0.03**	-0.84**	0.72**	0.04**	-9.65NS	0.03**	-0.08**	-18.00**
L19xT2	0.43**	-0.12**	0.03**	0.89**	-0.72**	-0.04**	9.66NS	-0.03**	0.08**	18.79**
L20xT1	0.19**	0.08**	-0.03**	-0.14**	1.21NS	0.13**	6.04**	-0.12**	0.05**	4.54**
L20xT2	-0.15**	-0.08**	0.03**	0.19**	-1.21NS	-0.13**	-6.03**	0.12**	-0.06**	-3.74**
L21xT1	-0.66**	0.53**	0.07**	0.23**	-0.40**	-0.07**	3.12**	-0.19**	-0.50**	-5.94**
L21xT2	0.69**	-0.54**	-0.07**	-0.18**	0.40**	0.07**	-3.11**	0.19**	0.49**	6.73**
L22xT1	0.09**	0.82**	0.07**	-0.18**	-0.42**	0.10**	-5.64**	0.32**	-0.20**	-12.43**
L22xT2	-0.05**	-0.83**	-0.07**	0.23**	0.42**	-0.10**	5.65**	-0.33**	0.20**	13.22**
L23xT1	-0.36**	-0.63**	-0.13NS	-1.47**	-0.50**	0.01**	-0.86**	0.39**	0.20**	-36.07NS
L23xT2	0.39**	0.62**	0.13NS	1.52**	0.51**	-0.02**	0.87**	-0.39**	-0.20**	36.86NS
L24xT1	-0.06**	-0.30**	-0.03**	-2.02NS	-0.65**	-0.02**	1.00**	0.13**	0.03**	-24.82**
L24xT2	0.09**	0.29**	0.03**	2.08NS	0.66**	0.01**	-0.99**	-0.13**	-0.03**	25.61NS
L25xT1	-0.35**	-0.38**	-0.03**	-0.58**	0.28**	-0.04**	1.25**	0.08**	0.23**	-0.39**
L25xT2	0.39**	0.38**	0.03**	0.64**	-0.28**	0.04**	-1.24**	-0.08**	-0.23**	1.19**
L26xT1	-0.16**	-0.90**	0.00**	0.85**	0.25**	-0.03**	-4.12**	0.03**	0.19**	-17.01**
L26xT2	0.19**	0.89**	0.00**	-0.79**	-0.25**	0.03**	4.13**	-0.03**	-0.19**	17.80**
L27xT1	-0.75**	0.38**	-0.11**	-0.15**	-0.22**	-0.09**	-1.77**	0.29**	0.14**	-26.90NS
L27xT2	0.79**	-0.39**	0.11**	0.20**	0.22**	0.08**	1.78**	-0.30**	-0.14**	27.70NS
L28xT1	1.05**	2.43NS	0.11**	-0.87**	0.13**	-0.11**	3.12**	-0.31**	-0.35**	7.44**
L28xT2	-1.02**	-2.44NS	-0.11**	0.92**	-0.13**	0.11**	-3.11**	0.31**	0.34**	-6.64**
L29xT1	0.02**	0.35**	0.02**	0.68**	1.05NS	-0.07**	-0.53**	0.02**	-0.12**	8.50**
L29xT2	0.02**	-0.36**	-0.02**	-0.63**	-1.05NS	0.07**	0.54**	-0.02**	0.12**	-7.71**
L30xT1	-0.28**	-2.29NS	-0.04**	1.35**	-0.38**	-0.12**	2.55**	-0.52NS	0.27**	3.00**
L30xT2	0.31**	2.29NS	0.04**	-1.30**	0.38**	0.12**	-2.54**	0.52NS	-0.27**	-2.20**
L31xT1	0.94**	1.04**	-0.01**	0.43**	-0.27**	0.19**	12.95NS	-0.27**	-0.12**	11.76**
L31xT2	-0.91**	-1.04**	0.01**	-0.38**	0.27**	-0.19**	-12.94NS	0.27**	0.11**	-10.97**
L32xT1	-0.53**	0.40**	0.04**	-0.88**	0.41**	0.16**	0.20**	-0.27**	-0.17**	14.49**
L32xT2	0.56**	-0.41**	-0.04**	0.93**	-0.41**	-0.16**	-0.19**	0.27**	0.17**	-13.70**
L33xT1	0.41**	1.11**	-0.05**	0.08**	-0.23**	-0.05**	-0.68**	-0.38**	-0.28**	2.14**

Lines x Testers	MD	NE	NEPP	NKPR	NRPE	PASP	PHT	RL	SL	TSW
L33XT2	-0.38**	-1.11**	0.05**	-0.03**	0.23**	0.05**	0.69**	0.38**	0.27**	-1.34**
L34xT1	-0.23**	0.40**	0.03**	0.41**	0.44**	0.10**	5.12**	-0.11**	0.58NS	13.26**
L34xT2	0.26**	-0.40**	-0.03**	-0.36**	-0.43**	-0.10**	-5.11**	0.11**	-0.58NS	-12.47**
L35xT1	-0.34**	-0.67**	0.00**	-1.07**	0.60**	0.02**	11.48NS	0.06**	0.12**	8.19**
L35xT2	0.38**	0.66**	0.00**	1.12**	-0.60**	-0.02**	-11.47NS	-0.07**	-0.12**	-7.40**
L36xT1	0.94**	-1.16**	0.05**	-0.31**	0.39**	-0.11**	2.38**	0.13**	-0.22**	8.78**
L36xT2	-0.91**	1.16**	-0.05**	0.36**	-0.39**	0.11**	-2.37**	-0.14**	0.22**	-7.99**
L37xT1	0.77**	-0.92**	-0.06**	0.59**	0.10**	0.14**	-2.73**	0.13**	-0.25**	3.00**
L37xT2	-0.73**	0.92**	0.06**	-0.54**	-0.10**	-0.15**	2.74**	-0.13**	0.25**	-2.20**
L38xT1	0.15**	1.90**	0.05**	0.52**	-0.92**	0.09**	5.82**	0.62NS	0.26**	7.20**
L38xT2	-0.12**	-1.91**	-0.05**	-0.46**	0.93NS	-0.09**	-5.81**	-0.63NS	-0.26**	-6.40**
L39xT1	-0.24**	0.31**	-0.01**	-0.85**	-0.08**	0.06**	-4.03**	-0.28**	0.11**	4.45**
L39xT2	0.27**	-0.31**	0.01**	0.90**	0.08**	-0.06**	4.04**	0.28**	-0.11**	-3.65**
L40xT1	0.11**	-0.54**	-0.04**	0.79**	-0.23**	0.08**	6.52**	-0.11**	-0.10**	22.00**
L40xT2	-0.08**	0.53**	0.04**	-0.74**	0.23**	-0.09**	-6.51**	0.11**	0.10**	-21.21**
SE	0.56	1.02	0.07	0.84	0.47	0.11	4.56	0.24	0.28	12.70
% (SCA_{LxT})	50.87	35.99	53.44	29.36	29.93	52.93	25.20	32.50	41.04	39.90

