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**Keywords:** SCA, GCA, hetrotic group.

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TESTCROSSPERFORMANCEANDCOMBININGABILITYOFMAIZEZEMAYS LINBREDLINESATBAKOWESTERNETHIOPIA

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# Test Cross Performance and Combining Ability of Maize (*Zea Mays L.*) Inbred Lines at Bako, Western Ethiopia

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**Abstract-** Information on combining ability and heterotic grouping for newly developed inbred lines is of paramount importance to design future breeding strategies for the development of hybrid and synthetic varieties. The objectives of the present study were to examine combining ability and to determine heterotic groups of the inbred lines for grain yield and other desirable traits. Twenty five inbred lines were used for the formation of the experimental crosses using line x tester mating design. The resulting 50 F1 crosses plus two standard checks (BH540 and BH543) were evaluated at Bako, Western Ethiopia in 2012 main cropping season. The entries were arranged in alpha lattice design with three replications. Data on grain yield, other agronomic traits and disease reactions were recorded under field condition. The highest grain yield was recorded from L24 x T1 (CML312/CML442) (9.97 t ha<sup>-1</sup>). The analysis due to mean squares for crosses was highly significant for all traits except for plant aspect, ear per plant, and number of plants per plot, and thousand kernel weights indicating the existence of genetic variability for all traits. GCA of line was significant for grain yield, agronomic traits and disease severity index. The mean square due to SCA for line by tester combinations were also significant for grain yield, stalk lodging, root lodging, ear rot, husk cover, maturity date, 50% silking day, and Turcicum leaf blight. Significant GCA and SCA effects were indicative of the importance of both additive and non additive gene effects in the control of the traits. However, in all traits, the proportion of GCA sum of square was higher than SCA sum of squares indicating the preponderance of additive gene effects in the control of all traits. Based on the SCA of crosses, the two testers used in this study successfully classified nine out of 25 tested inbred lines into two heterotic groups, A and B: six inbred lines belong to heterotic group A, while the remaining three belong to heterotic group B. These two group can be maximized heterosis by crossing inbred lines belonging to different heterotic groups/unrelated strains.

**Keywords:** SCA, GCA, heterotic group.

## 1. INTRODUCTION

Maize (*Zea mays L.*; 2n =20) is an important cereal crop of the world, belonging to the tribe Maydeae of the grass family *Poaceae*. It has great worldwide significance as human food, animal feed and as a source of hundreds of industrial products. Apart from the manufacture of mixed feed, maize

products include maize starch, maltodextrins, maize oil syrups of the large milling industry, and well-known products of the fermentation and distilling industries (Troyer 2004).

As the cultivation of early maize spread to different geographical regions from Mexico and Central America, where maize is widely believed to have originated, there was a rapid evolution of many races adapted to a wide variety growing conditions. It was introduced to West Africa in the early 1500s by Portuguese traders and then to Ethiopia during the 1600s and 1700s (Dowsell *et al.* 1996).

Cereals are the major crops produced in the country and they constitute the largest share of domestic food production. In 2011/12 main cropping season, cereals were cultivated on 9.6 million hectares producing 188.1 million Qt of food grains (CSA 2012). This represented 79.34% and 86.05% of the total area and production of food grains in the country, respectively. Among cereals, maize ranked second to *tef* in area coverage, and first in total production and productivity. Although it is one of the strategic crops for the achievement of food security in the country, more than 90% of the production is handled by small-scale farmers under rain-fed growing condition (CSA 2012).

Maize constitutes a major food source for the majority of the Ethiopian population, being the second most important cereal crop in area and first in total production in Ethiopia (CSA 2012). The per capital consumption of maize of maize in Ethiopia is about 60kg per annum; however, the level of consumption varies from place to place. In major maize producing areas, maize is staple food, and in other areas it is used in mixtures with other food grains (Mosisa *et al.* 2011).

Since 1952 maize research has been ongoing at different capacities to generate and recommend improved technologies for maize production. With the dissemination and utilization of improved maize technologies by the farmers, the national average yield has been increasing starting in late 1990s. Even though, the current average national maize yield of Ethiopia, 2.95 tones ha<sup>-1</sup> (CSA 2012), is better than the national yield of many African countries; it is still low compared to that of the world, China, and that of United States with average annual yield of 5.1, 5.6, and 9.7 tones ha<sup>-1</sup>, respectively (FAOSTAT 2008). This is due mainly due to

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the poor adoption of improved technologies by the predominantly small scale maize farmers', shortage of high yielding varieties, biotic and abiotic stresses (Mosisa *et al.* 2011). This indicates the need to develop high yielding maize varieties that perform well under both stress and non-stress conditions. In order to achieve this, potentially suitable parents and superior combinations must be identified.

During the early stages of maize breeding in Ethiopia, the main focus was the development of open pollinated varieties (OPVs) (Benti *et al.* 1993; Kebede *et al.* 1993). This was mainly due to the assumption that small-scale farmers did not have the skill required to manage hybrid maize (Gebre *et al.* 2002), unavailability of improved germplasm locally for hybrid development, lack of experience in hybrid development and absence of seed producers. Later, the high yield realized on the state farms with hybrids imported from Kenya, Zimbabwe and Malawi in the early 1980s together with high yield potential recorded from some experimental hybrids in the research centers convinced the breeders to go for wide development and testing of maize hybrids locally. This led to a shift in the breeding strategy from development of only OPVs to development of both hybrids and OPVs in the early 1980s, today, both hybrids and OPVs of different maturity groups are the main focus of the national maize research strategy, particularly for the mid-altitude and highland sub-humid maize growing areas of Ethiopia (Mosisa *et al.* 2011).

Development and release of maize varieties have been an eminent phenomenon in breeding programs mainly to accommodate a range of weather conditions, varying disease prevalence, and volume and distribution of rainfall. The main focus in this case is to come up with more advanced varieties than the existing ones in many aspects (Mosisa *et al.* 2011). Maize improvement involves formation, evaluation, selection, and recombination of genetically variable families or inbred lines (Pixley *et al.* 2006). Test cross performance of experimental lines is the prime selection criterion in hybrid breeding of maize (Mihaljevic *et al.* 2005). With a common tester, differences among the crosses are generally assumed to arise from genetic variability among the S0 plants or inbred lines crossed on to it (Genter and Alexander 1965). The superior individual lines identified after crossing with a tester can be inbred for potential use as a cross pollinated cultivar or as a parent of synthetic or hybrid cultivar (Fehr 1987). This could be achieved through ecological based development of superior inbred lines and identification of their best hybrid combinations.

Different methods of inbreeding are employed for the development of inbred lines, ear-to-row being the common method of inbred line development. The resulting inbred lines are used in the hybrid breeding program or for the development of synthetic (OPV) varieties. For such use, information on the performance

of the inbred lines, both per se and cross, is very crucial. Usually, the inbred lines are evaluated for their per se performance, a yield potential, resistance to major foliar diseases and flowering characteristics. At Bako National Maize Research Program, Ethiopia, the first cross performance of the materials (early test cross) is done when the inbred lines reach the S3 stage. At this stage, the inbred lines are crossed to the common testers of known heterotic groups (A and B) and the resulting test cross progenies are evaluated in multi-location trials. Finally, inbred lines with good cross performance are selected for further advancement and classified into heterotic group for further use in the breeding program.

In maize breeding program, analysis of general combining ability (GCA), specific combining ability and heterosis would help to identify best inbred lines for hybrid development and hybrid combinations for better specific combining ability. Combining ability is an effective tool which gives useful genetic information for the choice of parents in terms of their performance in series of crosses (Sprague and Tatum 1942). The development of populations with high combining abilities has a fundamental role in the efficient use of heterosis (Vasal *et al.* 1992). Therefore, germplasm evaluation is a decisive aspect in maize breeding programs.

Line x tester is useful in deciding the relative ability of female and male lines to produce desirable hybrid combinations (Kempthorne 1957). It also provides information on genetic components and enables the breeder to choose appropriate breeding methods for hybrid variety or cultivar development programmes. Information on combining ability effects helps the breeder in choosing the parents with high general combining ability and hybrids with high specific combining.

So far, combining ability effects in maize and heterotic classification of inbred lines has been extensively studied in Ethiopia for different sets of new inbred lines developed/introduced and adapted at different times (Nigussie and Zelleke 2001; Bayisa *et al.* 2005; Dagne *et al.* 2007; CIMMYT-Zimbabwe 2008; Worku *et al.* 2008). It is always mandatory for any breeding program to generate such information for any new batch of inbred lines generated or received outside of the program. Understanding the relative importance of general (GCA) and specific combining ability effects for different traits for newly developed inbred lines is of paramount importance to design future breeding strategies for the development of hybrid and/or synthetic varieties. The heterotic classification will also assist in determining the relationship existing among the different inbred lines.

Currently, at Bako National Maize Research Center there are a number of new batches of inbred lines generated through different methods of inbred line development. So far, little or no information is available

on these particular set of new inbred lines on their specific and general combining ability effects. Furthermore, these inbred lines are not grouped into the known heterotic groups. Therefore, keeping in view the above this study was conducted with two objectives: a) to estimate the general and Specific combining ability (GCA) of the new inbred lines of crosses for grain yield and other agronomic traits using Line x Tester mating design; and b) to classify the new inbred lines into different heterotic groups for future use in the breeding program.

## II. MATERIALS AND METHODS

### a) Description of Experimental Sites

The study was conducted at Bako Agricultural Research Centre, Western Ethiopia, in 2012 main cropping season. The centre is located 250 kilometres west of Addis Ababa. The locations represent sub-humid and mid-altitude maize growing mega-environments of sub-Saharan Africa (White *et al.* 2001). The site lies between 9°06' N latitude and 37°09' E longitude at an altitude of 1650 m.a.s.l. The soil of the centre is reddish brown clay (nitosol) with pH of 6.0 and 5.9 for top soil (0 – 30cm) and sub-soil (30 – 60cm), respectively. The total precipitation during the growing season (May to November 2012) was 828.5 mm, and the mean minimum and maximum temperatures were 14.4.1°C and 26.8.0°C, respectively. The long term total annual rainfall is 1245 mm, with mean, minimum and maximum temperatures of 13.5°C and 28°C, respectively.

### b) Experimental Materials

The experiment consisted of 52 maize crosses (including 50 test crosses formed by crossing 25 inbred lines to two testers in line x tester mating design in 2011) and two standard checks (BH543 and BH540). The inbred lines were developed at Bako Agricultural Research Center from available germplasm using ear-to-row and backcross inbred line development approaches. The two testers used; CML312/CML442 (Tester 1) and CML395/CML202 (Tester 2) are single crosses and obtained from CIMMYT. They are developed from commercial CIMMYT Maize Lines (CMLs) of known heterotic groups; viz. CML312 and CML442 are heterotic group A while CML395 and CML202 are heterotic group B. These single cross testers are commonly used by CIMMYT and many other national maize research programs in Africa (Dagne *et al.* 2008).

The most important stresses against which the inbred parents of the testers were selected include diseases (grey leaf spot, leaf rust and turicum leaf blight), low nitrogen, high density and drought. The lines x tester crosses were made at Bako Agricultural Research Center during the off-season of 2011/12. BH543 and BH540 are commercial maize hybrids

released for the mid-altitude and sub-humid maize agro-ecology of Ethiopia. BH543 is a three way-cross commercial hybrid released by Bako National Maize Research Project in 2005. It is a medium maturing hybrid that takes about 145 days for grain maturity at Bako and similar environments. The hybrid is a high yielding, tolerant/resistance to major maize diseases known in the country and well adapted to mid-altitude environments (1000-1700 m.a.s.l) receiving high rainfall. The other check BH540 is a popular single cross commercial hybrid released by the same center in 1995. It is a medium maturing hybrid that matures in about 140 days at the adaptation areas of BH543.

### c) Experimental Design and Field Management

A total of 52 entries, the 50 three way crosses plus two hybrid checks adapted to the mid-altitude agro ecology of Ethiopia were planted using alpha lattice (0, 1) design (Patterson and Williams 1976) with four plots per an incomplete block and 13 incomplete blocks in each three replicates. Each entry was placed in a two-row plot of 5.1 m long and 0.75 m apart with 0.3 m between plants.

Trial was hand planted with two seeds per hill, which was later be thinned to one seed per hill to get a total plant population of 44, 444 per hectare. Planting was done in the rainy season the 4th of June, 2012 after reliable moisture level of soil attained to ensure good germination and seedling development. All agronomic practices were done as per the recommendation for Bako research centre.

### d) Statistical analysis and procedures

*Data Collected and analysis of Variance:* Data were recorded on seventy different traits included: Days to 50% tasselling, Days to 50% silking, Days to 50% maturity, Ear rot percent, Husk covers percent, Grain yield, Ear height, Plant height, Disease score, Number of ears per plant, Ear aspect, Ear length, Ear diameter, Stalk lodging percent, Root lodging percent, Number of rows per ear and Number of kernels per row. Disease score and Ear aspect, were recorded visually and scale (1-5). Analysis of variance for all parameters studied was computed using the PROC MIXED procedure and test for significance differences among the genotypes was performed using SAS software (SAS 2008).

