COMBINING ABILITY AND HETEROSIS OF MAIZE INBRED LINES

MSc THESIS

BY

ABENEZER ABEBE TEFERA

NOVEMBER, 2018

JIMMA, ETHIOPIA

COMBINING ABILITY AND HETEROSIS OF MAIZE INBRED LINES

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Abenezer Abebe Tefera

MSc Thesis Summited to the School of Graduate Studies of Jimma University, College of Agriculture and Veterinary Medicine in Partial Fulfillment of the Requirements for the Degree of Master of Science (MSc) in plant breeding

Major advisor: Legesse Wolde (PhD)

Co-advisor: Wosene Gebreselassie (Asso. Prof)

November, 2018

Jimma, Ethiopia

DEDICATION

I dedicate this work to my late father Abebe Tefera for his due effort in the success of my life.

STATEMENT OF THE AUTHOR

First, I declare that this thesis is my bona fide work and that all sources of materials used in this thesis have been duly acknowledged. This thesis has been submitted in partial fulfillment of the requirements for an advanced MSc degree at Jimma University, College of Agriculture and Veterinary Medicine and is deposited in the University Library to be made available to users under the rules of the Library. I declare that this thesis is not submitted to any other institution anywhere for the reward of any academic degree, diploma or certificate. Brief quotations from this thesis are allowed without special permission, provided that accurate acknowledgement of the source is made. Requests for permission for extended quotation or reproduction of this manuscript in whole or in part may be granted by the head of the major department or the Dean of the School of Graduate Studies when in his or her judgment the proposed use of the material is in the interests of scholarship. In all other instances, however, permission must be obtained from the author.

Name: <u>Abenezer Abebe</u>   Place: <u>Jimma University</u>

Signature: _____   Date of Submission: _____

ACRONMYS AND ABBREVEATIONS

AARC	Ambo Agricultural Research Center
AGD-R	Analysis of genetics design in R-software
h^2b	Broad Sense Heritability
R^2	Coefficient of Determination
CV	Correlation Coefficient
EIAR	Ethiopian Institute of Agricultural Research
F_1s	First Filial Generation
GCA	General Combining Ability
rg	Genotypic Correlation
HARC	Holeta Agricultural Research Center
CIMMYT	International Maize and Wheat Improvement Center
NARS	National Agricultural Research System
rp	Phenotypic Correlation
U	Residual Effect
SCA	Specific Combining Ability
SAS	Statistical Analysis System
SH	Standard Heterosis

BIOGRAPHICAL SKETCH

The author was born in November 18, 1987 at Sire district of Arsi Zone, South Eastern Oromia region from his father Abebe Tefera and his mother Leke Gudeta. He attended elementary school education at Gesela Chacha and Sire Haile Aba Mersa elementary school from 1996 to 2003 G.C. Then he followed junior and senior secondary school education at Sire preparatory school from 2004 to 2007 G.C. Then he joined Aksum University and graduated with BSc degree in Plant Science and Protection in 2010 G.C.

After graduation, he was employed by Oromia Agricultural Research Institute from November 2010 to April 2014 G.C and served as cereal crop agronomist at Haro Sebu Agricultural Research Center, Qellem Wollega. In May 2014, he joined Ethiopian Institute of Agricultural Research (EIAR) and assigned to work at Holetta Agricultural Research Center as junior researcher. After two years of service, he joined Jimma University, College of Agriculture and Veterinary Medicine to pursue his MSc study in Plant breeding. The author is married and living with his spouse.