** = Highly significant (P<0.001);* = Significant (P<0.05);NS = non significant; L =Lines; T= Testers; SE= standard error of the difference; % (SCA_{LxT}) = proportional contribution of LxT to total cross variance; CLR = common leaf rust, DTA = Date to 50% anthesis; DTA= Date to 50% silking; EASP = ear spect; ED= ear diameter; EHT = ear height; EL = ear length; EPO = ear position; ER = ear rot; GY = grain yield; HC = bad husk cover; MD = 50% maturity date; NE = number of ear;NEPP = number of ear per plant; NKPR = number of kernel per row; NRPE = number of rows per ear; PASP = plant aspect; PHT = plant height; RL = root lodging; SL = stem lodging; TLB = turcicum leaf blight; TSW = thousand seed weigh

4.1.4. Proportional Contributions of GCA and SCA

The proportional contributions of line GCA, tester GCA, and line × tester (SCA) effects to the total variance among crosses are presented in Tables 5 and 6 and illustrated in Figure 1. Across all traits analyzed, the contribution of line GCA was consistently higher than that of tester GCA and L × T SCA, underscoring the predominance of additive genetic variance in this population. The highest proportional contributions of line GCA were observed for ear height (79.55%), ear length (78.96%), husk cover (78.74%), and date to 50% silking (77.78%), while the lowest was recorded for common leaf rust (33.03%). This pattern indicates that most yield-related and morphological traits are strongly influenced by additive gene action, whereas disease resistance traits such as leaf rust involve more complex inheritance.

Tester GCA contributions were comparatively smaller, ranging from 16.97% for common leaf rust to 0.04% for anthesis date and root lodging, confirming their role as discriminators rather than primary sources of variability. In contrast, L × T SCA contributions were substantial for several traits, reflecting the importance of non-additive gene action. The highest SCA contributions were recorded for ear rot (58.53%), number of ears per plant (53.44%), and plant aspect (52.93%), while the lowest was observed for ear length (16.21%).

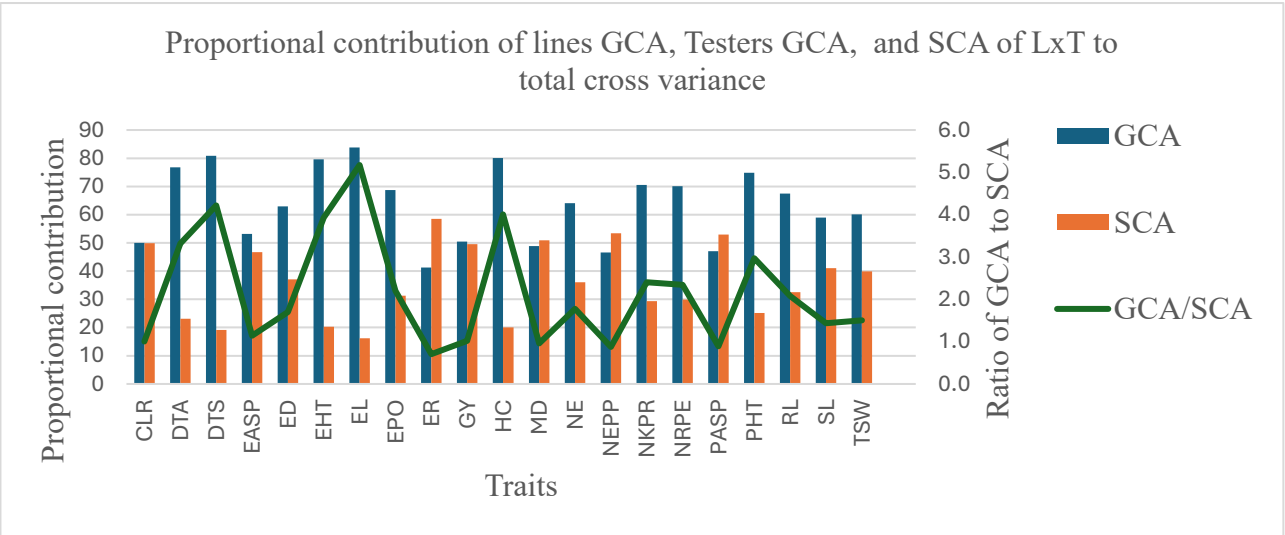


Figure **1**: Proportional contribution of GCA and SCA to the total crosses variance and the ratio of GCA to SCA

The highest ratio of general combining ability (GCA) to specific combining ability (SCA) was observed for ear length (5.2), which exceeded unity, indicating that the genetic variation for this trait is predominantly governed by additive gene action. A similarly high GCA/SCA ratio was recorded for days to 50% silking (4.5), further supporting the predominance of additive effects. In contrast, the lowest GCA/SCA ratio was obtained for ear rot (0.7), which is less than unity, signifying that the genetic variation for this trait is primarily controlled by non-additive gene action.

4.1.5. Heterotic grouping

Table 7 summarizes the heterotic grouping of the 40 maize inbred lines evaluated in this study. The grouping procedure followed the method proposed by Singh and Chaudhary (1985), whereby inbred lines were classified into heterotic groups based on the specific combining ability (SCA) effects for grain yield, computed from their across-location testcross performance with the two heterotic testers. Inbred lines exhibiting significant negative SCA effects with a given tester were assigned to the same heterotic group as that tester. Conversely, lines showing significant positive SCA effects with tester A (CML312) were classified into the opposite heterotic group (tester B, CML395), and vice versa.

Based on across-location grain yield SCA results, seventeen lines (L2, L3, L6, L7, L8, L10, L11, L14, L15, L16, L17, L22, L23, L24, L30, L34, and L39) exhibited significant negative SCA effects with tester A (CML312) and were therefore assigned to heterotic group A. Nineteen lines (L1, L4, L5, L9, L12, L13, L19, L20, L21, L25, L27, L28, L29, L32, L33, L36, L37, L38, and L40) showed significant negative SCA effects with tester B (CML395) and were classified into heterotic group B. Line L35 was categorized as A/B, since it displayed significant positive SCA effects with both testers. Three lines (L18, L26, and L31) remained unclassified, as they exhibited non-significant SCA effects with both testers.