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

*Classification of the inbred lines into different heterotic group:* Classifying maize inbred lines into heterotic groups is the initial step in maize breeding program

which would provide maximum exploitation of heterosis. Systematic studies on classifying inbred lines into heterotic groups have been reported (Vasal et al. 1992). Melchinger (1999) proposed that when large number of inbred lines is available and proven testers exist, the performance of the lines in test crosses with proven testers can be used as a main criterion for grouping of lines. Vasal et al. (1992) used this approach in evaluating the performance of test crosses of 92 tropical and 88 subtropical maize lines using two dent and two flint line testers. On the basis of ANOVA and SCA effect for grain yield of the testcrosses was used to classify the inbred 25 lines into two heterotic groups. An inbred line that expressed negative SCA effects when crossed to a certain tester implied that the inbred line belongs to the same heterotic group with the tester. On the other hand, if the same line manifests positive SCA effect with the same tester, it is classified into opposite heterotic group (Vasal et al. 1992).

### III. RESULTS AND DISCUSSIONS

#### a) Analysis of Variance

Analysis of variance showed highly significant differences ( $P < 0.01$ ) among tested materials for all the

traits except for number of plants, number of ear per plant, plant aspect and thousand kernel weight (Table 1). The existence of highly significant differences for all traits indicates the presence of inherent variation among the materials, which makes selection possible. In support of the present finding, earlier studies reported significant differences among genotypes for Grain yield tons per hectare (YLDT) and YLDT related traits in different sets of maize genotypes (Tuna 2004; Dagne et al. 2007; Nepir 2007).

In addition, highly significant differences were observed among entries for grey leaf spot (GLSSID) and Turicum leaf blight (TLBSID), indicating the variable reaction of the tested genotypes against the two diseases. The use of inbred lines from diverse sources of germplasm for generation of the crosses might have contributed to the significant difference observed among crosses for most of the traits considered. Similarly, Worku et al. (2008) and Legesse et al. (2009) reported significance difference in the genotypes they tested in combining ability study of maize inbred lines.

**Table 1 :** Mean squares of genotype and error for grain yield and other related traits in 25x2 lines by tester cross of maize at Bako (2012/13)

So.var	DF	DT	DS	MD	PH	EH	NP	PA
Rep	2	14.54**	9.31**	128.58**	1021.43**	535.55**	0.04	0.64
B(Rep)	36	1.14	2.21**	2.11	128.22**	72.41*	1.22	0.12
ENTRY	51	2.14**	2.33**	3.33**	301.68**	304.63**	1.37	0.12
ERROR	66	0.76	0.67**	1.30441	110.65**	63.79**	0.95	0.09
So.var	DF	ERP	ERP <sup>+</sup>	HCP	HCP <sup>+</sup>	TLBSID	TLBSID <sup>+</sup>	EL
Rep	2	0.61	0	0.5	0.0002	2.56	0.0003	1.99*
B(Rep)	36	1.90*	0.001	2.58*	0.001	204.94*	0.0246*	1.67*
ENTRY	51	6.20**	0.013	67.66**	0.036**	264.37**	0.0309**	3.55**
ERROR	66	1.16	0.001	1.92	0.0009	120.86	0.0143	1.47
So.var	DF	SLP	SLT <sup>+</sup>	RLP	RLP <sup>+</sup>	EA	YLDT	
Rep	2	3.33*	0.001	4.12*	0.002*	0.03	2.93**	
B(Rep)	36	2.66*	0.001	2.35*	0.001*	0.06*	0.31*	
ENTRY	51	50.31**	0.026**	23.78**	0.012**	0.31**	1.63**	
ERROR	66	2.19	0.001	2.88	0.001	0.07	0.38	
So.var	DF	GLSSID	GLSSID <sup>+</sup>	NEP	ED	NRE	TKW	
Rep	2	4863.56**	0.59**	0.06	0.002	0.03*	10932.7	
B(Rep)	36	246.79	0.03	1.12	0.066**	0.76	3306.61	
ENTRY	51	549.36**	0.07**	1.23	0.052**	1.31**	3804.59	
ERROR	66	175.91	0.02	0.87	0.027	0.51	3751.84	

+ Traits with transformed data

\*=significant at 0.05 probability level, \*\*=significant at 0.01 probability level

DT=day of 50% tassiling, DS=days of 50% silking, MD =Maturity date, PH=Plant height, EH=Ear height, NP=number of plant per plot, PA=Plant aspect, ERP= ear rot percent, HCP=husk cover percent, TLBSID=Turicum leaf blight severity index, EL=Ear length; SLP=stalk lodging percent, RLP= root lodging percent, EA=Ear aspect, YLDT=Grain yield tones per hectare, GLSSID=Gray leaf spot severity index, NEP= number ear per plot, ED=Ear diameter, NRE=Number of kernel rows per ear, TKW=Thousand kernel weight

#### b) Mean performance of crosses and checks

**Grain yield (YLDT):** The mean grain yield (YLDT) for genotypes tested under this experiment ranged from 6.8 t ha<sup>-1</sup> (L1xT1) to 9.97 t ha<sup>-1</sup> (L24xT1) with a mean value

of 8.23 t ha<sup>-1</sup> (Appendix 1). Among the crosses, 33 crosses showed significantly higher yield than the hybrid check BH540 and 26 crosses revealed significantly higher yield than the check hybrid BH 543. The best 11

crosses with yield advantages of 25% over the best check hybrid were L24xT1, L22xT1, L19xT2, L18xT1, L24xT2, L2xT2, L18xT2, L17xT1 L20xT1, L21xT1 and L22xT2.

**Fifty percent tasseling (TD) and silking days (SD):** The number of days to 50% tasseling ranged from 79.00 days (L3xT1) to 82.67 days (L24xT1) with overall mean of 81.04 days (table 2). Cross L24xT1 was late in tasseling and scored the longest day and became the highest yielder (9.97 t/ha) which could be due to high photosynthetic product accumulation during the longer growing period. The trait days to 50 percent silking showed a similar variation pattern with days to tasseling and ranged from 81 days (L7xT1, L8xT2 and L3xT1) to 84.67 days (L24xT1 and L17xT2). Crosses L3xT1, L7xT1 and L8xT2 had similar silking dates with that of hybrid check BH540. The rest 47 crosses revealed significantly higher days to silking as compared to hybrid check BH540. Crosses L3xT1, L7xT1 and L8xT2 were significantly earlier in silking than the check hybrid BH543.

**Maturity days (MD):** The days to maturity ranged from 147.67 (L6xT2 and L15xT2) to 153.33 days (L22xT1). Crosses L6xT2, L15xT2, L6xT1, L9xT2, and L8xT1 were earlier and showed similar maturity date to that of the check hybrid BH540. Twenty seven crosses showed significantly late maturity date when compared to the check hybrid BH540 while 23 crosses had similar maturity date as that of BH-540. Six crosses viz., L17xT1, L18xT2, L21xT1, L22xT2, L22xT1 and L24xT2 showed significantly late maturity date than hybrid check BH543 while L6xT1, L6xT2 and L15xT2 were significantly earlier than BH543 (Table 4). From the tested crosses, 41 crosses had similar maturity dates with hybrid check BH543. In this study, crosses with late maturity dates showed long days to tasseling as well as long days to silking day with longer anthesis silking interval and this might contributed to the late maturing of the crosses, while on contrary crosses with earlier anthesis and silking with shorter anthesis silking interval showed earlier maturity. Late maturing crosses could be used in breeding programs for the development of genotypes and better performing hybrids could be released for areas receiving sufficient precipitation for more than 155 days. Early maturing crosses also could be used for the development of early maturing varieties.

**Plant Height (PH):** The mean value for plant height ranged from 252.67 cm (L5xT1) to 299.33 cm (L17xT1) and the mean PH was 274.26 cm. Twenty five crosses exhibited significantly higher plant height than check hybrid BH543, while 15 crosses had similar plant height to BH543. From the tested crosses, 13 crosses were significantly taller than the check hybrid BH-540 while 37 crosses exhibited similar plant height to BH-540. In this study, crosses that showed significantly higher plant height gave higher grain yield, which could be attributed

to high photosynthetic products accumulation during long period for grain filling. Crosses L21xT1, L2xT2, L19xT2, and L20xT1 were in the range of high yielding crosses with intermediate height which is desirable in this particular trait.

**Ear height (EH):** L11xT1 was the cross with the lowest EH (126.33 cm) while L20xT2 had manifested the highest ear height (174.33cm). The mean EH for all genotypes was 145.33 cm. Among all the tested genotypes, 13 crosses exhibited significantly higher ear placement than the check hybrid BH540 while crosses L11xT1, L8xT1, L6xT1 and L9xT2 showed significantly lower ear height. Fourteen crosses showed significantly higher ear height than check hybrid BH543, while only L11xT1 cross showed significantly lower ear height. Crosses L2xT2 and L21xT1, which were among the top grain yielding hybrids, showed intermediate ear height. Plant and ear heights are the major concern to plant breeders since plants with increased ear and plant heights are vulnerable to lodging and hence yield reduction. Therefore, the variability existed in the tested crosses could help in the improvement of these traits. But it is evident that farmers use the maize Stover for different alternative uses like fire wood, fencing and livestock feed. In particular, farmers in crop-livestock mixed farming systems use the maize stover as animal feed and they usually prefer taller plants than shorter one to get large biomass. While trying to respond to the needs of farmers, care should be taken not to introduce taller varieties that are susceptible to lodging into the farming system where lodging is prevalent due to the occurrence of heavy wind.

**Stalk lodging Percentage (SLP):** L20xT1, L4xT2, L7xT2, L23xT1, L4xT1 and L19xT1 were crosses that manifested no stalk lodging (0%) while L15xT2 was most affected by stalk lodging (26.28%). The overall mean for this trait was 4.38%. Nine crosses showed significantly higher percentage of lodging to both hybrid checks, while 7 crosses exhibited significantly lower percent lodging. Among the tested crosses, six crosses scored 0% stalk lodging, which is a desirable feature that have been contributed either by the line or tester or due to the expression of hybrid vigor. The standard checks BH540 and BH543 exhibited stalk lodging percentage of 4.20 and 4.17, respectively.

**Root lodging percentage (RLP):** The mean for root lodging was 4.56% with minimum and maximum values of 0.0% (L21xT1) and 19.79% (L25xT1), respectively. Hybrid L25xT1 showed significantly higher root lodging to check hybrid BH540 and BH543. Among tested crosses, 49 showed significantly lower root lodging to BH540 and 43 crosses revealed significantly lower root lodging to BH543. L24xT1, L4xT1, L5xT2 and L2xT1 showed low percent root lodging next to L21xT1. The check hybrids, BH540 (11.69%) and BH543 (9.38%)

exhibited higher percent lodging next to cross L25xT1 (19.79%).

**Ear aspect (EA):** it is the visual evaluation of harvested ears for general performance with regard to diseases and uniformity. Ear aspect was scored on 1-5 scale and the mean values ranged from 1.33 for L18xT2, L19xT2, and L22xT1 to 2.5 for L9xT1 with overall mean of 2.08. Crosses L18xT2, L19xT2, L22xT1, L22xt2, L21xT2, L24xT2, L23xT2, L24xT1 and L19xT1 showed significantly lower score (1.33 to 1.5). They exhibited significantly lower score for trait crosses is in the desirable direction which implied these crosses showed clean, uniform, large and well filled ears and could be promoted to the next stage of trial evaluation if they are high yielding and have performed well in other traits. However, the check hybrids BH540 and BH543 showed intermediate score of 2.5 and 2.17, respectively.

**Ear rot percentage(ERP):** Mean ER value ranged from 0.0% for L18T2, L22xT2, L21xT2, L17xT2, L20xT1, L16xT2, L7xT2, L23xT1, L6xT1 and L19xT1 to 6.22% for L4xT2 with the overall mean of 2.27%. Among the tested crosses, 21 showed significantly higher ear rot percent to the hybrid BH540 while 4 crosses were significantly higher in ear rot percent to hybrid check BH543. In addition, 33 crosses showed significantly lower score as compared to BH543. These shows there are promising materials that are less affected by ear rot as compared to the standard checks. Based on their yield and overall performance, these materials could be advanced to advanced stages of trials to confirm their performance across locations and years.