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ABSTRACT

Maize is one of the high priority crops to feed the ever increasing population in Africa, however, its production is limited by shortage of high yielding varieties coupled with biotic and abiotic stresses. Ambo Agricultural Research Center developed a number of inbred lines and crosses whose genetic information has not yet studied. This the study was initiated to estimate combining ability, heterosis, and traits association of maize inbred lines and crosses using line by tester analysis. Fifty entries consists 48 F_1 single crosses developed from 24 inbred lines and 2 testers using line x tester design and two commercial check hybrids used in the study. The experiment was conducted using alpha lattice design with two replications at Ambo and Holeta Agricultural Research Center. Analysis of variance revealed existence of significant genetic variation among genotypes for all studied traits except for plant aspect (PA). Location x entry interaction for most of the traits was not significant which suggests hybrid performance was consistent across tested locations. Crosses L23 x T1 and L11 x T1 were the best performing genotypes for grain yield with mean values of 10.17and 9.50 t ha^{-1}, respectively. Line x tester analysis of variance showed that mean squares due to GCA of lines were significant ($p< 0.01$ or $p< 0.05$) for all studied traits. Mean squares of tester GCA and SCA were significant for most of studied traits. This indicates that additive and non-additive gene effects had contributed for the variation of the crosses. However, higher proportional contribution of additive gene action for all studied traits was obtained. Mean squares of GCA line x loc and GCA tester x loc interaction were significant for some of studied traits which implies that the trend of variation of GCA lines and testers were different across locations. Broad sense heritability ranged from 28.19 to 88.76% and majority of the studied traits showed medium to high heritability, indicating higher genetic effect than environmental effect. But, grain yield had lower broad sense heritability estimate of 28.19%. Number of ears per plant, ear height, ear diameter and number of kernels per row had positive association, and exerted positive direct and indirect effects on grain yield, indicating possibility of simultaneous improvement of these traits and grain yield. Several lines and crosses were identified as good general and specific combiners for yield and yield related traits. Lines L23, L11, L15 and crosses L2xT1, L3xT1, L8xT1, L11xT1, L23xT1 and L13xT2 were found to be good general and specific combiners, respectively. L11xT1 and L23xT1 had significantly higher standard heterosis for grain yield over the best hybrid check (Kolba) with values of 22.18% and 32.44%, respectively. Based on the direction of sca effects, 24 lines each were categorized under ''A'' and ''B''. In conclusion, better performing testcrosses, inbred lines with desirable gca effects and known heterotic groups, cross combinations with desirable sca effects and heterosis for grain yield and yield related traits could be used as source of useful genetic material for future maize breeding activities.

Keywords: Combining ability, Heterosis, Inbred lines, Line by tester, Maize

1 INTRODUCTION

Maize (*Zea mays* L.) is a diploid (2n = 20) crop belongs to the family of grasses *Poaceae* and tribes *Maydeae* and naturally it is cross pollinated crop. The crop is grown over a wide range of environmental conditions (Downsell *et al*., 1996).

Maize has great world-wide importance as human food, industrial raw material and animal feed. Because of its high yield potential and wider adaptation, maize is one of the strategic crops for the achievement of food security. Prasanna *et al*. (2001) noted that the crop is a vital source of calorie, protein, and some important vitamins and minerals to billions of people world-wide, particularly in Africa, South America and Asia. Approximately 88% of maize produced in Ethiopia is consumed as food, both as green and dry grain (Tsedeke, 2015). The per capita consumption of maize is 50 kg year^{-1} per annum in Ethiopia (Mosisa *et al*., 2012).

Maize is cultivated globally as one of most important cereal crops and ranks third next to wheat and rice. In 2016/2017 cropping season, the total world production of maize was 1,068.79 MT, with the United States producing 384.78 MT, China 219.55 MT, Brazil 97.00 MT, European Union 60.71 MT, South Africa 16.40 MT and Ethiopia harvesting 6.35 MT of the total production of maize (FAS, 2017). CSA (2017) reported that in Ethiopia by 2016/17 main cropping season out of the total grain crop area (12,574,107.33 hectare), 81.27% was under cereals of which maize share as large area as 16.98%, after tef (24%). Regarding total annual production, cereals contributed 87.42% (253,847,239.63 quintals) in which maize ranked first 27.02% (78,471,746.57 quintals) followed by teff and sorghum (CSA, 2017). Over 5.8 million hectares of potential suitable land was identified for the highland maize hybrids in the country (Demeke *et al*., 2011). The crop is increasingly grown to the highlands of Ethiopia where it has been a minor crop in the past. Zeng *et al.* (2013) pointed out that increased productivity and production of maize has significant positive impact on poverty reduction in sub-Saharan African countries including Ethiopia.