Inbred lines within the same heterotic group are genetically similar, whereas lines between groups are genetically divergent. This divergence provides the basis for exploiting heterosis, as crossing lines from opposite groups is expected to generate high-yielding hybrids.

Table7: Heterotic grouping of maize inbred lines based on across location grain yield specific combining ability.

Lines	SCA Tester A (CML312)	SCA Tester B (CML395)	HG	Lines	SCA Tester A (CML312)	SCA Tester B (CML395)	HG
L1	0.33**	-0.32**	B	L21	0.03**	-0.02**	B
L2	-0.29**	0.29**	A	L22	-0.09**	0.1**	A
L3	-0.01**	0.01**	A	L23	-0.52**	0.52**	A
L4	0.03**	-0.03**	B	L24	-0.35**	0.36**	A
L5	0.1**	-0.1**	B	L25	0.33**	-0.33**	B
L6	-0.08**	0.08**	A	L26	-0.63NS	0.64NS	.
L7	-0.44**	0.44**	A	L27	0.21**	-0.21**	B
L8	-0.13**	0.14**	A	L28	0.18**	-0.18**	B
L9	0.24**	-0.24**	B	L29	0.04**	-0.04**	B
L10	-0.31**	0.31**	A	L30	-0.15**	0.15**	A
L11	-0.47**	0.47**	A	L31	0.71NS	-0.7NS	.
L12	0.3**	-0.3**	B	L32	0.22**	-0.21**	B
L13	0.36**	-0.35**	B	L33	0.07**	-0.07**	B
L14	-0.04**	0.05**	A	L34	-0.15**	0.16**	A
L15	-0.39**	0.4**	A	L35	0**	0.01**	A/B
L16	-0.31**	0.32**	A	L36	0.21**	-0.21**	B
L17	-0.33**	0.34**	A	L37	0.32**	-0.31**	B
L18	0.7NS	-0.7NS	.	L38	0.06**	-0.05**	B
L19	0.14**	-0.13**	B	L39	-0.05**	0.05**	A
L20	0.04**	-0.03**	B	L40	0.21**	-0.21**	B

**=highly significant (P<0.01); * = Significant (P<0.05); NS = Non significant; L = Lineas; HG = Heterotic group

4.2. Discussion

The present study was undertaken to estimate the general and specific combining ability of forty maize inbred lines and to classify them into heterotic groups for the development of high-yielding, moisture-stress-tolerant hybrids. The combined analysis of variance revealed highly significant differences among genotypes, lines, testers, and line × tester interactions for grain yield and most agronomic traits, confirming that the parental lines used in this study possess substantial genetic variability that can be exploited through hybrid breeding. The simultaneous significance of GCA and SCA mean squares indicates that both additive and non-additive gene actions are operative in the inheritance of grain yield and yield-related traits in this population, consistent with the theoretical framework of Sprague and Tatum (1942) and Falconer (1960), who established that GCA reflects additive gene effects while SCA reflects dominance and epistatic deviations. The significant line × location and tester × location interactions further demonstrate that genotype × environment interaction influences the expression of these traits, underscoring the necessity of multi-environment testing before any line or hybrid is recommended for moisture-stress-prone production systems, in agreement with Hosana et al. (2015).

The general combining ability results showed that line effects exceeded tester effects in magnitude and proportional contribution for nearly all traits evaluated, indicating that the additive component of genetic variance resided predominantly in the inbred lines rather than in the two testers. Twenty lines exhibited positive and significant GCA effects for grain yield, with the line component contributing 47.94% of the total cross variance, suggesting that careful selection and recycling of parental lines, rather than tester choice alone, will drive genetic gain in this breeding programme. This predominance of additive gene action for grain yield and most yield components agrees with the findings of Legesse et al. (2017) and Gemechu (2019) in Ethiopian mid-altitude maize, and with Tamirat et al. (2014) in lowland maize evaluated at the same Melkassa location, all of whom reported strong additive control of grain yield, ear traits, and kernel traits. The exceptionally high proportional contribution of lines to ear length (78.96%), ear height (79.55%), and husk cover (78.74%) further demonstrates that these morphological and agronomic traits can be improved efficiently through recurrent selection among the inbred lines, while the comparatively modest tester contribution to most traits (generally below 5%, except for common leaf rust at 16.97%) confirms that CML312 and

CML395 functioned mainly as discriminating testers rather than as primary sources of genetic variability, consistent with the rationale of Matzinger (1953) for the use of narrow-base testers in inbred line evaluation.

Negative GCA and SCA effects for days to anthesis, days to silking, and days to maturity were considered favourable in this study, since earlier flowering and maturity allow hybrids to complete their reproductive cycle before the onset of terminal moisture stress, a strategy generally referred to as drought escape (Banziger and Diallo, 2004; Badu-Apraku et al., 2012). The substantial proportion of variance attributable to lines for silking date (77.78%) indicates that the early-flowering lines identified in this study, several of which also combined well for grain yield, represent valuable parental material for developing short-cycle hybrids adapted to the erratic and short rainy seasons characteristic of Melkassa and Dhera. The corresponding non-additive effects observed for the same traits, with forty crosses showing negative and significant SCA for both anthesis and silking dates, suggest that specific line × tester combinations can shorten the flowering period beyond what would be predicted from the additive effects of the parents alone, a pattern also reported by Dereje (2020) in central Rift Valley maize germplasm evaluated under similarly moisture-limited conditions.

Specific combining ability effects were significant for grain yield and several yield-related traits, confirming that non-additive gene action, arising from dominance and epistatic interactions between specific line and tester combinations, also plays an important role in hybrid performance. Thirty-seven crosses exhibited positive and significant SCA effects for grain yield, with the line × tester interaction contributing 49.54% of the total cross variance, a proportion nearly equal to that attributed to lines, indicating that grain yield in this population is governed by a near balance of additive and non-additive gene effects. This finding has direct practical implications; because SCA effects are specific to individual cross combinations and cannot be reliably predicted from the GCA of the parents alone, the superior crosses identified in this study, particularly those combining favourable SCA with high-GCA parents, should be advanced through further yield trials rather than selected on the basis of parental performance alone. A similar co-occurrence of significant GCA and SCA effects for grain yield has been reported by Assefa et al. (2017), Annor et al. (2019), and Nasser and Mafouasson (2020) in maize evaluated under drought and multiple-stress environments, reinforcing that both the

selection of superior parents and the testing of specific hybrid combinations are necessary components of an effective breeding strategy for moisture-stressed environments.