**Husk cover percentage (HCP):** Poor husk cover, increases the susceptibility of genotypes for ear rot and field infestation of weevil before harvest. Generally, materials with good husk cover could promote to the next stages of trial evaluation. In the current study, mean values for husk cover ranged from 0.0% (L10xT1, L10xT2, L11xT1, L25xT2, L24xT2, L1xT2, L18xT2 and L2xT2) to 24.16% (L3xT2). The mean value for husk cover was 5.19%. Four crosses scored significantly higher percent while 46 crosses showed significantly lower husk cover percent to hybrid BH540. Among the tested crosses, 23 exhibited higher score while 27 crosses showed significantly lower husk cover percent when compared to check hybrid BH543. In this experiment, entries that manifested the highest husk cover percentages are the ones that showed the highest score for ear rot.

**Turcicum leaf blight severity index (TLBSI):** The mean values scored for TLBSI ranged from 20% for L13xT2 to 72% for L17xT1 with mean value of 35.82% severity index. The level of infection varies from slight to severe leaf infection and none of the entries showed complete resistant to *Turcicum* leaf blight. The low severity was recorded for L13xT2, L10xT1, L8xT1, L4xT1, L6xT1, and L9xT1 with severity percent of 20, 21.33, 22.67, 22.67,

24.00 and 25.33, respectively. From the tested crosses 16 crosses showed significantly higher leaf infection when compared to hybrid check BH540 while 24 crosses exhibited similar in reaction to TLBSI. BH-543 showed severe index (61.33%) while, BH-540 showed moderate severity index (22.67%). The highest index for BH543 is because of the susceptibility of one of its parents for *turcicum* leaf blight. As a result of that, this variety is also affected by this disease when grown in *turcicum* hot spot areas. There is a need for proper positioning of this variety in order to avoid the growing of it in areas where the occurrence of the disease is high.

**Gray leaf spot severity index (GLSSI):** Mean value of GLSSI ranged from 20% for L18xT2 to 78.67% for L16xT1. Over all mean value for the trait was 35.24%. Among the tested crosses, 10 crosses showed significantly higher severity index percent due to grey leaf spot when compared to hybrid check BH540. The only cross showed significantly higher GLSSI was L16xT1 while 15 crosses revealed significantly lower GLSSI when compared to BH543. Crosses L18xT2, L22xT2, L25xT1, L21xT1, L7xT2, L5xT2 and L11xT2 revealed relatively low leaf infection and could be used in the development of resistant genotypes against grey leaf spot. Check hybrid BH543 (45.33%) exhibited high leaf infection above the overall mean (35.24%). Therefore, care should be exercised not to grow this variety in areas where the incidence of occurrence of both *Turcicum* leaf blight and gray leaf spot is high.

**Ear length (EL):** Of all the genotypes tested, L19xT2 attained the maximum ear length (21.3 cm) while L1xT2 was genotypes with shortest ear length (16.6 cm). The overall mean for all the genotypes evaluated was 18.62 cm. Among all crosses, 16 showed significantly higher ear length as compared to BH540. Among the tested crosses, L19xT2, L19xT1, L20xT1 and L24xT2 showed significantly higher ear length compared to BH543 while L1xT2 and L25xT2 exhibited lower ear length. Crosses L19xT1, L24xT2, L20xT1 and L19xT2 were crosses with the best ear length and are among the 11 best crosses with larger ear length.

**Ear diameter(ED):** L25xT2 manifested the highest ear diameter (5.17cm) of all the genotypes studied. On the other hand, L14xT2 has shown the least ear diameter of 4.47cm. The average ear diameter for all the genotypes included in this study was 4.79 cm. L25xT2, L3xT2, L25xT1, L17xT2 and L18xT2 showed significantly higher ear diameter than BH540 while 13 crosses exhibited higher ear diameter than BH543.

**Number of kernels row per ear (NKRE):** NKRE was a significant difference between crosses. It varies from 13.07 to 16.67 with average 14.46. The minimum NKRE was recorded from L14xT2 cross and the maximum was from L23xT2 cross.

**Number of kernel per row (NKR):** The number of kernels per row ranged from 36.60 (L25xT2) to 47.00 (L20xT2) and had mean value of 41.24 for the trait. Out of 50 crosses tested, 21 showed significantly higher number of kernels per rows when compared with BH540 while 9 crosses showed significantly higher NKR when compared with BH543. The two check hybrids, BH540 and BH543 showed 38.07 and 39.73 kernels per row which was below the overall mean (41.24) of tested genotypes.

A number of crosses showed better performances for more than one trait as compared to

the best hybrid check used in the study. Therefore, crosses that had high grain yield could be used in the breeding program to improve the grain yield and other traits of interest. Similarly, hybrids that were late in anthesis and silking, longer in ear and plant heights could be used as sources of genes for development of late maturing and longer statured varieties. In agreement with the present results, investigators in their studies identified experimental varieties performing better than the best check for most yield and related traits (Nepir 2007; Wegary et al. 2010).

**Table 2 :** Mean Minimum, Maximum, CV (%) and F-test values of grain yield and related traits evaluated

Traits	MEAN	MIN	MAX	CV (%)	LSD (5%)	F-test
TD	81.04	78.67	82.67	1.08	1.43	**
SD	82.60	79.67	84.67	0.99	1.34	**
MD	150.22	147.67	153.33	0.76	1.86	**
PH(cm)	274.26	252.67	299.33	3.84	17.15	**
EH(cm)	145.33	126.33	174.33	5.50	13.02	**
SLP (%)	4.38	0.00	26.28	33.77	2.41	**
RLP (%)	4.56	0.00	19.79	37.25	2.77	**
EA(scale)	2.08	1.33	2.5	12.77	0.43	**
ERP (%)	2.27	0.00	6.23	47.32	1.75	**
HCP (%)	5.19	0.00	24.16	26.67	2.26	**
YLDT(tones)	8.23	6.80	9.97	7.50	1.01	**
TLBSI	35.82	20.00	72.00	30.69	17.92	**
GLSSI	35.24	20.00	78.67	37.63	21.62	**
EL(cm)	18.62	16.60	21.30	6.51	1.98	**
ED(cm)	4.79	4.47	5.17	3.40	0.27	**
NKRE	14.46	13.07	16.67	4.95	1.17	**
NKR	41.24	36.60	47.60	5.12	3.44	**
Traits	MEAN	MIN	MAX	CV (%)	LSD (5%)	F-test
TD	81.04	78.67	82.67	1.08	1.43	**
SD	82.60	79.67	84.67	0.99	1.34	**
MD	150.22	147.67	153.33	0.76	1.86	**
PH(cm)	274.26	252.67	299.33	3.84	17.15	**
EH(cm)	145.33	126.33	174.33	5.50	13.02	**
SLP (%)	4.38	0.00	26.28	33.77	2.41	**
RLP (%)	4.56	0.00	19.79	37.25	2.77	**
EA(scale)	2.08	1.33	2.5	12.77	0.43	**
ERP (%)	2.27	0.00	6.23	47.32	1.75	**
HCP (%)	5.19	0.00	24.16	26.67	2.26	**
YLDT(tones)	8.23	6.80	9.97	7.50	1.01	**
TLBSI	35.82	20.00	72.00	30.69	17.92	**
GLSSI	35.24	20.00	78.67	37.63	21.62	**
EL(cm)	18.62	16.60	21.30	6.51	1.98	**
ED(cm)	4.79	4.47	5.17	3.40	0.27	**
NKRE	14.46	13.07	16.67	4.95	1.17	**
NKR	41.24	36.60	47.60	5.12	3.44	**

\*=significant at 0.05 probability level \*\*=significant at 0.01 probability level a Figures in parenthesis were transformed values.

TD=50% Tasseling days, SD=50% silking days MD =Maturity day, PH=Plant height, EH=Ear height, SLP=stalk lodging percent, RLP= root lodging percent, EA=Ear aspect, ERP= ear rot percent, HCP=husk cover percent, TLBSI=Turicum leaf blight severity index, GLSSI=Gray leaf spot severity index, YLDT=Grain yield tones per hectare, EL=Ear length, ED=Ear diameter, NKRE=Number of kernel rows per ear, NKR=Number of kernels per row



c) *Combining Ability*

The mean squares due to crosses were partitioned into lines, testers and line by tester mean squares using the line by tester procedure (Singh and Chaudhary 1979; Dabholkar 1999). As a result, mean squares due to GCA of lines and tester, and SCA of crosses were determined (Table 3). The analysis indicated that both additive and non-additive gene effects were involved in the control of most of these traits. However, the proportion of GCA sum of squares was higher than that of SCA for all traits. This showed the greater contribution of the additive gene effects to genetic variability of the traits than the non-additive genetic variance in the crosses.

The mean squares due to GCA of line and SCA of line x tester were significant ( $P < 0.01$ ) and ( $P < 0.05$ ) respectively for grain yield (YLDT). However, mean square due to GCA of tester showed non-significant difference for grain yield. Significant GCA and SCA mean squares implied the importance of additive and non-additive gene actions in governing grain yield. In the analysis, significant GCA and SCA mean squares were observed for grain yield (table 3). In agreement with the present study, Nepir (2007) using line x tester analysis of QPM versions of early generation highland maize inbred lines and reported significant GCA mean squares due to lines at Holeta. Dagne *et al.* (2007) and Abakemal *et al.* (2011) reported the importance of both additive and non-additive gene actions in governing grain yield in maize. Legesse *et al.* (2009) reported significant GCA mean squares due to lines and testers and significant SCA mean squares for grain yield. On the contrary, Pswarayi and Vivek (2008) using diallel analysis among CIMMYT's early maturing maize germplasm reported significant GCA mean squares and non-significant SCA mean squares for grain yield. On the contrary, Asefa *et al.* (2008) found non-significant GCA effects for grain yield in line by tester study of transition highland inbred lines at Kulumsa. Worku *et al.* (2008) reported the mean squares due to GCA effects for grain yield to be more important than SCA effects under high-N conditions. Legesse *et al.* (2009) also found significant GCA mean squares of lines and testers and significant SCA mean squares for grain yield. Tamirat *et al.* (2014) reported that GCA Mean squares were significant, but SCA mean squares were non-significant for all traits what they were studied.

The mean square due to GCA of line and tester was significant ( $P < 0.01$ ) for GLSSI. The mean square due to SCA was significant ( $P < 0.05$ ) for TLBSI. However, GCA of line and tester and SCA for GLSSI were not significant. Similarly, Dagne *et al.* (2007) observed highly significant GCA and SCA effects for GLSSI in maize inbred lines. The contribution of GCA effects were higher than SCA effects for GLSSI in the present study as GCA contributed 80.28% and SCA contributed 19.72% of the cross sum of squares. Worku

*et al.* (2008) also reported higher proportion of GCA effect as compared to SCA for GLSSI. Legesse *et al.* (2009) found highly significant SCA mean squares for GLSSI. From the results of this finding, GLSSI tolerant varieties could be developed from inbred lines having desirable GCA effects.

The mean squares due to GCA of lines for PH showed highly significant differences ( $P < 0.01$ ). However, mean square of GCA of testers and SCA of line x tester did not showed significant differences. EH the mean square due to GCA of line was highly significant differences ( $P < 0.01$ ) and GCA of tester showed significant differences ( $P < 0.05$ ) among genotypes. Similar results were reported by Leta *et al.* (1998) in Ethiopian maize composites who observed a highly significant GCA effects for both PH and EH while the SCA effect was non-significant. Worku *et al.* (2008) reported high mean square due to GCA and SCA effects under high-N.

In this study, GCA mean squares of line explained 91.29% of the variation for EH. The proportional contribution of GCA for the total variation was higher indicating the importance of additive gene effects than the non additive (table 4). Similarly, Worku *et al.* (2008) also observed higher proportion of GCA sum of squares than SCA sum squares for secondary traits (ear height and plant height) in large number of (635) CIMMYT tropical mid altitude inbred lines evaluated under contrasting nitrogen (both low and high nitrogen) environments. The highly significant ( $p < 0.05$ ) GCA observed for PH in the present study was in accordance with the findings of Sughroue and Hallauer, (1997), Dagne *et al.* (2007), and Amiruzzaman *et al.* (2010).

The mean square of GCA of line and tester for ERP did not showed significant differences. However, the mean square due to SCA of line by tester showed highly significant ( $P < 0.01$ ) differences. Non additive gene effects were found to be important for the control of ERP as manifested by a highly significant SCA effects. Worku *et al.* (2008) also observed higher proportion of GCA mean squares for ERP than SCA.

The mean square estimates due to GCA of lines for ED and EL showed highly significant differences ( $P < 0.01$ ) and significant differences ( $P < 0.05$ ) for tester ED. The result of the present study is in line with the findings of Dagne *et al.* (2007). In the present study, GCA accounted for about 81.10% of the total sum of squares for ED. This indicated the greater contribution of additive genetic portion for the total variation observed in the crosses for this trait. Several investigators reported the importance of both additive and non-additive gene effects in the inheritance of ED. Dange *et al.* (2007), Assefa *et al.* (2008) and Abdel-Moneam *et al.* (2009) observed highly significant GCA and SCA for ED and EL. On the contrary, Ojo *et al.* (2007) reported a non significant GCA and SCA effect for ED and EL.