Considering its importance, wide adaptation, total production and productivity, maize is one of the high priority crops to feed the increasing population of the country. However, national average yield in Ethiopia is still as low as 3.675t ha^{-1} (CSA, 2017) compared to that of the developed world 10.96t ha^{-1} (FAS, 2017) and this warrants the importance of increasing

maize productivity as high national priority issue. For such yield gap, a number of production constraints are responsible. The shortages of high yielding varieties or potential parent materials and the effect of biotic and abiotic stresses are the major constraints limiting maize production and productivity (Mosisa *et al.*, 2012). This implies the need for developing high yielding maize varieties from suitable parents and crosses which will perform well under stress and non-stress conditions.

Identification of suitable inbred lines and superior cross combinations require knowledge of combining ability, heterosis, heritability and traits association. Information from combining ability (GCA and SCA) analysis can show the type of gene action involved in controlling quantitative characters thereby assisting breeders in selecting suitable parent materials and crosses (Hallauer and Miranda, 1988). Feng *et al.* (2015) pointed out that understanding the magnitude of hybrid vigor (heterosis) helps us for effective selection of best combinations of parents for predicting breeding goal. Likewise, determination of heritability and association of traits are important for the selection of favorable plant types for effective maize breeding programs (Munawar *et al.*, 2013). Estimation of heritability has been used to identify selection methods, prediction of any gains from selection and establish magnitude of the genetic effects (Nzuve *et al.*, 2014). Mallikarjuna *et al.* (2011) and Zeeshan *et al.* (2013) also noted that correlation and path coefficient analysis were used to measure the level of relationships between the traits, give reliable and useful information on nature, extent and direction of selection.

Parental lines selection can be performed by particular mating designs such as line x tester, North Carolina (NC) designs I, II and III, and diallel. Through such designs, the genetic influences of a line can be partitioned into additive and non-additive components (Fasahat, 2016). Line x tester analysis as suggested by Kempthorne (1957) is useful in deciding the relative ability of female and male lines to produce desirable hybrid combinations (Girma *et al.*, 2015). Line x tester programs have been applied to provide a systematic approach for the detection of suitable parents and crosses for investigated characters (Liaqat *et al.*, 2015). Guimarães *et al.* (2012) also indicated that testers have been used in maize breeding programs to form heterotic groups, assess the combining ability and to identify superior hybrid combinations.Classification of inbred lines into heterotic groups would also facilitate exploitation of heterosis and lead to development of high yielding maize hybrids.

Combining ability, standard heterosis, trait association and classification of inbred lines has been studied in Ethiopia for different sets of new maize inbred lines (Dagne *et al.*, 2007; Worku *et al.*, 2008; Girma *et al.*, 2015; Tolera *et al.,* 2017). However, it is always mandatory for any breeding program to generate such information for any new batch of inbred lines developed or received outside of the program. In line with this, highland maize breeding program at Ambo Agricultural Research Center (AARC) in collaboration with CIMMYT recently developed inbred lines and crosses whose genetic information has not been studied. Hence, this study was conducted to address the following objectives:

General Objective

- To identify suitable inbred lines and crosses for yield and yield related traits of maize.

Specific Objective

- To estimate general and specific combining abilities of maize inbred lines and crosses (F_1), respectively.

- To generate information on the heterotic group of inbred lines

- To evaluate the heterotic performances of the F_1 hybrids for yield and yield related traits over the standard checks.