The GCA/SCA ratio provides further insight into the relative importance of additive versus non-additive gene action for individual traits. Ratios greater than unity, such as those obtained for ear length (5.2) and days to 50% silking (4.5), indicate that additive gene action predominates in the inheritance of these traits and that they should respond well to simple selection-based breeding methods such as pedigree selection or recurrent selection among the lines. In contrast, the low ratio recorded for ear rot (0.7) signals that non-additive gene action is more influential for this trait, implying that exploitation of hybrid vigour through specific cross combinations, rather than line selection alone, would be more effective for traits showing this pattern. These results parallel the conclusions of Sprague and Tatum (1942) and Hallauer et al. (2010), who emphasized that the relative magnitude of GCA and SCA variance should guide the choice between population improvement and hybrid breeding strategies for a given trait.

The classification of the forty inbred lines into heterotic groups A and B, based on their across-location SCA effects for grain yield with testers CML312 and CML395, provides a practical basis for systematic hybrid development in this breeding programme. Seventeen lines, namely L2, L3, L6, L7, L8, L10, L11, L14, L15, L16, L17, L22, L23, L24, L30, L34, and L39, each exhibited significant negative SCA effects with tester A (CML312) and were accordingly assigned to heterotic group A, while nineteen lines, namely L1, L4, L5, L9, L12, L13, L19, L20, L21, L25, L27, L28, L29, L32, L33, L36, L37, L38, and L40, each exhibited significant negative SCA effects with tester B (CML395) and were assigned to heterotic group B. The use of proven, narrow-base CIMMYT testers of known heterotic relationship to classify new lines is consistent with the line × tester-based grouping approach recommended by Singh and Chaudhary (1985) and successfully applied in similar Ethiopian and African studies (Elmyhun et al., 2020; Konaté, Baffour and Traoré, 2017; Zelleke et al., 2018; Tolera et al., 2017). Lines assigned to opposite heterotic groups are expected to be more genetically divergent and, when intercrossed, to produce hybrids with greater heterotic expression than crosses between lines of the same group, thereby reducing the number of redundant cross combinations that must be evaluated and increasing the efficiency of the hybrid development pipeline (Melchinger, 1999; Zambezi et al., 1986). The classification of line L35 into both groups A and B, owing to its

significant positive SCA with both testers, and the failure of lines L18, L26, and L31 to show significant SCA with either tester, indicate that these three lines are either genetically intermediate between the two heterotic pools or possess tester-independent combining ability for grain yield; such lines warrant further characterization, ideally supported by molecular marker data, before they are confidently assigned to a specific heterotic group or discarded from the breeding pipeline (Reif et al., 2003; Xia et al., 2004).

Taken together, the combining ability and heterotic grouping results generated in this study provide breeders with the additive and non-additive genetic information needed to design hybrid combinations and to organize the available inbred lines into complementary heterotic pools for sustained genetic gain under moisture-stress conditions. The identification of lines with simultaneously favourable GCA for grain yield, early flowering, and a defined heterotic group classification offers an efficient starting point for advancing the most promising single-cross hybrids to multilocation variety trials, while continued use of molecular markers alongside the phenotypic line × tester approach used here would further refine heterotic grouping and improve the precision of parental selection in subsequent breeding cycles (Eathington et al., 2007).

5. SUMMARY AND CONCLUSIONS

This study was conducted to estimate the general and specific combining ability of forty advanced maize inbred lines and to classify them into heterotic groups for systematic hybrid development under the low-moisture stress conditions of Ethiopia. A total of 126 genotypes, comprising 80 lines × tester crosses, four standard checks, and 42 parental lines, were evaluated at Melkassa and Dhera during the 2019/20 main cropping season using an alpha-lattice design with three replications.

Combined analysis of variance across the two locations revealed highly significant ($P<0.01$) or significant ($P<0.05$) differences among genotypes for grain yield and most agronomic traits in both the hybrid and parental line trials, confirming the presence of substantial exploitable genetic variability in the study material. Mean squares due to GCA of lines and testers, as well as SCA of line × tester interactions, were significant for grain yield and most yield-related traits, demonstrating that both additive and non-additive gene actions condition the inheritance of these traits in this population.

Twenty inbred lines exhibited positive and highly significant ($P<0.01$) GCA effects for grain yield, with the line component accounting for 47.94% of the total cross variance, while nineteen lines showed negative and significant GCA effects. Tester 1 (CML312) displayed a positive and significant GCA effect for grain yield, although the tester component contributed only 2.46% of the total variance, confirming that the additive genetic variance in this population resided predominantly in the inbred lines rather than in the testers.

Thirty-seven crosses exhibited positive and highly significant ($P<0.01$) SCA effects for grain yield, with the line × tester interaction contributing 49.54% to the total cross variance, while an equal number of crosses showed negative and highly significant SCA effects. Three crosses (L31×T1, L18×T1, and L26×T2) recorded the highest positive SCA values but were not statistically significant, and three crosses (L26×T1, L18×T2, and L31×T2) showed the highest negative, non-significant SCA effects.

Based on across-location SCA effects for grain yield, seventeen lines (L2, L3, L6, L7, L8, L10, L11, L14, L15, L16, L17, L22, L23, L24, L30, L34, and L39) were classified into heterotic group A on account of their significant negative SCA with tester A (CML312), while nineteen lines (L1, L4, L5, L9, L12, L13, L19, L20, L21, L25, L27, L28, L29, L32, L33, L36, L37, L38,

and L40) were classified into heterotic group B based on their significant negative SCA with tester B (CML395). Line L35 was assigned to both groups (A/B) owing to its significant positive SCA with both testers, whereas lines L18, L26, and L31 remained unclassified because they showed non-significant SCA with either tester.

The simultaneous presence of significant GCA and SCA effects, together with GCA/SCA ratios exceeding unity for most traits, confirms that additive gene action predominates in the inheritance of grain yield and the majority of agronomic traits evaluated, although non-additive effects remain important for specific cross combinations. The successful classification of the forty inbred lines into two complementary heterotic groups provides a practical foundation for designing future hybrid combinations and reducing the number of redundant crosses that must be evaluated in this breeding programme.

It is recommended that the information on parental line combining ability and heterotic grouping generated in this study be complemented with molecular marker data to validate and refine the heterotic classification, particularly for the three unclassified lines and for line L35, which combined favourably with both testers. Future breeding efforts should also extend testing of these inbred lines and their derived hybrids across a wider range of moisture-stressed environments to confirm their stability and adaptation before any candidate hybrid is advanced for variety release.

6. REFERENCES

A.R. Hallauer, M.J. Carena, and J.B.M. Filho. (2010). Quantitative Genetics in Maize Breeding. Hand Book of Plant Breeding. J. Prohens, F. Nuez and M.J. Carena (Eds) Vol (6), *Springer,* Science Business Media.