Estimate of GCA effects of line and tester for NKRE revealed a highly significant ( $p < 0.01$ ) mean square and non-significant SCA effects (Table 6). The proportional contribution of line GCA sum of squares to the cross sum of squares was higher (83.07%), indicating the higher share of additive gene effects to the total variation observed in crosses for NKRE in this particular set of cross combinations. Several workers reported a significant GCA effects for the traits (Dagne *et al.* 2007; Abdel-Moneam *et al.* 2009; Amiruzzaman *et al.* 2010). Similar to the present study, Bayisa, (2005) and Dange *et al.* (2007) reported a significant GCA and non significant SCA effect for NKRE.

The mean squares due to GCA of line and SCA for SD showed highly significant differences ( $P < 0.01$ ) and non-significant difference for tester. The present finding is in agreement with the findings of Assefa *et al.* (2008). Many other authors also reported (Abebe 1983; Mulatu *et al.* 1993; Beyene 1998) reported the importance of both additive and non-additive gene effects for the control of the trait. TD or SD, the greatest share of variability observed in crosses was contributed by the GCA of lines which accounted, 70.60% for TD and 77.00 for SD of the total sum of squares. Similar to the current result, Mosisa *et al.* (2008) observed higher proportion of GCA for most of the secondary traits they studied including TD and SD.

The mean square of GCA of lines for TD) revealed significant differences ( $P < 0.05$ ). However, tester did not revealed significant differences. Mean square of GCA of line contributed 70.30% of the total sum of square. The SCA effects due to line x tester showed non-significant differences. Similarly, Wagary (2002), Bayissa (2005) Tuna (2004) and Bhatnagar *et al.* (2004) reported significance differences of mean squares due to GCA of anthesis days.

The mean square of GCA of line for maturity date (MD) showed highly significant ( $P < 0.01$ ) and showed non-significant for tester GCA effects. The mean square due to SCA of line x tester showed significant ( $P < 0.05$ ). The present finding is in agreement with the findings of Legesse *et al.* (Legesse *et al.* 2009). Many other authors also reported (Abebe 1983; Kebede *et al.* 1993; Beyene 1998; Nigusie 1999; Nigussie and Zelleke 2001) the importance of both additive and non-additive gene effects for the control of the trait. In preset study, the greatest share of variability observed in crosses was contributed by the GCA of lines which accounted, 78.7% of the total sum of squares.

The mean square of GCA of line for HCP revealed highly significant ( $P < 0.01$ ). However, GCA of tester was not significant. The mean square due to SCA for line by tester showed highly significant differences ( $P < 0.01$ ). This result is consistent with the findings of Worku *et al.* (2008) who reported the significances of

GCA mean squares for secondary trait. The proportional contribution of lines GCA to the cross mean of squares was higher indicating the higher share of additive gene effects to the total variation observed in crosses for HCP in this particular set of cross combinations.

Estimate of GCA effect of line for SLP was highly significant ( $p < 0.01$ ). However, GCA of tester was not significant. The mean square of SCA due to line x tester showed highly significant ( $p < 0.01$ ). The finding is in accordance with the findings of various workers. Bhatnagar *et al.* (2004) reported the predominance of additive gene action for root lodging and the predominance of both additive and non additive gene action for stalk lodging. In this study, sum of squares explained 78.1% of the variation for SLP.

The mean square of SCA due to line x tester for RLP showed highly significant ( $p < 0.01$ ). However, GCA of line and tester did not showed significant differences. The result of present study is in agreement with Bhatnagar *et al.* (2004) who reported the predominance of additive gene action for root lodging and the predominance of both additive and non additive gene action for stalk lodging.

The estimate of GCA effects of line for NKR revealed highly significant differences ( $P < 0.01$ ). However, mean square due to GCA of tester and SCA of line x tester did not show significant differences. The present result was in agreement with Dange *et al.* (2007) who reported a non significant SCA effect for NKR in their study for heterosis and combining ability for grain yield and its components in selected maize inbred lines. Similarly, ear length showed highly significant mean square due to GCA of lines ( $P < 0.01$ ). The present study is in line with the findings of Wagary (2002) and Dagne *et al.* (2007).

The Mean square due to GCA of line for ear aspect revealed highly significant differences ( $P < 0.01$ ). However GCA of tester and SCA of line x tester did not show significant differences.

Table 3 : Mean square for GCA of lines, testers and SCA of line x tester for 17 characters in 25 x 2 line by tester crosses evaluated at Bako (2012/13)

	DF	MF	FF	MD	PH	EH	EA
Rep	2	14.54**	9.31**	128.58**	1021.43**	535.56**	0.030
Block (Rep)	36	1.140	1.46**	2.11*	128.22**	72.410	0.063
Entry	51	2.14**	2.33**	3.33**	301.68**	304.63**	0.31**
Cross	49	0.59**	1**	1.86**	146.93**	155.5**	0.14**
GCA line	24	0.85*	1.57**	2.99**	247.42**	284.33**	0.23**
GCA tester	1	0.180	0.020	0.020	15.300	132.29*	0.110
SCA (L x T)	24	0.350	0.48**	0.81*	51.910	27.640	0.040
Check	1	13.50**	10.670	8.17*	140.167	13.500	0.167
Cross vs. Check	1	4.813	15.898	6.896	862.450	108.000	0.390
Pooled error Entry	66	0.765	0.671	1.304	110.654	63.791	0.071
Pooled Error Crosses	62	0.250	0.220	0.450	38.230	22.080	0.020
Pooled error checks	2	0.500	0.667	0.167	76.167	6.500	0.042
	DF	SLP	SLP <sup>+</sup>	RLP	RLP <sup>+</sup>	ERP	ERP <sup>+</sup>
Rep	2	3.334	0.001	4.122	0.002	0.612	0.000
Block (Rep)	36	2.659	0.001	2.352	0.001	1.90*	0.00*
Entry	51	50.31**	0.03**	23.79**	0.01**	7.00**	0.01**
Cross	49	21.65**	0.01**	9.33**	0**	3.32**	0.01**
GCA line	24	34.53**	0.02**	9.870	0.00	3.950	0.010
GCA tester	1	10.520	0.000	0.350	0.00	0.330	0.000
SCA (L x T)	24	9.24**	0.01**	9.17**	0**	2.82**	0.01**
Check	1	0.002	0.000	8.050	0.003	6.30**	0.01**
Cross vs. Check	1	0.238	0.004	223.131	0.101	0.187	0.001
Pooled error Entry	66	2.189	0.001	2.879	0.001	1.159	0.001
Pooled Error Crosses	62	0.760	0.000	0.890	0.000	0.410	0.000
Pooled error checks	2	0.002	0.000	2.014	0.001	0.047	0.000

0.05 probability level \*\*=significant at 0.01 probability level , MF=male flowering, FF=female flowering, MD =Maturity date, PH=Plant height, EH=Ear height, EA=Ear aspect, SLP=stalk lodging percent, RLP= root lodging percent, ERP= ear rot percent

Continuo table

	DF	HCP	HCP <sup>+</sup>	YLDT	TLBSID	TLBSID <sup>+</sup>	NKR
Rep	2	0.503	0.000	2.93**	2.564	0.000	4.185
Block (Rep)	36	2.577	0.001	0.309	204.94*	0.02*	3.687
Entry	51	67.66**	0.04**	1.63**	264.37**	0.03**	14.62**
Cross	49	28.91**	0.02**	0.64**	106.84**	0.01**	6.05**
GCA line	24	46.34**	0.02**	1.13**	139.170	0.020	10.55**
GCA tester	1	5.000	0.000	0.010	205.400	0.020	3.420
SCA (L x T)	24	12.49**	0.01**	0.23*	70.4*	0.01*	1.650
Check	1	206.15**	0.08**	0.240	2242.667	0.277	4.167
Cross vs. Check	1	47.401	0.031	9.393	238.281	0.031	34.085
Pooled error Entry	66	1.920	0.001	0.381	120.865	0.014	4.465
Pooled Error Crosses	62	0.670	0.000	0.130	37.530	0.000	1.470
Pooled error checks	2	1.186	0.000	0.020	514.667	0.069	11.247
	DF	GLSSID	GLSSID <sup>+</sup>	EL	ED	NKRE	
Rep	2	4863.56**	0.59**	1.989	0.002	2.37*	
Block (Rep)	36	246.789	0.030	1.670	0.07**	0.759	
Entry	51	549.36**	0.07**	3.55**	0.05**	1.31**	
Cross	49	214.28**	0.03**	1.49**	0.02**	0.5**	
GCA line	24	270.8**	0.03**	2.61**	0.03**	0.77**	
GCA tester	1	1930.07**	0.24**	0.000	0.04*	1.8**	
SCA (L x T)	24	86.270	0.010	0.450	0.010	0.170	
Check	1	560.667	0.077	4.507	0.042	2.667	
Cross vs. Check	1	1.117	0.000	3.234	0.070	3.309	

Pooled error Entry	66	175.906	0.021	1.470	0.027	0.513
Pooled Error Crosses	62	55.090	0.010	0.490	0.010	0.170
Pooled error checks	2	1260.66	0.158	1.322	0.207	0.187

\*= significant at 0.05 probability level \*\*=significant at 0.01 probability level, HCP=husk cover percent, YLDT= Grain yield tones per hectare, TLBSID=Turicum leaf blight severity index, NKR=Number of kernels per row, GLSSID=Gray leaf spot severity index, EL=Ear length, ED=Ear diameter, NKRE=Number of kernel rows per ear,

i General combining ability estimates

**Grain yield:** The GCA estimates of parental lines ranged from -1.39 to 1.42 for grain yield. The female parent, L24 was the best general combiner for GY with a highly significant ( $P<0.01$ ) and positive GCA effect of 1.42 t ha<sup>-1</sup> followed by L22 and L18 with GCA effect of 1.20 and 1.11 t ha<sup>-1</sup>, respectively (table 4). In addition, L2, L17, L19, L20, L21, L22 and L24 had highly significant ( $P<0.01$ ) positive GCA effects of 0.88 and 0.81, respectively. These inbred lines are desirable parents for hybrid development as well as for inclusion in the breeding programs, as the lines may contribute favorable alleles in the synthesis of new varieties. Parental lines L1, L4, L6, L7, L8, L9, L10, L11, L12 and L25 showed significantly negative GCA effects to the undesirable direction. Among the testers (males), none of them showed significant GCA effects for grain yield per hectare. Result of the current study are in accordance with the findings of Amiruzzaman *et al.* (2010), Legesse *et al.* (2009), Nepir (2007), Tuna (2004) and Dagne *et al.* (2007) who reported significant positive and negative GCA effects for grain yield.

**Fifty percent silking and tassling days:** The GCA estimates of parental lines ranged from -1.66 to 1.84 for silking days. The female parent L24, L17, L22, L2, L20, were the best general combiners for SD with high and significant difference ( $P<0.01$ ). L24 and L17 had high positive GCA effect of 1.84 days respectively. These inbred lines had the tendency to increase late maturity. On the other hand, L7, L8, L9, L11, L13, L18, L19 and L25 showed highly significant GCA effects. Hence, the inbred lines had contributed to earliness in maturity in

their crosses as these lines showed negative and highly significant negative GCA effects of -1.16 days, -1.66 and -1.16, respectively. Similarly, Gudeta (2007) and Wagary (2010) reported significant positive and negative GCA effects for silking in their combining ability study.

The GCA estimates of parental lines ranged from -1.06 to 1.44 for Tasseling days. The female parents L24, L16, L1, L2, L10, L12, L15, L17, L20, L21 and L22 revealed significant and positive GCA effects contributed to late maturity. Lines L3, L25, L19, L8, L6, L7 and L18 showed significant and negative GCA effects contributed to early maturity and were best combiners for early maturity as they showed the tendency to increase early flowering. None of the testers showed significant GCA effects for both silking and tasseling. Result of the current study are in accordance with the findings of Nepir (2007) and Dagne (2007) who reported significant positive and negative GCA effects for anthesis in their combining ability study.

The GCA estimates of lines ranged from -2.34 to 2.66 days for maturity date (MD). L22 showed highly significant positive GCA effect of 2.66 days. In addition, L17, L18, L19, L24 showed highly significant ( $P<0.01$ ) GCA of 1.16 whereas, L6, L8, L11, L14 and L15 revealed highly significant GCA effects in the negative direction. The female line (L6) could be used in breeding program for the introgression of gene for early maturing. Testers showed non-significant effects to MD. The result of this study is in accordance with Legesse (2009) who found desirable GCA effects for physiological maturity in combining ability of highland transition maize inbred line.