2 LITERATURE REVIEW

2.1 Hybrids Maize Development

Development of hybrid maize has been one of the outstanding agricultural technological successes of the century (Tolessa *et.al.*, 1996). Hallauer *et al.* (2010) noted that growers played major role in selecting and fixing different maize traits. Their movement and exchange of maize germplasm was permitted introgression of divergent varieties. Several workers (Jenkins, 1978; Hallauer and Miranda, 1981) have also studied various aspects of maize hybridization. Shull (1908) described hybrid vigor via two crossbred inbred lines and produced a stronger single cross hybrid offspring with higher yields. He also pointed out that producing hybrid seed on female inbred lines was not commercially feasible. However, Jones (1918) suggested the use of double cross hybrids from two single hybrids to lower seed costs. Sprague and Dudley (1988) noted that Henry Wallace the founder of Pioneer Hi-Bred Seed Company produced and sold the first hybrid maize in the USA in 1926. In Ethiopia, a strong foundation was laid for the hybrid maize breeding program in the mid-1980s and early 1990s as breeders in Ethiopia purify introduced inbred lines and began generating inbreed lines for hybrid development (Mandefro *et al.*, 2002). The shifts from open pollinated varieties to hybrid commercial maize production took place in 1994 and thereafter accounted for the sharply improved national average yields of maize (Mosisa *et al.*, 2011). Highland maize breeding program released seven maize varieties like AMB02SYN1 (Hora),AMH800 (Arganne), AMH850 (Wenchi), AMH851 (Jibat), AMH760Q (Webi), AMH853 (Kolba) and AMH852Q (Huluka) from 1999 to 2015 (Demissew *et al.*, 2013 and MoANR, 2016). The introduction of hybrid seed in production system triggered the emergence and establishment of several seed industries in Ethiopia (Mosisa *et al.*, 2011).

Maize hybrid seed provides farmers with varieties containing improved genetics such as high yield potential and unique trait combinations to counter diseases and adverse growing conditions (Macrobert *et al.*, 2014). Exploitation of hybrid vigor will depend on the direction and magnitude of heterosis and the type of gene action involved. The magnitude of heterosis provides information on extent of genetic diversity of parents in developing superior F_1s (Praveen *et al.*, 2014). The success of hybrid maize development depends on the ability of the breeding program to rapidly isolate inbred lines that combine well in hybrid

combinations and to identify appropriate heterotic combinations for maximizing hybrid vigor (Dagne, 2008).

Mosisa *et al*. (2011) noted that inbred lines generating and identification of their best hybrid combination are the major focus of maize improvement activities. Shushay (2011) described that maize hybrid development starts with creation of source segregating breeding population for inbred lines generating. Any inbred line value in hybrid breeding ultimately depends on its ability to combine very well with other lines to produce superior hybrids (Liaqat *et al*., 2015). Although both inbred and non-inbred progenitors can be used to form new heterotic groups, inbred progenitors will provide better source germplasm suitable for hybrid development (Rahman *et al*., 2013).

New inbred lines can be tested by crossing to an inbred line from an opposite heterotic group (Flint-Garcia *et al*., 2009).Hallauer and Miranda (1988) suggested that continues inbreeding increase variability among lines and decreases within inbred lines. Each cycle of selfing increases homozygosity by half and at seventh generation of selfing nearly homozygous and homogeneous reach (Hallauer *et al*., 2010). Haddadi *et al*. (2012) noted that in maize hybrid development, the recognition of parental inbred lines to develop superior hybrids is costly and time consuming phase.Early testing of S_2 lines is considered an efficient approach by maize breeders to identify good performing lines which are then evaluated for grain yield and yield related traits (Rahman *et al*., 2013). Based on their performance as well as combining ability effects from crossing with testers, elite lines can be selectedthat may serve as parents of hybrids or for the formation of synthesis varieties.