Abadassi J, Herve Y (2000). Introgression of temperate germplasm to improve an elite tropical maize population. Euphytica 113:125–133

Abenezer Abebe Tefera; Legesse Wolde Beyene; Wosene Gebreselassie Abtew (2020). Combining Ability Analysis of Maize Inbred Lines in Ethiopia. Agriculture and Food Sciences Research, 7(2): 113-124.

Abrha and Dagne Wagari (2013). Line x tester analysis of maize inbred lines for grain yield and yield related traits. Asian Journal of Plant Science and Research, 3(5).

Acquaah, George(2012). Principles of plant genetics and breeding / George Acquaah. — 2nd ed.

Aguiar, A. M., Carlini-garcia, L. A. and Resende, A. (200. 'Combining ability of inbred lines of maize and stability of their respective single-crosses',.

Alemeshet Lemma (2014). Combining ability of elite maize (*zea mays l.)* inbred lines for intercropping compatibility with common bean (phaseolus vulgaris l.) in Central rift valley of Ethiopia.Haramaya University,Msc thesis.Harmaya, Ethiopia.

Allison, J.C.S. and Curnow, R.N., (1966). On the choice of tester parent for the breeding of synthetic varieties of maize (Zea mays L.) 1. Crop Science, 6(6), .

Amare Seyoum,Dagne Wegari and Sentayehu Alemerew (2016) 'Test cross performance and combining ability of elite highland maize (Zea Mays L.) Inbred Lines at Jimma, South West Ethiopia', International Journal of Trend in Research and Development, 3(2), pp. 13–26. Available at: internal-pdf://2.13.217.53/Amare_et_al_2016_Test cross performance and co.pdf.

Andayani, N. N. et al. 2018 'Line × tester analysis across equatorial environments to study combining ability of Indonesian maize inbred', Asian Journal of Agriculture and Biology, 6(2), .

Annor, B. et al. (2019) 'Testcross performance and combining ability of early maturing maize inbreds under multiple-stress environments', Scientific Reports. Springer US, 9(1), pp. 1–11. doi: 10.1038/s41598-019-50345-3.

Assefa T, Zeleke H, Afriye T, Otyama P., 2017. Line ×Tester Analysis of Tropical High Land Maize (*Zea mays* L.) Inbred Lines Top Crossed with Three East African Maize Populations. *American Journal of Plant Sciences* .

Badu-Apraku, B., Akinwale, R.O., Franco, J. and Oyekunle, M., (2012). Assessment of reliability of secondary traits in selecting for improved grain yield in drought and low-nitrogen environments. Crop Science, 52(5), .

Banziger, M and A.O. Diallo. (2004). Progress in developing drought and N stress tolerant maize cultivars for eastern and southern Africa. In: D.K. Friesen and A.F.E. Palmer (Eds.). Integrated Approaches to Higher Maize Productivity in the New Millennium. Proceedings of the 7th Eastern and Southern Africa Regional Maize Conference. 5-11 February 2002, CIMMYT/KARI, Nairobi, Kenya. .

Beck, D.L., Vasal, S.K. and Crossa, J. (1991). Heterosis and combining ability among subtropical and temperate intermediate- maturity maize germplasm. Crop Sci., 31:68-73.

Belfield, S. and C. Brown. (2008). Field Crop Manual: Maize; a Guide to Upland Production in Cambodia. Cambodian Agricultural Research and Development Institute and the State of New South Wales (NSW) Department of Primary Industries. 50p.

Benson, T. Engida, E., Thurlow, J. (2014). The economy-wide effects of teff, wheat and maize production in increases in Ethiopia: results of economy-wide modeling. IFPRI Discussion Paper 01366. International Food Policy Research Institute.Washington, DC.

Bitew Tilahun (2016). Heterosis and Combining Ability of Mid-Altitude Maize (*Zea mays* L.) Inbred Lines for Grain Yield, Yield Related Traits and Reaction to Turcicum Leaf Blight (*Exserohilum turcicum Leonard and Suggs*) at Bako, Western Ethiopia. MSc. Thesis. Haramaya University, Haramaya, Ethiopia. 28-80.

Bos, I. and Caligari, P., (2007). Selection methods in plant breeding. Springer Science & Business Media.

Brown, W.L., M.S. Zuber, L.L. Darrah and D.V. Glover (1985). National maize hand book-origin adaptation and types of maize. .

Carangal, V.R., Ali, S.M., Koble, A.F., Rinke, E.H. and Sentz, J.C., (1971). Comparison of S1 with Testcross Evaluation for Recurrent Selection in Maize 1. Crop Science, 11(5),

Carena, M.J. and Hallauer, A.R. (2001b) Response to inbred progeny selection in Leaming and Midland Yellow Dent maize populations. Maydica 46:1–10.

Christian R, Angelika C, Christoph GJ, Frank T, Albrecht EM (2012). Genomic and metabolic prediction of complex heterotic traits in hybrid maize.

Christian R, Angelika C, Christoph GJ, Frank T, Albrecht EM (2012). Genomic and metabolic prediction of complex heterotic traits in hybrid maize.

CIMMYT and IITA, (2010). MAIZE-Global alliance for improving food security and the livelihoods of the resource-poor in developing world. Draft proposal submitted by CIMMYT and IITA, to the CGIAR Consortium Board.

CSA. (2016). The Federal Democratic Republic Of Ethiopia Central Statistical Agency Agricultural Sample Survey Report On Crop And Livestock Product Utilization (Private Peasant Holdings, Meher Season), (Vii).CSA, Addis Ababa, Ethiopia

CSA. (2019). The Federal Democratic Republic of Ethiopia Central Statistical Agency Agricultural sample survey: Report on area and production of major crops (private peasant holdings, meher season). Statistical bulletin, (1). Addis Abeba.

Dagne Wegari., Vivek, B.S., Tadesse, B., Abdissa, K., Worku, M. and Wolde, L., (2011). Combining ability and heterotic relationships between CIMMYT and Ethiopian maize inbred lines. Ethiopian Journal of Agricultural Sciences, 21(1-2).

Dagne Wegari., Zelleke, H., Labuschagne, M.T., Hussien, T. and Singh, H., (2007). Heterosis and combining ability for grain yield and its components in selected maize inbred lines. South African Journal of Plant and Soil, 24(3).

Davis, R.L. (1927): Report of the plant breeder.Rep. Puerto Rico. Agric. Exp. Sta.

Delgado-Salinas, J. Caballero and A. Casas. (2004). Crop domestication in Mesoamerica. Goodman (ed.) Encyclopedia of Plant and Crop Science. Marcel Dekker, Inc., New York.