Table 4 : Estimates of general combining ability (GCA) effect of lines and tester for grain yield and agronomic traits in 25x2 line by tester crosses evaluated at Bako(2012/13)

Lines	TD	SD	MD	PH	EH	SLP	EA
1	0.44*	0.34	-0.34	-7.23**	-4.99*	3.3**	0.34**
2	0.44*	0.84**	0.16	-0.73	0.51	1.12**	0.18**
3	-1.06**	-0.66**	0.16	-11.56**	-8.83**	-3.33**	0.34**
4	-0.06	-0.16	-0.84**	-5.39*	-11.16**	-4.39**	0.09
5	-0.06	-0.16	-0.34	-16.56**	-9.33**	-2.84**	0.01
6	-0.56**	-0.16	-2.34**	-13.39**	-15.33**	-2.4**	0.26**
7	-0.56**	-1.16**	-0.84**	-14.56**	-12.66**	-0.71*	-0.24**
8	-1.06**	-1.66**	-1.34**	-3.06	-12.16**	-0.87*	0.43**
9	-0.06	-0.66**	-0.84**	-9.39**	-12.49**	0.14	0.26**
10	0.44*	0.34	0.16	2.61	0.84	2.8**	0.26**
11	-0.06	-0.66**	-1.34**	-11.06**	-14.99**	-0.93**	0.34**
12	0.44*	0.34	-0.84**	5.27*	-3.16	0.07	0.26**
13	-0.06	-1.16**	-0.34	-5.9*	1.51	7.21**	0.09
14	-0.06	-0.16	-1.34**	-8.06**	-5.83**	1.21**	0.34**

15	0.44*	-0.16	-1.34**	12.94**	9.67**	15.97**	0.09
16	0.94**	0.34	0.66*	2.77	-3.32	0.65	0.18**
17	0.44*	1.84**	1.16**	21.27**	14.01**	-0.87*	-0.16**
18	-0.56**	-0.66**	1.66**	17.44**	21.84**	-1.87**	-0.41**
19	-1.06**	-0.66**	1.16**	0.61	5.51**	-3.87**	-0.66**
20	0.44*	0.84**	0.66*	12.11**	20.51**	-2.81**	-0.07
21	0.44*	0.34	2.16**	-9.9**	-4.33*	-0.9*	-0.49**
22	0.44*	1.34**	2.66**	14.94**	11.01**	-1.42**	-0.66**
23	-0.06	0.34	0.66*	11.77**	20.51**	-1.34**	-0.32**
24	1.44**	1.84**	1.16**	13.94**	17.67**	-1.86**	-0.57**
25	-1.06**	-0.66**	-0.34	1.11	-4.99*	-2.02**	0.09
SE <sup>1</sup>	0.20	0.19	0.27	2.47	1.88	0.35	0.06
SEd	0.29	0.27	0.39	3.57	2.71	0.50	0.08
Tester							
1	-0.06	0.02	-0.02	0.55	-1.63**	-0.46**	0.05**
2	0.06	-0.02	0.02	-0.55	1.63**	0.46**	-0.05**
SE <sup>2</sup>	1	1	1	1	1	1	1
SEd	0.08	0.08	0.11	1.01	0.77	0.14	0.02

1GCA lines standard error. 2 GCA testers standard error.

TD=number of days to 50% tasseling SD= number of days to 50% silking , MD =Maturity date, PH=Plant height, EH=Ear height, SLP=stalk lodging percent, EA=Ear aspect, SLP=stalk lodging percent

Continue Table 4

Lines	HCP	YLDT	GLSSID	EL	ED	NKRE	NKR
1	-4.54**	-1.39**	-7.23*	-1.83**	-0.04	-0.96**	-1.77**
2	-2.59**	0.69**	6.77*	-1.4**	0.07	-0.83**	-0.18
3	17.69**	-0.11	-10.56**	-0.42	0.27**	1.24**	0.17
4	2.58**	-0.61**	-10.56**	-0.05	0.04	0.24	0.93
5	0.55	0.16	-7.89**	-1.08**	-0.01	0.64**	-0.57
6	-0.11	-0.98**	-7.23*	-1.4**	0.01	0.04	-2.98**
7	0.89**	-0.63**	7.44*	0.09	0.02	0.17	-2.03**
8	3.4**	-0.76**	-6.56*	0.2	-0.12**	0.11	-3.47**
9	3.44**	-0.56**	15.44**	-0.18	-0.04	0.18	-1.43**
10	-5.08**	-0.33*	2.77	-0.93**	-0.16**	0.44**	-3.27**
11	-3.12**	-0.86**	-3.23	-0.11	-0.03	0.31	-0.86
12	-1.59**	-0.36*	14.11**	0.85**	-0.08	-0.16	0.94
13	-0.96**	0.01	2.77	0.03	-0.04	-0.49**	0.5
14	5.58**	-0.18	8.11**	-0.33	-0.17**	-0.89**	-0.63
15	-2**	0.02	18.11**	-0.11	-0.11**	-0.46**	1.1*
16	-4.07**	-0.05	29.44**	-1.56**	0.04	-1.03**	-1.86**
17	-3.61**	0.47**	8.1**	1.42**	0.19**	0.11	1.97**
18	-3.12**	1.11**	-13.89**	0.14	0.08	0.11	0.07
19	3.13**	0.81**	-7.9**	2.45**	-0.17**	-0.33	3.24**
20	4.92**	0.42**	2.11	1.62**	-0.04	-0.42*	5.7**
21	-0.55	0.71**	-11.89**	0.32	-0.13**	0.38*	1.47**
22	-2.58**	1.2**	-13.89**	1.68**	0.08	0.31	3.34**
23	-0.6	0.64**	8.11**	0.92**	0.09*	1.51**	0.97
24	-3.57**	1.42**	-8.56**	1.25**	-0.03	0.11	2.1**
25	-4.1**	-0.88**	-13.89**	-1.55**	0.31**	-0.36*	-3.47**
SE <sup>1</sup>	0.33	0.14	2.97	0.28	0.04	0.16	0.48
SEd	0.47	0.21	0.00	0.40	0.56	0.24	0.70
Tester							
1	-0.32**	0.02	6.21**	0	0.03**	0.19**	-0.26*
2	0.32**	-0.02	-6.21**	0	-0.03**	-0.19**	0.26*

SE <sup>2</sup>	1	1	1	1	1	1	1
SEd	0.13	0.06	1.21	0.11	0.02	0.07	0.20

1GCA lines standard error. 2 GCA testers standard error.

\*=significant at 0.05 probability level \*\*=significant at 0.01 probability level, HCP=husk cover percent, ERP= ear rot percent, GLSSID=Gray leaf spot severity index EA=Ear aspect, YLDT=Grain yield tons per hectare, EL=Ear length, ED=Ear diameter, NKRE=Number of kernel rows per ear, NKR=Number of kernels per row.

**Plant height:** The GCA estimate of parental lines ranged from -16.56 to 21.75 cm for plant height (PH). L18, L17, L20, L22, L15, L23, L12, and L24 showed positive and significant GCA effects indicating that these lines significantly contributed to taller plant stature. On the other hand, L5, L6, L3, L11, L9, L1, L4, L9, L14, L21, and L7 showed negative GCA effects, indicating that these lines contributed to reduced plant stature in their crosses. None of the testers showed significant GCA effects for PH. In line with the present study Tuna (2004) and Wagary (2010) found significant positive and negative GCA effects for plant height.

**Ear height (EH):** The GCA estimate of parental lines ranged from -15.33 to 21.84cm for ear EH. Parental lines: L18, L19, L15, L20, L23, L24, L17 and L22 showed positive and significant GCA effects indicating that these lines significantly contributed to taller plant stature. On contrary, L11, L6, L7, L9, L8, L4, L5, L1, L14 and L3 showed negative GCA effects, indicating that these lines contributed to reduce plant ear height in their crosses. Regarding the testers, T2, showed positive GCA effects for EH, indicating that this tester contributed to increased plant stature whereas T1 depicted negative and significant GCA effects for EH. Similarly, Tuna (2004) and Wegary et al. (2010) found significant positive and negative GCA effects for plant height.

**Grey leaf spot severity index (GLSSI):** The GCA estimate of parental lines ranged from -13.89 to 29.44 for GLSSI. Parental lines, L18, L22, L25, L21, L3, L4, L24, L5, L6, L1, L8 and L19 and revealed GCA effect of -13.89, -13.89, -13.89, -11.89, -10.56, -10.56, -8.56, -7.9 -7.89, -7.23, -6.56, -7.9 respectively. These inbred line had greater tolerances to GLS as the line had negative significant GCA effects while, L16, L15, L9, L12, L2, L7, L14, L17 and L23, showed positive and significant GCA effects to undesirable direction as these increased the susceptibility of crosses they involved, which was evident from their highly significant positive GCA effect of 29.44, 18.11, 15.44, 14.11, 6.77, 7.44, 8.11, 8.1, 8.11 respectively. The result of this study is in agreement with Menkir (2005), Asefa et al (2008) and Legesse et al. (2009).

**Ear length (EL):** The GCA estimate of parental lines ranged from -1.83 to 2.45cm for EL. Parental lines, L19, L17, L20, L22, L23, L12, and L24 showed positive and significant GCA effects to the desirable direction and contribute to increased grain yield in its hybrid combinations. On contrary, L1, L2, L5, L6, L10, L16 and L25 showed negative SCA effects. Similarly, Dagne et al.

(2007) reported significant positive and negative GCA effects for this trait.

**Ear diameter(ED):** The GCA estimate of parental lines ranged from - 0.17 to 0.31cm for ED. Parental lines, L25, L3, L23 and L17 showed positive and significant GCA effects to the desirable direction and contribute to increased grain yield in its hybrid combinations. On contrary, L8, L10, L14, L15, L19 and L21 showed negative and significant GCA effects which is undesirable. The GCA estimate for testers showed that, T1 revealed positive and significant GCA effect While, T2 showed negative significant GCA effect. This result revealed T1 contributed towards the increments of yield in its hybrid combinations. The present study is in agreement with Dagne et al. (2007), and Nepir (2007), who reported significance positive and negative GCA effects for ear diameter.

**Number of kernels row per ear (NKRE):** The GCA estimate of parental lines ranged from -1.03 to 1.51 for NKRE. Parental lines L23, L3, L5 and L10 revealed positive and significant GCA effects to the desirable direction and contributed to increased grain yield in its hybrid combinations. L1, L2, L13, L14, L15, L16, L20 and L25 showed negative and significant GCA effects. The GCA estimate for testers showed that, T1 revealed positive and significant GCA effect While, T2 showed negative significant GCA effect. T1 contributed towards the increments of yield in its hybrid combinations. Similar results were found by Dagne et al. (2007), Tuna (2004) and Nigusie (1999).

**Number of Kernels per row (NKR):** The GCA estimate of parental lines ranged from -3.47 to 3.34 for NKR. Parental line, L22, L19, L17, L24, L20, L21 and L15 showed positive and significant GCA effects to the desirable direction and contributed to increased grain yield in its hybrid combinations. On the other hand, L1, L6, L7, L8, L9, L10, L16 and L25 revealed negative and significant GCA effects. The GCA estimate for testers showed that, T1 revealed negative and significant GCA effect While, T2 showed high and positive significant GCA effect. This result revealed T2 contributed towards the increments of yield in its hybrid combinations. The current result is in agreement with Dagne et al. (2007) and Nepir (2007).

**Stalk lodging percent (SLP):** The GCA estimate of parental lines ranged from -4.39 to 15.97 for SLP. Parental lines, L15, L13, L14, L1, L2, and L10 showed positive and significant GCA effects to the undesirable and vulnerable effect. On the other hand parental lines,

L3, L4, L5, L6, L7, L8, L11, L17, L18, L19, L20, L21, L22, L23, L24 and L25 revealed negative and significant GCA effects which is to the desirable direction and could be used in breeding program for the development of stalk lodging tolerant improved maize varieties. Regarding testers, T1 showed high and negative GCA effect which is desirable while, T2 showed positive and GCA effect which contributed towards lodging. The current result agrees with Bhatnagar et al. (2004) who found significant differences among GCA effects for the same trait.

**Ear aspect (EA):** The GCA estimate of parental lines ranged from -0.66 to 0.43 for EA. Parental lines, L8, L1, L3, L11, L9, L12, L2, L6, L10, L16 and L14 showed high and positive significant GCA effects to the undesirable direction. On the other hand, L7, L19, L22, L24, L23, L21, L18 and L17 revealed a high and negative GCA effect which is to the desirable direction with good ear character that could be used in breeding programs for trait.

**Husk cover percentage (HCP):** The GCA estimate of parental lines ranged from -5.08 to 17.69 for HCP. Parental lines, L3, L20, L19, L14, L9, L8, L7, and L4 showed high and positive significant GCA effects to the undesirable direction contributed to open husks. On the other hand, L10, L1, L16, L25, L24, L22, L18, L17, L11, L12, L13, L15 and L2 revealed negative and significant GCA effect which is to the desirable direction plants with good ear character that could be exploited in breeding programs for unopened husk cover.