2.2 Line x Tester Mating Design

The parental lines selection can be performed by particular mating designs such as line x tester, North Carolina (NC) designs I, II and III, and diallel (Fasahat *et al*., 2016). Line x tester mating design was developed by Kempthorne (1957) which provided reliable information on the general and specific combining ability effects of parents and their hybrid combination. It is an extension of the top cross method in which several testers are used under LxT mating design (EL-Gazzar *et al*., 2013). It involves hybridization between inbreed lines (f) and testers (m) in one to one strategy to produce f x m = fm hybrids.

The materials considered as testers would consist of inbred lines, single cross hybrids and heterogeneous materials.These materials fall into two broad groups namely broad genetic base as well as narrow genetic base testers (Fasahat *et al*., 2016).Smith (986) suggested that if a tester with low frequency (or absence) of favorable alleles is used in the testcrosses, those lines with greater frequency of favorable alleles can be identified.

The line x tester mating design has been widely used by plant breeders (Shams *et al*., 2010). Shanthi *et al*. (2002) evaluated the nature of gene action and combining ability for yield and yield components in maize lines developed through line x tester design and found the preponderance of non-additive gene action. Shushay (2014) also used line x tester mating design in order to evaluate forty eight crosses generated from crossing of 24 elite maize inbred lines with two testers for yield and yield component traits.

Several researchers (Singh and Chaudhary, 1985: Hallauer and Miranda, 1988; Rafiq *et al*., 2010; Shushay, 2011; Praveen, 2013; Tessemma *et al*., 2014; Girma *et al*., 2015; Tolera *et al*., 2017; Dufera *et al*., 2018) used line x tester mating design for the evaluation of genetic potential of different set of maize inbred lines in hybrid combination.

2.3 Heterosis

Heterosis, or hybrid vigor, is the increased performance of hybrid progeny compared to their inbred parents (East and Shull, 1908). Conventionally, dominance and over-dominance were the two most prominent genetic hypotheses for manifestation of heterosis (Feng *et al*., 2015). Falconer and Mackay (1996) also suggested that heterosis can be manifested due to dominance, over-dominance or epistasis.

Heterosis has been extensively studied in maize because of its large expression for grain yield (100-200%) and intensive exploitation in hybrid breeding of maize. It can be expressed as mid-parent heterosis (MPH), heterobeltiosis (BPH) and standard heterosis (SH) and estimated as deviation of F_1 value from the mid-parent, better-parent and standard check values, respectively. The hybrids with over 20% of standard heterosis have high commercial value in almost all crops with special reference to maize (Ram *et al*., 2015).

Singh *et al.* (2010) evaluated heterotic expression and combining ability for 15 yield and related traits in maize involving 66 F1 crosses produced in LxT mating design. They found high percentage of better parent heterosis and standard heterosis for grain yield per plant in some of the crosses and also reported that SCA variance was greater than GCA variance for all characters.

Melkamu *et al.* (2013) studied combing ability, gene action and heterosis estimation in quality protein maize using twelve F_1 hybrids and two standard checks. Accordingly, they reported the higher magnitude of standard heterosis of 107.3% for grain yield, 23.3% for kernel rows per ear, 27% for plant height and 29.7% for ear height.

Shushay (2014) reported that estimation of heterosis over best standard checks for 48 crosses were computed and found significant difference among genotypes. Out of the tested crosses, 31 crosses exhibited positive and significant to highly significant heterosis over the best standard check (BHQPY-545) for grain yield which ranged from -32.16 to 89.24%. he identified crosses with positive and significant standard heterosis for number of rows per ear, for 1000 kernel weight and for number of ears per plants.

Praveen *et al.* (2014) estimated heterosis for 60 hybrids obtained by crossing 20 inbred lines with three testers using line x tester mating design along with 23 parents and three standard checks in maize. In line with this, they reported that out of 60 hybrids, 46 hybrids showed significantly negative standard heterosis for days to 50% tasseling. Moreover, 32 hybrids showed significant and positive heterosis over one of standard checks for number of kernel rows per ear.