Dereje Ayalneh (2020). Heterosis and combining ability for yield and yield related traits in maize (*zea mays* l.) inbred lines in centeral rift valley of Ethiopia.Haramya University,Msc thesis.Haramaya Ethiopia.

DeVries, J. and G. Toenniessen. (2001). Securing the Harvest: Biotechnology, Breeding and Seed Systems for African Crops. CABI Publishing, Wallingford, UK.

Dhillon, B. S., Prasanna, B. M. (2001). Maize. In V. L. Chopra (ed.). Breeding Field Crops: Theory and Practice. Oxford and IBH, New Delhi. Doebley,

Dhliwayo T, Pixley K, Menkir A, Warburton M (2009). Combining Ability, Genetic Distances , and Heterosis among Elite CIMMYT and IITA Tropical Maize Inbred Lines. Crop Sci. 49:1201-1210.

Diekmann, M. and Putter, C.A.J., (1996). FAO/IPGRI Technical guidelines for the safe movement of germplasm no. 15: Musa, Food and Agriculture Organization of the United Nations, Rome. International Plant Genetic Resources Institute, Rome.

Doebley, J. (1990). Molecular evidence for gene flow among Zea species. Bioscience 40: 443-448.

Duvick, D.N., and K.G. Cassman (1999). Post-green revolution trends in yield potential of temperate maize in the north-central United States. Crop Sci. 39:1622–1630.

Eathington, S.R., Crosbie, T.M., Edwards, M.D., Reiter, R.S. and Bull, J.K., (2007). Molecular markers in a commercial breeding program. Crop Science.

Eberhart, S.A., Salhuana, W., Sevilla, W.R. and Taba, S. (1995). Principles for tropical maize breeding. Maydica, 40: 339-355.

Ejigu, Y. G., Tongoona, P. B. and Ifie, B. E. (2017) 'Performances of selected tropical white maize single- cross hybrids for yield and yield attributing traits', (September). doi: 10.5897/JPBCS2016.0624.

Elmyhun, M. et al. (2020) 'Combining ability performance and heterotic grouping of maize (Zea mays) inbred lines in testcross formation in Western Amhara , North', Cogent Food & Agriculture. doi: 10.1080/23311932.2020.1727625.

Falconer, (D.S.) (1960). Introduction to quantitative genetics. Ronald Press, New York.

Falconer, D.S., Mackay, T.F.C. and Frankham, R., (1996). Introduction to quantitative genetics. 4th ed London. England: Longman group.

FAOSTAT (2010). The statistical database [Online]. Available at http://faostat.fao.org. FAO, Rome

FAOSTAT. (2008). Statistical Database of the Food and Agriculture of the United Nations. http://www.fao.org [Online].

FAOSTAT. (2016). Statistical databases and data-sets of the Food and Agriculture Organization
of the United Nations.

FAOSTAT. (2019). Statistical databases and data-sets of the Food and Agriculture Organization
of the United Nations.

Farg, S. A. and Aboyousef, H. A. (2019) 'Combining Ability of some White Maize Inbred Lines for Grain Yield and some Other Traits', 10(12), pp. 1059–1063. doi: 10.21608/jpp.2019.71550.

Farg, S. A. and Aboyousef, H. A. (2019) 'Combining Ability of some White Maize Inbred Lines for Grain Yield and some Other Traits', 10(12), pp. 1059–1063. doi: 10.21608/jpp.2019.71550.

Farhan Ali, Irfan Ahmed Shah, Hidayatur Rahman, Mohammad Noor, Durrishahwar, Muhammad Yasir Khan, IhteramUllah and Jianbing Yan (2012). Heterosis for yield and agronomic attributes in diverse maize germplasm. *ISSN*: 1835-2707.

Felix, M.,M. Stephen, M. Murenga A. Leah. (2010). Maize Production and Improvement in SubSaharan Africa. ABSF 2: 16-17.

Galinat, W. C. (1988). The origin of corn. In G. F. Sprague and J. W. Dudley (eds). Corn and Corn Improvement. Amer. Soc. Agron., Madison, Wisconsin, USA.

Gemechu Getachew' (2019). Combining ability and heterosis in maize inbred lines (zea mays l.) For yields in mid altitude sub-humid agroecology of Ethiopia, Department Of Plant Science and Biotechnology Faculty of Biological Sciences University Of Nigeria, Nsukka (Msc Thesis).

George Aquaah (2007).Principles of plant Genetics and breeding.Victoria Australia.

George H. Shull, The Composition of a Field of Maize, *Journal of Heredity*, Volume os-4, Issue 1, January 1908, Pages 296–301, https://doi.org/10.1093/jhered/os-4.1.296

Gichuru, L. et al. (2011) 'Combining ability of grain yield and agronomic traits in diverse maize lines with maize streak virus resistance for Eastern Africa region Faculty of Agriculture , University of Nairobi , Kenya', pp. 432–439. doi: 10.5251/abjna.2011.2.3.432.439.

Girma Damisse., Tadele T. and Abraham T. (2008). Importance of husk covering on field infestation Of maize by Sitophilus (Zea mays.L) Motsch (Coleoptera: Curculionidae) at Bako,Western Ethiopia.African J. Biot. 7(20): 3777-3782

Gudata Napir. (2007). Heterosis and combining abilities in QPM varieties of early generation high land maize (Zea mays L.) inbred lines. M.Sc. Thesis. Haramaya University of Agriculture, School of Graduate Studies. Haramaya, Ethiopia.

Gudata, N., (2007). Heterosis and combining abilities in QPM varieties of early generation high land maize (*Zea mays* L.) inbred lines. M.Sc. Thesis. Haramaya University of Agriculture, School of Graduate Studies. Haramaya, Ethiopia, 185.

Habtamu Zelleke (2015). 'Heterosis and combining ability for grain yield and yield component traits of maize in eastern Ethiopia', Current Agriculture Research Journal 3(2).

Hallauer AR, Marccelo J, Carena JB, Mirnda F (2010). Quantative genetics in maize breeding. (M JC. Prohens, Jamie, Fernando Nuez, Ed.) (6th ed.). Springer, New York Dordrecht Heidelberg London.

Hallauer, A.R. (1997). Maize improvement. In M.S. Kang (ed.) Crop Improvement for the 21st Century. Research Signpost, Trivandrum, India.

Hallauer, A.R. and Miranda, J.B., 1981. Fo. (1988). Quantitative genetics in maize breeding. *Iowa State Univ Press, Ames, IA. Jenkins, JN, WL Parrott, JC McCarty Jr & RL Shepherd, 1988a. Registration of three noncommercial germplasm lines of upland cotton tolerant to tobacco budworm.*

Hallauer, A.R., Carena, M.J. and Miranda Filho, J.D., (2010). *Quantitative genetics in maize breeding* (Vol. 6). Springer Science & Business Media.