#### ii Specific combining ability estimates

**Grain yield:** Crosses L2xT2, L5xT2, L11xT2, L12xT1, L14xT1, L17xT2, L19xT1, L20xT2 and L22xT2 (table 5) revealed positive and significant SCA effects for grain yield with SCA values of 0.42, 0.55, 0.47, 0.37, 0.35, 0.43, 0.63, 0.41 and 0.43t/ha, indicating that these crosses were good specific combinations for grain yield. Crosses with the higher value of SCA effect also showed higher values of mean grain yield performance, indicating good correspondence between SCA effects and mean grain yield. Hence, such cross combinations

could effectively be exploited in hybrid breeding program in maize research. On the other hand, five cross combinations L19xT2, L5xT1, L11xT1, L17xT1, L20xT1, L14xT2, L12xT2, L2xT1 and L22xT1 expressed negative and significant SCA effects for grain yield which is undesirable as these crosses showed a tendency to reduce grain yield performance. The finding of the current study are in agreement with that of Nigussie (1999) who reported significant positive and negative SCA effects for grain yield in 8 x 8 diallel study of drought tolerant maize populations at Melkasa. and Dagne et al. (2007) also reported similar results for grain yield. However, Pswarayi and Vivek (2008) and Jumbo and Carena (2008) reported non-significant positive and negative SCA effects for grain yield which is inconsistent with the present study.

**Fifty percent silking:** Crosses, L3xT1, L4xT1, L7xT2, L10xT1, L15xT1, L17xT1, L20xT2, L14xT2, L13xT1, L6xT2, L5xT1, L2xT1 and L18xT1, manifested positive and significant SCA effects for silking. This indicated these crosses were good specific combiners for lateness in female flowering (silking). On the other hand crosses L3 x T2, L4xT2, L7 x T1, L10 x T2, L15 x T2, and L17 x T2, expressed negative and significant SCA effects indicating earliness in flowering (Table 10). These are the best hybrids that could be used for developing early maturing hybrids. This finding agrees with Tuna (Tuna 2004), Nepir (2007) and Wegary et al. (2010) who found positive and negative SCA effects for silking.

**Maturity day (MD):** The SCA effect for MD ranged from -1.48 to 1.48. Crosses L10xT2, L13xT1, L15xT1, L16xT2 and L20xT1 manifested negative and significant SCA effects indicating that these crosses were good specific combinations for early maturity date. Hence, such cross combinations could effectively be exploited in hybrid breeding program in maize research for reduced maturity dates. On the other hand, cross combinations L5xT2, L10xT1, L13xT2, L15xT2, L16xT1 and L20xT2 expressed positive and significant SCA effects for maturity date which are undesirable as these crosses showed a tendency to increase maturity date.

**Table 5 :** Estimates of Specific combining abilities of 25 x 2, Line x tester crosses evaluated for yield, agronomic and disease traits at Bako (2012/13)

Entry	CODE	SD	MD	SLP	RLP	ERP	HCP	YLDT	TLBSID
1	L1xT2	-0.02	0.02	-1.13**	-1.03**	-0.51	0.86*	-0.10	0.00
2	L1xT1	0.02	-0.02	1.13**	1.03**	0.51	-0.86*	0.10	2.70
3	L2xT1	0.48*	-0.48	1.96**	-1.06**	1.49**	2.81**	-0.42**	3.97
4	L2xT2	-0.48*	0.48	-1.96**	1.06**	-1.49**	-2.81**	0.42**	-3.97
5	L3xT2	-1.02**	-0.48	0.44	-1.16**	0.93**	-1.07**	0.22	-2.69
6	L3xT1	1.02**	0.48	-0.44	1.16**	-0.93**	1.07**	-0.22	2.69
7	L4xT2	-0.52**	-0.48	0.46	-1.13**	-2.17**	-1.25**	-0.02	-4.03
8	L4xT1	0.52**	0.48	-0.46	1.13**	2.17**	1.25**	0.02	4.03

9	L5xT1	0.48*	-0.98**	-0.01	2.52**	0.45	-2.13**	-0.55**	3.97
10	L5xT2	-0.48*	0.98**	0.01	-2.52**	-0.45	2.13**	0.55**	-3.97
11	L6xT2	0.48*	0.02	0.49	-0.05	-1.23**	0.39	-0.05	-4.03
12	L6xT1	-0.48*	-0.02	-0.49	0.05	1.23**	-0.39	0.05	4.03
13	L7xT1	-0.52**	0.52	4.13**	1.77**	1.88**	0.22	0.1	-1.36
14	L7xT2	0.52**	-0.52	-4.13**	-1.77**	-1.88**	-0.22	-0.1	1.36
15	L8xT2	-0.02	0.02	2.02**	-2.49**	-1.05**	1.85**	0.03	-8.69**
16	L8xT1	0.02	-0.02	-2.02**	2.49**	1.05**	-1.85**	-0.03	8.69**
17	L9xT1	-0.02	0.52	1.93**	-0.57	-0.1	-0.22	0.03	-3.36
18	L9xT2	0.02	-0.52	-1.93**	0.57	0.1	0.22	-0.03	3.36
19	L10xT2	-1.02**	-1.48**	-1.49**	0.41	-0.07	0.32	-0.04	-4.70
20	L10xT1	1.02**	1.48**	1.49**	-0.41	0.07	-0.32	0.04	4.70
21	L11xT2	-0.02	0.02	-0.03	0.45	-1.06**	-1.64**	0.47**	3.30
22	L11xT1	0.02	-0.02	0.03	-0.45	1.06**	1.64**	-0.47**	-3.30
23	L12xT2	-0.02	-0.48	1.91**	0.93*	-0.1	1.82**	-0.37*	-8.03**
24	L12xT1	0.02	0.48	-1.91**	-0.93*	0.1	-1.82**	0.37*	8.03**
25	L13xT1	0.48*	-0.98**	-4.04**	-3.4**	-1.21**	2.29**	-0.23	7.31**
26	L13xT2	-0.48*	0.98**	4.04**	3.4**	1.21**	-2.29**	0.23	-7.31**
27	L14xT2	0.48*	0.02	-1.91**	-1.00*	0.01	-6.05**	-0.35*	1.97
28	L14xT1	-0.48*	-0.02	1.91**	1.00*	-0.01	6.05**	0.35*	-1.97
29	L15xT2	-0.52**	1.02**	-5.47**	0.00	1.51**	2.42**	-0.02	-0.69
30	L15xT1	0.52**	-1.02**	5.47**	0.00	-1.51**	-2.42**	0.02	0.69
31	L16xT1	-0.02	1.02**	-1.52**	-1.54**	-0.59*	0.32	-0.02	2.64
32	L16xT2	0.02	-1.02**	1.52**	1.54**	0.59*	-0.32	0.02	-2.64
33	L17xT2	-0.52**	0.52	2.94**	1.42**	0.96**	0.81*	0.43**	20.64**
34	L17xT1	0.52**	-0.52	-2.94**	-1.42**	-0.96**	-0.81*	-0.43**	-20.64**
35	L18xT1	0.98**	0.02	1.86**	-0.67	0.41	2.28**	0.07	6.64**
36	L18xT2	-0.98**	-0.02	-1.86**	0.67	-0.41	-2.28**	-0.07	-6.64**
37	L19xT2	-0.02	0.52	-0.06	-0.62	-1.63**	-0.78*	-0.63**	0.64
38	L19xT1	0.02	-0.52	0.06	0.62	1.63**	0.78*	0.63**	-0.64
39	L20xT2	0.48*	1.02**	-1.12**	0.36	-0.59*	-7.72**	0.41**	0.64
40	L20xT1	-0.48*	-1.02**	1.12**	-0.36	0.59*	7.72**	-0.41**	-0.64
41	L21xT1	-0.02	0.52	0.92*	-3.14**	1.91**	0.78*	0.07	-3.36
42	L21xT2	0.02	-0.52	-0.92*	3.14**	-1.91**	-0.78*	-0.07	3.36
43	L22xT2	-0.02	0.02	-0.49	2.43**	1.95**	-1.20**	0.43**	-4.03
44	L22xT1	0.02	-0.02	0.49	-2.43**	-1.95**	1.20**	-0.43**	4.03
45	L23xT1	-0.02	0.02	-2.59**	0.88*	-1.58**	1.80**	0.03	0.64
46	L23xT2	0.02	-0.02	2.59**	-0.88*	1.58**	-1.80**	-0.03	-0.64
47	L24xT1	0.48*	-0.48	1.02**	-0.59	0.44	1.83**	0.25	-4.03
48	24xT2	-0.48*	0.48	-1.02**	0.59	-0.44	-1.83**	-0.25	4.03
49	L25xT2	-0.02	0.02	-0.24	7.3**	-0.10	1.30**	0.21	-0.69
50	L25xT1	0.02	-0.02	0.24	-7.3**	0.10	-1.30**	-0.21	0.69
SCASE		0.19	0.27	0.35	0.38	0.26	0.33	0.14	2.45
SEd		0.38	0.55	0.71	0.77	0.52	0.67	0.29	5.00

\*=significant at 0.05 probability level, \*\*=significant at 0.01 probability level

SD=Silking day, MD =Maturity date, SLP=stalk lodging percent, RLP= root lodging percent,

HCP=husk cover percent, ERP= ear rot percent, TLBSID=Turicum leaf blight severity index, YLDT=Grain yield tones per hectare,

stalk lodging(SLP): Crosses L1xT2, L2xT2, L7xT2, L8xT1, L16xT1, L17xT1, L18xT2, L20xT2, and L23xT1 revealed negative and significant SCA effects for SLP with SCA



values of -1.13, -1.96, -4.13, -2.02, -1.93, -1.49, -1.91, -4.04, -1.91, -5.47, -1.52, -2.94, -1.86, -1.12, -2.59 respectively, indicating that these crosses were good specific combinations for reduced stalk lodging. On the other hand, crosses L1xT1, L2xT1, L7xT1, L8xT2, L9xT1, L10xT1, L12xT2, L13xT2, L14xT1, L15xT1, L16xT2, L17xT2, L18xT1, L20xT1, L23xT2, L24xT1 revealed positive and significant SCA effects for stalk lodging which are undesirable as these crosses showed increased stalk lodging. The current results are in accordance with Bhatnagar et al. (2004) who found significant SCA effects in the study of combining ability of QPM inbred lines.

*Root lodging percent (RLP)*: Crosses L1xT2, L2xT1, L3xT2, L4xT2, L5xT2, L7xT2, L8xT2, L13xT1, L16xT1, L17xT1, L21xT1, L22xT1, L25xT1 expressed negative and significant SCA effects for RLP with SCA values of -2.81, -1.07, -1.25, -2.13, -1.85, -1.64, -1.82, -2.29, -6.05, -2.42, -2.28, -7.72, -1.20, -1.80, -1.83, -1.30 respectively, indicating that these crosses were good specific combinations for resistance to root lodging. On the other hand, crosses L1xT1, L2xT2, L3xT1, L4xT1, L7xT1, L8xT1, L13xT2, L16xT2, L17xT2, L21xT2, and L25xT2 revealed positive and significant SCA effects for root lodging percent which are undesirable as these crosses showed higher root lodged percent in their hybrid combinations. Similarly, Bhatnagar et al. (2004) reported SCA significance for the same trait.

*Husk cover percent (HCP)*: Crosses L2xT2, L1xT1, L5xT1, L3xT2, L4xT2, L5xT1, L8xT1, L11xT2, L12xT1, L13xT2, L14xT2, L15xT1, L17xT1, L18xT2, L19xT2, L20xT2, L21xT2, L22xT2, L23xT2, L24xT2, L25xT1 expressed negative and significant SCA effects for HCP indicating that these crosses were good specific combinations for resistance to husk cover. On the other hand, crosses L1xT2, L1xT2, L5xT2, L3xT1, L4xT1, L11xT1, L12xT2, L13xT1, L14xT1, L15xT2, L17xT2, L18xT2, L19xT1, L20xT1, L22xT1, L23xT1, L24xT1, L25xT2 revealed positive and significant SCA effects for husk cover percent which are undesirable as these crosses showed higher opened husk percent in their hybrid combinations.

*Ear rot percent (ERP)*: Crosses L2xT2, L3xT1, L4xT2, L6xT2, L7xT2, L8xT2, L11xT2, L13xT1, L15xT1, L17xT1, L19xT2, L21xT2, L22xT1, L23xT1 expressed negative and significant SCA effects for ear rot percent (ERP) with SCA values of 1.49, 0.93, 2.17, 1.23, 1.88, 1.05, 1.06, 1.21, 1.51, 0.96, 1.63, 1.91, 1.95, 1.58 respectively, indicating that these crosses were good specific combinations for resistance to ERP. Hence, such cross combinations could effectively be exploited in hybrid breeding program in maize research for developing ear rot free genotypes. The result of this finding agrees with Worku et al. (2008) who found significant GCA effect for the same trait.