Ram *et al.* (2015) studied heterosis and combining ability for 99 genotypes including 80 F_1 hybrids along with their 18 parents and a check quality protein maize hybrid. For grain yield, 15, 62 and 70 crosses exhibited positive heterosis over standard check, better parent and mid parent, respectively. Accordingly, they reported standard heterosis for grain yield which ranged from -56.45 to 53.31%. Moreover, 22, 40 and 70 crosses for days to tasseling revealed negative standard, better parent and mid parent heterosis, respectively.

Ziggiju *et al.* (2017) estimated standard heterosis of eleven maize pipeline hybrids with two standard checks for grain yield and yield related traits and reported that standard heterosis ranged from -38.72 to 33.65% for grain yield.

2.4   Combining Ability and Gene Action

Information on combining ability for newly developed inbred lines is paramount important to design future breeding strategies for the development of hybrid and synthetic varieties (Girma *et al.*, 2015). It is an important method to know gene actions which can be partitioned as additive and non-additive gene action. Based on concept of combining ability, genetic variance is partitioned into two components; i) variance due to general combining ability ii) variance due to specific combining ability. General combining ability (GCA) is the average performance of a genotype in hybrid combination, whereas specific combining ability (SCA) is certain combinations perform relatively better or worse than would be expected on the basis of the average performance (Liaqat *et al.*, 2015).

Shams *et al.* (2010) studied the combining ability and gene action for 36 hybrids developed from twelve maize inbred lines and three tester using line x tester mating design including parents. They observed hybrids with desirable SCA effect which is significant and positive SCA effects for ear weight, kernel number per row and grain yield.

Amiruzzaman *et al.* (2013) studied heterosis, general and specific combining ability for different traits like plant height, grain yield, days to anthesis and ear height of different maize inbred lines. Following this, they found that general and specific combining abilities variances were high for all traits that indicated the important of additive and dominance genes in the inheritance of these traits.

Haydar and Paul (2014) pointed out that the estimated ratio between GCA and SCA was more than unity indicating the predominance of additive gene action for characters like days to 50% tasseling and silking, days to maturity, ear height, ear length, kernels per row and yield per plant. However, for plant height, cob diameter and kernel row per cob non-additive gene action found to be predominance.

Tessema *et al*. (2014) evaluated 72 crosses created via line x tester mating design and three standard checks for 11 traits using alpha lattice design. Then they reported that GCA mean squares were significant, while SCA mean squares were non-significant for all traits. They also found higher GCA/SCA mean squares ratio which stated the preponderance of additive gene effects in the inheritance of all traits. Furthermore, the inbred lines GCA effects for grain yield and days to 50% anthesise were ranged from -0.98 to 1.88 t ha^{-1} and 4.20 to 2.79d, respectively. Finally, they identified desirable inbred lines for grain yield and days to 50% anthesise with best GCA effects which might be used as parents for hybrid and synthetic variety development.

Ofori *et al*. (2015) evaluated six maize inbred lines with their 15 hybrids resulted from diallel mating design. They found non-significant GCA and SCA effects for all traits except for grain yield, which revealed significant additive gene effect. Based on GCA effect estimation, they identified three parental lines with best general combiners for grain yield. Hence, they suggested that the parents may be used in hybridization programmes for grain yield and some yield related traits.

Niyonzima *et al.* (2015) observed that combining ability analysis showed the predominant role of non-additive gene action for inheritance of all the characters studied. They found best crosses that involved high x low, high x high and low x low performing parental combinations. Furthermore, they suggested that the promising single cross hybrids having a parental combination of high x high and high x low *gca* effects could be used for the improvement of parental lines for desired characters by selecting in advanced generations.

Zare *et al*. (2011) studied the gene action for some agronomic traits in maize and found that non-additive gene effects were predominant for controlling the majority of traits. Particularly, they reported that physiological maturity, plant height and number of kernels per row were controlled by non-additive gene action while ear length governed by additive gene action.