Hassan, R.M., M. Mekuria and W. Mwangi. (2001). Maize breeding research in eastern and southern Africa: Current status and impacts of past investments made by public and private sectors 1966-1997. CIMMYT, Mexico, D.F., Mexico.

Haullauer, A.R., Russell, W.A. and Lamkey, K.R. (1998) Corn breeding. In:Corn and corn improvement. 3rd edition. (Eds. G.F. sprange and J.W. Dudley) Agron. Monogr.18. Madison, WI. ASA, CSSA and SSSA, 677 South Segoe Road, Madison, WI, 53711, USA.

Heisey, P.W. and G.O. Edmeades. (1999). Maize production in drought stressed environments: Technical options and research resource allocation. CIMMYT 1997/98 World Maize Facts and Trends. CIMMYT, Mexico, D. F., Mexico.

Hosana, G. C., Alamerew, S., Tadesse, B., & Menamo, T. (2015). *Test Cross Performance and Combining Ability of Maize (Zea Mays L .) Inbred Lines at Bako , Western*

Ethiopia Test Cross Performance and Combining Ability of Maize ZeaMaysL Inbred Lines at Bako Western Ethiopia. (June).

Jenkins, M.T. and Brunson, A.M., (1932). Methods of testing inbred lines of maize in crossbred combinations. Journal of the American society of agronomy.

Johnson, L.J. and Hayes, H.K., (1936). combining ability of inbred lines of golden bantam sweet corn. Journal of the American Society of Agronomy.

Joshi, V. N., R. B. Dubey and S. Marker (2002). Combining ability for polygenic traits in early maturity hybrids of maize (*Zea mays* L.). *Indian J. Plant Breed*. Genet. 62: 312-315.

Kempthorne O. 1957. *An introduction to Genetic Statistics*, John Wiley and Sons, New York.

Konaté, L., Baffour, B.A. and Traoré, D., (2017). Combining ability and heterotic grouping of early maturing provitamin A maize inbreds across Striga infested and optimal environments. Journal of Agriculture and Environment for International Development (JAEID).

Lamkey, K.R. and Edwards, J.W., (1999). Quantitative genetics of heterosis.

Legesse Wolde., Keno, T., Tadess, B., Worku, M. and Wogari, D., (2017). Combing ability analysis of among early generation maize inbred lines. Ethiopian Journal of Agricultural Sciences.

Librando, R.P. and Magulama, E.E., (2008). Classifying white inbred lines into heterotic groups using yield combining ability effects. USM R & DJ, 16(1).

Lile, S.M. and Hallauer, A.R., (1994). Relation between S2 and later generation testcrosses of two corn populations. Journal of the Iowa Academy of Science: JIAS, 101(1).

Mamud Aman (2018). Line × tester analysis of maize (*zea mays l.)* inbred lines for grain yield and yield related traits in mid-altitude agro-ecology of Ethiopia. Haramaya Unvversity,Msc thesis.Haramaya,Ethiopia

Mandal, B.C., (2014). Maize breeding and seed production manual. *Food and Agriculture Organization, United Nations, DPR Korea*.

Matsuoka, Y., Y. Vigouroux, M.M. Goodman, G.J. Sanchez, E. Buckler, and J. Doebley. (2002). A single domestication of maize shown by multilocus microsatellite genotyping. Proc. Natl. Acad. Sci. USA 99(9):6080–6084.

Matzinger D.F. (1953). Comparison of three types of testers for the evaluation of inbred lines of corn. Agron. J. 45:493-495.

Mealkassa Agricultural Research Center (2019).Progress review document of soil fertility research process.

Melchinger AE (1999). Genetic diversity and heterosis. In: Coors JG, Pandey S (eds) The genetics and exploitation of heterosis in crops. CSSA-SP, Madison.

Melchinger, A.E. and Gumber, R.K. (1998) Overview of heterosis and heterotic groups in agronomic crops. pp. 29-44. In: K.R. Lamkey, J.E. Staub (Eds.), Concepts and Breeding of Heterosis in Crop Plants. CSSA, Madison, WI.

Ministry of Agriculture and Rural Development; Animal and Plant Health Regulatory Directorate. Crop Variety Registry issue no.17; June, 2014.Addis Ababa, Ethiopia.

Moll, R.H., Lonnquist, J.H., Velez, F.J and Johnson, C. (1965) the relationship of heterosis and genetic divergence in maize.

Morris ML, Tripp R, Dankyi AA (1999). Adoption and Impacts A Case Study of the of Improved Ghana Grains Maize Production Development Project Technology: Adoption and Impacts of Improved Maize Production Technology: A Case Study of the Ghana Grains. Economics Program paper 99- 01. Mexico, D.F.: CIMMYT.

Nasser, L. M. and Mafouasson, H. (2020) 'Combining Ability of Early-Maturing Yellow Maize Inbreds under Combined Drought and Heat Stress', (November). doi: 10.3390/agronomy10101585.

Nepir, G., Wegary, D. and Zeleke, H. (2015) 'Heterosis and combining ability of highland quality protein maize inbred lines', Maydica, 60(3).

Paliwal, R.L. and M.E. Smith (2002). Tropical maize: Innovative approaches for sustainable productivity and production increases. In M.S. Kang (ed.) Crop Improvement: Challenges in the Twentyfi rst Century. Food Products Press, an imprint of Haworth Press, Binghamton, New York.

Pandey, S. and Gardner, C.O., (1992). Recurrent selection for population, variety, and hybrid improvement in tropical maize. In Advances in Agronomy (Vol. 48, pp. 1-87). Academic Press.

Pingali, P.L and S. Pandey (2001). Meeting world maize needs: Technological opportunities and priorities for public sector. CIMMYT 1999/2000 World Maize Facts and Trends. CIMMYT, Mexico, D. F., Mexico.

Poehlman, J. M., Sleper, D. A. (1995). Breeding Field Crops. 4th Edn. Iowa State Univ. Press, Ames.

Raina, K., (2018). Genetic evaluation of newly developed inbred lines in maize (Zea mays L.) (Doctoral dissertation, Sher-e-Kashmir University of Agricultural Sciences and Technology of Jammu, Jammu).

Raj, R. N., Devi, C. P. R., & Gokulakrishnan, J. (2019). *GENETICS AND PLANT BREEDING G × E interaction and Stability Analysis of Maize Hybrids Using Eberhart and Russell Model*. *12*(March), 1–6. https://doi.org/10.30954/0974-1712.03.2019.1.