*Turicum leaf blight severity index (TLBSI)*: Crosses L8xT2, L12xT2, L13xT2, L17xT1, L18xT2, revealed negative and significant SCA effects for TLB with SCA values of 8.69, 8.03, 7.31, 20.64, 6.64 respectively, indicating that these crosses were good specific combinations for resistance to TLB. Hence such cross combinations could effectively be exploited in hybrid breeding program in maize research for developing tolerant maize genotypes to Turicum leaf blight. On the other hand, crosses L8xT1, L12xT1, L13xT1, L17xT2, and L18xT1, revealed positive and significant SCA effects for Turicum leaf blight which are undesirable as these crosses showed higher percent incidence in their hybrid combinations. On contrary to this finding, Legesse et al. (2009) reported non-significant SCA effects for the same trait.

In Summary, the preponderance of GCA effects for expression of YLDT and yield related traits considered in this study indicated the possibility for improvement of these traits through simple selection procedures. However, the chance of success could be hampered in the presence of substantial amount of epistatic component. In such cases selection procedure would not be fruitful in immediate progenies and process has to be delayed to later generations when appreciable homozygosity is achieved (Sofi et al. 2006). For complex traits like YLDT and similar traits, recurrent selection procedure that exploits both the additive and non additive component of genetic variation are more appropriate in bringing about a better improvement. Similar suggestion was made by Worku et al. (2008) for secondary traits.

#### d) *Heterotic Grouping of inbred lines*

Study on test cross performance and combining ability of maize (*Zea mays L.*) inbred lines was undertaken and evaluated for performance, general and specific combining ability and heterotic groups using line by tester mating design. Twenty five inbred lines were crossed to two CIMMYT testers: Tester 1 (CML 312/CML442) and Tester 2 (CML395/CML202) which belongs to maize heterotic group A and B, respectively. Heterotic grouping designate broad classes in maize with diverse genetic base that are complimentary and result in expression of heterosis after crossing. On the other hand, synthetic varieties are developed from inbred lines belonging to the same heterotic group.

In heterotic grouping, an inbred line express negative SCA effect when crossed to a certain tester implies that both the line and the tester belong to the same heterotic group, while the reverse is true when the SCA effect is positive (Vasal et al. 1992). Table 6 shows that six inbred lines expressed significant negative SCA effects and three inbred lines expressed positive SCA effects when crossed to CML312/CML442 and when crossed to CML395/CML202, six inbred lines expressed

positive and three expressed negative SCA effects. The study exhibited that the six inbred lines belong to heterotic group A, while the remaining three belong to heterotic group B.

In order to maximize genetic diversity and therefore heterosis during hybrid variety development using these inbred lines, one parent should come from the six inbred lines belonging to heterotic group A while

the other parent should be from the three inbred lines belonging to heterotic group B. In the case of the development of synthetic varieties, inbred lines belonging to the same heterotic group should be used. Likewise, Legesse et al. (2009) using population and inbred line testers separated inbred lines into different heterotic groups on the basis of grain yield SCA values.

**Table 6 :** Grain yield mean, SCA effect and heterotic group of 9 maize inbred lines teste crosses to CML312/CML442 and CML395/CML202 tested for one year at Bako (2012/13)

Line	Tester (CML312/CML442)		Tester 2(CML395/CML202)		Heterotic group
	Grain yield	SCA	Grain yield	SCA	
1	6.80	0.1	6.97	-0.1	---
2	8.57	-0.42**	9.37	0.42**	A
3	8.40	-0.22	7.93	0.22	---
4	7.67	0.02	7.67	-0.02	---
5	7.90	-0.55**	8.97	0.55**	A
6	7.27	0.05	7.33	-0.05	--
7	7.77	0.1	7.53	-0.1	--
8	7.57	-0.03	7.47	0.03	--
9	7.77	0.03	7.67	-0.03	--
10	7.93	0.04	7.97	-0.04	--
11	7.90	-0.47**	6.93	0.47**	A
12	7.57	0.37*	8.27	-0.37*	B
13	8.07	-0.23	8.50	0.23	--
14	7.77	0.35*	8.43	-0.35*	B
15	8.30	0.02	8.30	-0.02	--
16	8.23	-0.02	8.23	0.02	--
17	9.20	-0.43**	8.30	0.43**	A
18	9.47	0.07	9.30	-0.07	--
19	8.47	0.63**	9.70	-0.63**	B
20	9.13	-0.41**	8.27	0.41**	A
21	9.07	0.07	8.90	-0.07	--
22	9.93	-0.43**	9.03	0.43**	A
23	8.97	0.03	8.87	-0.03	--
24	9.97	0.25	9.43	-0.25	--
25	7.63	-0.21	7.17	0.21	--

\*=significant at 0.05 probability level, \*\*=significant at 0.01 probability level

#### IV. CONCLUSION AND RECOMMENDATION

The analysis of variance showed the genotypes were significantly different at ( $P < 0.01$  or  $P < 0.05$ ) for all traits tested except for number of ear per plant. Moreover, Mean squares due to crosses were significant for all traits studied. In addition, significant differences were not found among the checks and checks vs crosses for most traits.

Out of the 50 crosses, 30 crosses recorded more than 10 percent higher grain yield advantage as compared to the best check BH543. The mean performance for crosses revealed L24xT1, L22xT2, L19xT2, L18xT1, L24xT2, L2xT2, L18xT2, L17xT1, L20xT1, L21xT1 and L22xT2 with mean grain yield of 9.97, 9.93, 9.70, 9.47, 9.43, 9.37, 9.30, 9.20, 9.13, 9.07, 9.03 t ha<sup>-1</sup>. These hybrids could be included in further

investigation for grain yield and related traits and could be possible candidates of future release after verifying their yield stability across more environments.

Mean squares due to GCA of lines and SCA of line by tester interactions were also significant ( $P < 0.01$ ) or ( $P < 0.05$ ) for most studied traits. This indicated that both additive and non-additive genetic variances were important in the control of traits revealed in the crosses. Mean squares due to GCA of testers were significant for EH, GLSSI, ED and NKRE. It showed non-significant differences for the rest of the traits. The additive gene effects were responsible for variability observed in grain yield and most agronomic traits.

Based on combining ability analysis L2, L17, L18, L19, L20, L21, L22, L23 and L24 were found the best general combiners for grain yield. Inbred lines with a high GCA effect for grain yield are desirable for

hybrids and open pollinated varieties development as well as for inclusion in breeding program.

Inbred lines with significant positive GCA effects were found for NKRE, NKR, EL and ED, suggesting presence of divergence to improve these traits. Thus, the inbred lines L17, L19, L20, L21 L22 and L24 showed significant positive GCA effects for increase NKR. For NKRE significant positive GCA effects were shown by inbred lines L3, L5, L10 and L23. L12, L17, L19, L20, L22, L23 and L24 showed significant positive GCA effects for EL. For ED L3, L17, L23 and L25 recorded significant positive GCA effects.

For days to anthesis/Tasseling, L3, L6, L7, L8, L18, L19 and L25 and for silking L7, L8 and L13 were the best combiners, indicating that these lines had favorable allele frequency for early maturity. Inbred lines L5, L6, L3, L11 and L7 were good general combiners for shorter plant height, which are desirable for lodging resistance.

For grain yield crosses L2xT2, L5xT2, L11xT2, L12xT1, L14xT1, L19xT1, L20xT2 and L22xT2 had good specific combining ability. These hybrids could be included for further studies for the improvement of grain yield and related traits.

Crosses L8xT2, L12xT2, L13xT2, L17xT1 and L18xT2 displayed negative and significant SCA effects for TLB, indicating that these crosses were good specific combinations for resistance to Turcicum leaf blight (TLB). Hence, such cross combinations could effectively be exploited in hybrid breeding program in maize research for developing tolerant maize genotypes to Turcicum leaf blight.

Based on the SCA and GCA effects for grain yield, only nine maize inbred lines were established into A and B heterotic groups. These heterotic groups could serve as sources for developing inbred line and hybrids. However, the testers used in the current study could not clearly discriminate most of the inbred lines into distinct heterotic groups. Therefore, further studies should explore the possibility of separating these and other inbred lines into distinct heterotic groups using the currently used and other more divergent testers.

From this study, it can be concluded that better performing testcrosses, inbred lines with desirable GCA and cross combinations with desirable SCA effects for grain yield and other grain yield related traits were successfully identified. These germplasm constitute a source of valuable genetic material that could be used for future breeding work. In general, the results of this study could be useful for researchers who need to develop high yielding varieties of maize particularly adapted to the mid altitude areas of Ethiopia.

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*Appendix 1:* Mean value of 25x2 line by tester crosses of maize evaluated for grain yield and other related traits at Bako (2012/13)

ENTRY	Crosses	TD	SD	MD	PH	EH	SLP	SLP <sup>+</sup>	RLP	RLT <sup>+</sup>	EA	ERP	ERP <sup>+</sup>
1	L1xT2	81.33	83.00	149.67	263.00	139.00	9.27	0.31	7.96	0.28	2.33	3.95	0.19
2	L1xT1	82.00	83.33	149.67	272.00	142.00	6.10	0.24	6.07	0.24	2.50	3.10	0.18
3	L2xT1	81.33	83.67	150.00	285.00	147.00	7.01	0.26	1.04	0.10	2.33	6.09	0.24
4	L2xT2	81.67	82.67	151.33	263.00	145.00	4.01	0.20	3.00	0.17	2.17	2.94	0.17
5	L3xT2	81.00	83.33	150.67	261.33	139.00	1.08	0.10	6.26	0.25	2.33	3.13	0.18
6	L3xT1	79.00	81.00	149.67	265.00	134.33	1.04	0.10	4.11	0.20	2.50	5.15	0.22
7	L4xT2	81.00	83.00	150.00	273.00	132.33	0.00	0.00	3.13	0.18	2.33	6.23	0.25
8	L4xT1	81.33	82.33	149.00	265.67	136.33	0.00	0.00	1.04	0.10	2.00	2.06	0.14
9	L5xT1	81.33	83.33	149.33	252.67	131.33	1.08	0.10	6.22	0.25	2.17	2.08	0.14
10	L5xT2	80.67	82.33	151.33	263.67	141.00	2.02	0.14	1.01	0.10	2.00	1.01	0.10
11	L6xT2	79.67	82.00	147.67	262.00	131.33	1.96	0.14	2.94	0.17	2.17	2.29	0.15
12	L6xT1	81.33	82.67	148.00	260.67	129.00	2.02	0.14	3.01	0.17	2.50	0.00	0.00
13	L7xT1	80.00	81.00	149.67	259.67	130.67	7.35	0.27	6.86	0.26	1.83	3.92	0.20
14	L7xT2	80.67	82.00	149.33	260.67	135.00	0.00	0.00	3.16	0.18	1.83	0.00	0.00

ENTRY	Crosses	TD	SD	MD	PH	EH	SLP	SLP <sup>+</sup>	RLP	RLT <sup>+</sup>	EA	ERP	ERP <sup>+</sup>
15	L8xT2	79.67	81.00	149.33	274.67	138.67	1.96	0.13	6.90	0.26	2.50	5.97	0.24
16	L8xT1	79.67	81.33	148.67	268.67	128.00	5.08	0.23	2.08	0.14	2.50	4.04	0.20
17	L9xT1	80.67	82.33	149.67	272.67	137.00	6.00	0.24	2.02	0.14	2.50	4.01	0.20
18	L9xT2	81.00	82.00	148.67	258.00	129.00	3.06	0.18	3.00	0.17	2.17	4.04	0.20
19	L10xT2	82.00	83.67	151.67	275.67	145.00	9.13	0.30	2.08	0.14	2.33	1.01	0.10
20	L10xT1	80.67	82.33	148.67	279.00	147.67	5.24	0.23	3.06	0.18	2.33	1.04	0.10

21	L11xT2	81.33	82.33	148.67	264.67	134.67	3.95	0.19	4.96	0.22	2.33	3.95	0.19
22	L11xT1	81.33	82.33	149.00	262.67	126.33	2.97	0.17	6.03	0.24	2.50	2.00	0.14
23	L12xT2	81.67	83.00	150.00	277.33	138.33	3.00	0.17	3.98	0.20	2.33	1.01	0.10
24	L12xT1	81.33	82.67	148.67	282.67	146.33	5.91	0.24	6.00	0.25	2.33	0.98	0.10
25	L13xT1	80.67	82.00	148.67	274.33	147.00	7.10	0.27	2.00	0.14	2.50	2.05	0.14
26	L13xT2	80.67	81.33	150.67	263.33	147.00	16.10	0.41	8.63	0.30	1.83	4.31	0.21
27	L14xT2	81.00	82.33	149.00	269.33	140.00	7.96	0.28	5.02	0.22	2.50	3.00	0.17
28	L14xT1	81.00	82.67	149.00	264.00	139.33	3.23	0.18	3.19	0.18	2.33	3.19	0.18
29	L15xT2	81.67	82.67	147.67	290.67	159.33	26.28	0.54	3.95	0.20	2.33	2.02	0.14
30	L15xT1	81.33	82.33	150.00	284.67	151.00	14.43	0.39	4.11	0.20	2.00	5.21	0.23