Rawlings, J.O. and D.L. Thompson. (1962). Performance level as a criterion for the choice of
maize testers. *Crop Sci*. 2: 217-220.

Reif, J.C, Melchinger, A.E., Xia, X.C., Warburton, M.L., Hoisington, D.A., Vasal, S.K., Srinivasan, G., Bohn M. and Frisch, M. (2003) Genetic distance based on simple sequence repeats and heterosis in tropical maize populations. Crop science 43(4):1275-1282.

Reif, J.C., Gumpert, F.M. Fischer, S. and Melchinger, A.E. (2007) Impact of interpopulation divergence on additive and dominance variance in hybrid populations. Genetics 176:1931–1934.

Ron, P.J. and Hallauer, A.R. (1997) Utilization of exotic maize germplasm. Plant Breed Rev 14:165–187.

SAS Institute, Inc., (2008). SAS proprietary Software. SAS Institute, Inc, CARY, NC, Canada.

Schnell F.W. (1961) Heterosis and inbreeding effect. Schriftenreihe des Max-Planck-Instituts für Tierzucht und Tierernährung .

Sentayehu Alemerew (2015). Hetrosis and combining ability of sub tropical maize inbred lines.

Sharma, S.M., S. Narwal, R. Kumar and S. Dass. (2004). Line x tester analysis in maize (*Zea*
mays L.). *Forage Res*. 30: 28-30.

Shull, G.H. (1909). A pure line method of corn breeding. Rep. Am. Breeders Assoc. 5:51–59.

Shull, G.H. (1952) Beginnings of the heterosis concept. pp. 14- 48. In: J.W. Gowen (Ed.), Heterosis. Iowa State College Press, Ames, IA.

SILVA, J.C. and HALLAUER, A.R., 1975. Estimation of epistatic variance in Iowa Stiff Stalk Synthetic maize. Journal of Heredity, 66(5).

Singh, R.K., and B.D. Chaudhary. (1985). Biometrical Methods in Quantitative Genetic Analysis. Kalyani Publishers, New Delhi.

Singode, A., Ahmad, B., Srivastava, E. and Mahajan, V. (2017). 'Heterotic Grouping in Early Maturing Indian Maize Lines', International Journal of Agriculture Innovations and Research 6 (1): 2319-1473

Smalberger, S. and A.S. du Toit. (2004). Identification of maize cultivars tolerant to low soil fertility in south Africa. In: D.K. Friesen and A.F.E. Palmer (Eds.). Integrated Approaches to Higher Maize Productivity in the New Millennium. Proceedings of the 7th Eastern and Southern Africa Regional Maize Conference. 5-11 February 2002, CIMMYT/KARI, Nairobi, Kenya.

Sofi P, Rather AG. (2006). Genetic analysis of yield traits in local and CIMMYT inbred line crosses using Line x Tester analysis in maize (*Zea mays L*). *Asian J Plant Sci* 5(6): 1039-1042.

Sprague, (G.F.), and (L.A.) Tatum (1942). General vs specific combining ability in single crosses of corn. J. Am. Soc. Agron. 34: 923-932.

Sprague, G. F., Eberhart, S. A. (1977). Corn breeding. In G. F. Sprague and J. W. Dudley (eds.).

Sprague, G.F. (1939). An estimation of the number of top crossed plants required for adequate representation of corn variety. J. Am. Soc. Agron. 38: 11-16.

Tamirat T, Alamerew S, Wegary D, Menamo T (2014) Test Cross Mean Performance and Combining Ability Study of Elite Lowland Maize (Zea mays L.) Inbred Lines at Melkassa, Ethiopia. Adv Crop Sci Tech 2: 140. doi: 10.4172/2329- 8863.1000140

Tolera Keno and Berhanu Ertiro (2017) 'Combing ability analysis of among early generation maize inbred lines', Ethiopian Journal of Agricultural Sciences, 27(2),.

Tolera Keno and Dufera Tulu (2018) 'Test cross performance and combining ability of newly introduced quality protein maize (Zea mays) inbred lines for grain yield and agronomic traits evaluated in mid-altitude agro-ecological zones of Ethiopia', (May 2020). doi: 10.1080/02571862.2018.1537009.

Tolera, Keno, Mosisa, W. and Habtamu, Z., (2017). Combining ability and heterotic orientation of mid altitude sub-humid tropical maize inbred lines for grain yield and related traits. *African Journal of Plant Science,* 11(6): 229-239.

Troyer, A.F. (2001). Temperate corn – Background, behavior, and breeding. In: Specialty corn (Hallauer, A.R., ed). CRC Press, New York.

Vasal SK, Srinivasan G, Crossa J, Beck DL (1992a) Heterosis and combining ability of CIMMYT's subtropical and temperate early maturity maize germplasm.

Vasal, S.K. and Srinivasan, G., Beck, D.L., Crossa, J., Pandey, S. and Leon, C de (1992b) Heterosis and combining ability of CIMMYT's tropical late white maize germplasm.

White, P.J. (1994). Properties of corn starch. 29-54. In: A.R. Hallauer (ed.). Specialty Corns. CRC Press Inc Boca Raton, USA.

Wilkes, G. (2004). Corn, strange and marvelous: but is a definitive origin known In Corn: Origin, History, Technology, and Production, C. W. Smith, J. Betran, and E. C. A. Runge, (eds.).Wiley, Hoboken, NJ.

Worku Mosisa., Abdurehman Jemal., Tulu Leta., Tuna Haji., Wolde Leggese., Yihun Kassa.,
Abera Wonde., Guta, A., Tariku S., Asefa T. and Birhanu Tadesse (2002). Development of improved maize germplasm for the mid and low altitude sub-humid agro-ecologies of Ethiopia. Enhancing the Contribution of Maize to Food Security in Ethiopia: *Proceedings of the Second National Maize Workshop of Ethiopia:* 12-16 November 2001, Addis Ababa, Ethiopia CIMMYT.

Xia XC, Reif JC, Hoisington DA, Melchinger AE, Frisch M, Warburton ML (2004). Genetic Diversity among CIMMYT Maize Inbred Lines Investigated with SSR Markers: I. Lowland tropical maize.

Zambezi, B.T., Harner, E.S. and Martin, F.G. 1986. Inbred lines as testers for general combining ability in maize. Crop Science 26: 908-910.

Zelleke, H., Tello, M.A. and Wegary, D., (2018). Line× Tester Analysis of Maize Zea mays L. Inbred Lines for Grain Yield and Yield Related Traits in Mid-Altitude Agro-Ecology of Ethiopia (Doctoral dissertation, Haramaya University).

Zhang, S.H. (1998) Maize production and research for the next century in China: Progres