ENTRY	Crosses	TD	SD	MD	PH	EH	SLP	SLP <sup>+</sup>	RLP	RLT <sup>+</sup>	EA	ERP	ERP <sup>+</sup>
31	L16xT1	81.67	83.33	151.67	280.33	142.67	3.06	0.18	3.06	0.18	2.33	0.00	0.00
32	L16xT2	82.33	83.33	150.33	274.67	141.67	7.01	0.27	5.97	0.24	2.17	1.01	0.10
33	L17xT2	80.67	84.67	150.67	292.67	153.67	1.04	0.10	4.10	0.20	2.00	0.00	0.00
34	L17xT1	82.33	84.33	152.33	299.33	165.33	6.00	0.24	7.12	0.27	1.83	2.08	0.14
35	L18xT1	81.33	82.67	151.67	288.33	163.67	3.92	0.20	1.96	0.14	2.00	0.98	0.10
36	L18xT2	80.33	81.33	152.33	296.00	171.00	1.11	0.11	3.14	0.18	1.33	0.00	0.00
37	L19xT2	80.00	82.00	150.67	270.67	156.00	1.04	0.10	6.16	0.25	1.33	3.09	0.17
38	L19xT1	80.33	82.00	151.67	280.00	146.00	0.00	0.00	5.05	0.22	1.50	0.00	0.00
39	L20xT2	81.33	82.67	150.33	298.67	174.33	3.16	0.18	2.08	0.14	2.00	1.01	0.10
40	L20xT1	82.33	83.67	151.67	275.00	157.67	0.00	0.00	2.97	0.17	2.00	0.00	0.00
41	L21xT1	81.00	82.67	152.67	261.33	133.00	3.95	0.19	0.00	0.00	1.67	3.98	0.20
42	L21xT2	81.67	83.00	151.67	268.33	149.33	3.03	0.17	6.12	0.24	1.50	0.00	0.00
43	L22xT2	82.33	83.67	152.67	285.33	157.00	3.92	0.20	3.13	0.18	1.50	0.00	0.00
44	L22xT1	81.00	83.67	153.33	294.00	156.00	2.02	0.14	8.15	0.29	1.33	4.07	0.20
45	L23xT1	81.00	82.67	151.33	280.33	159.67	0.00	0.00	4.01	0.20	2.00	0.00	0.00
46	L23xT2	81.33	82.67	151.33	292.67	172.33	6.09	0.24	2.08	0.14	1.50	3.00	0.17
47	L24xT1	82.67	84.67	151.33	291.00	161.33	3.09	0.17	1.01	0.10	1.50	2.02	0.14
48	L24xT2	82.33	84.33	152.33	286.33	165.00	1.96	0.13	2.02	0.14	1.50	0.98	0.10

49	L25xT2	80.00	82.00	149.67	268.67	143.00	3.06	0.17	5.03	0.22	2.33	1.04	0.10
50	L25xT1	80.00	81.67	150.00	283.00	138.00	1.67	0.13	19.79	0.46	2.00	1.01	0.10
51	BH-540	78.67	79.67	148.00	267.33	142.67	4.20	0.21	11.69	0.35	2.50	1.08	0.10
52	BH-543	81.67	82.33	150.33	257.67	139.67	4.17	0.21	9.38	0.31	2.17	3.13	0.17
MEAN		81.04	82.6	150.22	274.26	145.33	4.38	0.18	4.56	0.2	2.08	2.27	0.13
MINIMUM		78.67	79.67	147.67	252.67	126.33	0.00	0	0.00	0.00	1.33	0.00	0.00
MAXIMUM		82.67	84.67	153.33	299.33	174.33	26.28	0.53	19.79	0.46	2.5	6.23	0.25
CV(%)		1.08	0.99	0.76	3.84	5.5	33.77	17.81	37.25	18.05	12.77	47.32	19.97
LSD (5%)		1.43	1.34	1.86	17.15	13.02	2.41	0.05	2.77	0.06	0.43	1.75	0.04

+ Traits with transformed data

\*=significant at 0.05 probability level, \*\*=significant at 0.01 probability level

TD=50% days to tasseling SD=50% days to silking, MD =Maturity date, PH=Plant height, EH=Ear height, SLP=stalk lodging percent, RLP= root lodging percent, EA=Ear aspect, , ERP= ear rot percent

Continue appendix 1

ENTRY	Crosses	HCP	HCT	YLDT	TLBSI	TLBSI+	GLSSI	GLSSI+	EL	ED	NKRE	NKR
1	L1xT2	0.00	0.00	6.97	42.67	0.71	21.33	0.48	16.60	4.80	13.73	39.00
2	L1xT1	1.08	0.10	6.80	41.33	0.70	34.67	0.62	17.03	4.70	13.33	40.13
3	L2xT1	4.99	0.22	8.57	42.67	0.71	46.67	0.75	17.10	4.80	13.60	41.40
4	L2xT2	0.00	0.00	9.37	30.67	0.58	37.33	0.65	17.40	4.93	13.73	40.90
5	L3xT2	24.16	0.51	7.93	29.33	0.57	21.33	0.48	18.13	5.13	16.00	40.60
6	L3xT1	21.39	0.48	8.40	28.00	0.55	28.00	0.55	18.33	5.00	15.47	42.40
7	L4xT2	9.23	0.31	7.67	26.67	0.54	20.00	0.46	19.20	4.80	14.40	43.33
8	L4xT1	6.10	0.24	7.67	22.67	0.49	29.33	0.56	18.00	4.87	15.07	41.20
9	L5xT1	3.19	0.18	7.90	56.00	0.86	34.67	0.62	17.50	4.87	15.07	39.13
10	L5xT2	8.08	0.29	8.97	44.00	0.72	20.00	0.46	17.63	4.70	15.20	42.40
11	L6xT2	4.90	0.21	7.33	28.00	0.55	30.67	0.58	17.13	4.80	13.73	38.43
12	L6xT1	5.05	0.22	7.27	24.00	0.51	25.33	0.52	17.37	4.80	15.33	38.27
13	L7xT1	5.88	0.24	7.77	32.00	0.60	65.33	0.95	18.70	4.93	14.93	40.27
14	L7xT2	6.07	0.24	7.53	30.67	0.59	20.00	0.46	18.77	4.70	14.40	38.33
15	L8xT2	6.95	0.26	7.47	36.00	0.64	22.67	0.49	19.47	4.67	14.40	38.40
16	L8xT1	10.02	0.32	7.57	22.67	0.49	34.67	0.63	18.23	4.67	14.80	37.33
17	L9xT1	7.99	0.29	7.77	25.33	0.53	61.33	0.91	18.33	4.80	15.07	39.53
18	L9xT2	9.06	0.30	7.67	28.00	0.55	40.00	0.68	18.60	4.70	14.27	40.27
19	L10xT2	0.00	0.00	7.97	26.67	0.54	28.00	0.55	17.30	4.63	14.93	36.93
20	L10xT1	0.00	0.00	7.93	21.33	0.48	48.00	0.77	18.13	4.63	14.93	39.20
21	L11xT2	3.92	0.20	6.93	26.67	0.54	20.00	0.46	18.27	4.73	14.80	39.87
22	L11xT1	0.00	0.00	7.90	37.33	0.66	44.00	0.73	18.80	4.80	14.80	41.07
23	L12xT2	1.99	0.14	8.27	41.33	0.70	42.67	0.71	19.83	4.70	14.27	42.87
24	L12xT1	4.99	0.22	7.57	29.33	0.57	56.00	0.86	19.17	4.73	14.40	41.67
25	L13xT1	6.09	0.25	8.07	38.67	0.67	41.33	0.70	18.53	4.77	14.00	41.33
26	L13xT2	2.15	0.15	8.50	20.00	0.46	34.67	0.62	18.83	4.73	14.00	42.33
27	L14xT2	17.03	0.43	8.43	37.33	0.65	34.67	0.62	18.63	4.47	13.07	41.27
28	L14xT1	4.30	0.21	7.77	45.33	0.74	52.00	0.83	18.00	4.77	14.13	40.13
29	L15xT2	0.98	0.10	8.30	32.00	0.60	44.00	0.72	17.80	4.60	13.93	42.13
30	L15xT1	5.18	0.23	8.30	34.67	0.62	62.67	0.95	19.27	4.77	14.13	42.73
ENTRY	Crosses	HCP	HCP+	YLDT	TLBSI	TLBSI+	GLSSI	GLSSI+	EL	ED	NKRE	NKR
31	L16xT1	1.01	0.10	8.23	34.67	0.62	78.67	1.09	17.00	4.93	13.60	38.27
32	L16xT2	1.01	0.10	8.23	25.33	0.52	50.67	0.79	17.17	4.73	13.33	40.67
33	L17xT2	0.98	0.10	8.30	26.67	0.53	45.33	0.73	20.00	5.00	14.27	45.07
34	L17xT1	1.96	0.14	9.20	72.00	1.02	41.33	0.69	20.13	4.97	14.93	41.53
35	L18xT1	3.92	0.20	9.47	49.33	0.78	22.67	0.49	18.60	4.77	15.07	40.93
36	L18xT2	0.00	0.00	9.30	32.00	0.60	20.00	0.46	18.97	4.97	14.13	41.87
37	L19xT2	9.31	0.31	9.70	25.33	0.53	25.33	0.52	20.90	4.57	13.73	44.47
38	L19xT1	7.11	0.27	8.47	30.67	0.59	29.33	0.56	21.30	4.67	14.60	44.67

39	L20xT2	18.0 4	0.44	8.27	41.33	0.69	22.67	0.49	19.30	4.67	13.87	47.60
40	L20xT1	1.96	0.14	9.13	46.67	0.75	52.00	0.82	21.23	4.83	14.27	46.47
41	L21xT1	4.99	0.22	9.07	50.67	0.79	20.00	0.46	18.77	4.73	14.67	41.67
42	L21xT2	4.07	0.20	8.90	53.33	0.82	26.67	0.53	19.17	4.60	15.07	43.93
43	L22xT2	4.02	0.20	9.03	44.00	0.72	20.00	0.46	20.33	4.77	14.13	44.87
44	L22xT1	0.98	0.10	9.93	40.00	0.68	22.67	0.49	20.33	4.97	15.47	44.47
45	L23xT1	5.97	0.25	8.97	45.33	0.74	60.00	0.90	20.20	4.93	16.67	42.47
46	L23xT2	3.00	0.17	8.87	40.00	0.69	26.67	0.53	18.93	4.83	15.33	42.13
47	L24xT1	3.03	0.17	9.97	38.67	0.67	25.33	0.52	18.57	4.83	14.67	41.33
48	24xT2	0.00	0.00	9.43	42.67	0.71	28.00	0.55	21.23	4.70	14.53	45.53
49	L25xT2	0.00	0.00	7.17	28.00	0.55	22.67	0.49	16.60	5.17	14.27	36.60
50	L25xT1	1.96	0.14	7.63	30.67	0.58	20.00	0.46	17.60	5.03	14.00	39.13
51	BH-540	13.8 1	0.38	6.80	22.67	0.49	26.00	0.52	17.03	4.77	13.07	38.07
52	BH-543	2.09	++	7.20	61.33	0.92	45.33	0.75	18.77	4.60	14.40	39.73
MEAN		5.19	0.19	8.23	35.82	0.64	35.24	0.63	18.62	4.79	14.46	41.24
MINIM UM		0	0	6.8	20	0.46	20	0.46	16.6	4.47	13.07	36.6
MAXIM UM		24.1 6	0.51	9.97	72	1.02	78.67	1.09	21.3	5.17	16.67	47.6
CV(%)		26.6 7	14.99	7.5	30.69	18.79	37.63	23.1	6.51	3.4	4.95	5.12
F-TEST		**	**	**	**	**	**	**	**	**	**	**
LSD (5%)		2.26	0.05	1.01	17.92	0.2	21.62	0.24	1.98	0.27	1.17	3.44

+ Traits with transformed data

\*=significant at 0.05 probability level, \*\*=significant at 0.01 probability level

HCP=husk cover percent, YLDT=Grain yield tones per hectare, TLBSID=Turcicum leaf blight severity index, GLSSID=Gray leaf spot severity index, EL=Ear length, ED=Ear diameter, NKRE=Number of kernel rows per ear, NKR=Number of kernels per row





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