EL-Gazzar *et al*. (2013) evaluated forty eight crosses along with two commercial checks and reported that additive gene effects were more important for silking date, plant height, ear height, grain yield, number of ears/plant and ear diameter whereas non-additive gene effects

were more important for ear length. Moreover, they also found that a non-additive gene effects were more interacted with locations than additive gene effects for all studied traits.

Several workers were estimated the combining ability and determined the gene action for different set of maize materials. However, the combining ability and gene action of 24 new inbred lines and 48 crosses considered in this study were not investigated.

2.5   Heterotic Grouping

A heterotic group may be defined as a group of related or unrelated genotypes from the same or different populations which display a similar combining ability when crossed with genotypes from other germplasm groups (Acquaah, 2009). Knowledge of the heterotic groups and patterns is important in plant breeding as it helps breeders to utilize germplasm in a more efficient and consistent manner through exploitation of complementary lines for maximizing the outcomes of a hybrid breeding program.Hallauer and Miranda (1988) pointed out the importance of heterotic patterns for the selection of inbred lines as potential parents in hybrids. A heterotic pattern is a specific pair of heterotic groups which express high heterosis in hybrid combinations (Warburton *et al.,* 2002). Badu-Apraku *et al.* (2013) also highlighted the importance of classifying the parental lines used in a breeding program into heterotic groups as this could help to determine the usefulness of these lines for the development of high yielding hybrids.

Different heterotic grouping techniques are available. Thus, pedigree analysis, geographic isolation inference, measurement of heterosis and combining ability, and molecular analysis techniques have been used to determine genetic distance among genotypes and to assign germplasm into heterotic groups (Vasal *et al.*, 1992; Parentoni *et al.*, 2001; Reif *et al.*, 2003).

Girma *et al.* (2015) gouped maize inbred lines into group "A" and "B" based on SCA of grain yield in their study of testcross performance and combining ability in maize inbred lines. Menkir *et al.* (2004) also assigned 23 inbred lines into different heterotic groups based on SCA effects and test cross mean grain yield. Gurung *et al.* (2009) classified ten inbred lines into three main groups A, B and AB heterotic groups based on SCA of grain yield and mean grain yield. Tolera *et al.* (2017) also grouped maize inbred lines into A, B and AB group based on the direction of specific combining ability in which lines exhibited positive

SCA with tester A were allocated to the opposite heterotic group B and vice versa, whereas lines displaying positive SCA to both were designated as AB group.

2.6 Heritability

Heritability can be expressed as narrow sense and broad sense. Narrow sense heritability is the ratio of additive genetic variance to the phenotypic variance (Fehr, 1991). Broad sense heritability is the proportion of the total genotypic variance to the phenotypic variance (Fehr, 1991; Falconer and Mackay, 1996). Novoselovic *et al.* (2004) pointed out that breeder need to know how much variation in crop is genetic and to what extent this variation is heritable as efficiency of selection mainly depends on additive genetic variation, environment and genotype by environment interaction.

Wannows *et al.* (2010) estimated heritability for different maize traits and reported higher values like 85% for plant height, 83% for ear height, 82% for physiological maturity, 73% for ear length, and moderate value for silking dates (34%) and grain yield (39%). Hallauer and Miranda (1988) also found moderate heritability (41%) for grain yield and high heritability of 66% and 81% for ear height and plant height, respectively. However, Smalley *et al.* (2004) reported low heritability estimates of 7% for grain yield, moderate heritability estimates of 51% for ear height and 56% for plant height. Saleh *et al.* (2002) suggested that low heritability estimates are an indication that environmental factors have played a major role compared to genetic factors.

Zare *et al.* (2011) studied the gene action of some agronomic traits for seven inbred lines and 42 hybrids and estimated both broad-sense and narrow-sense heritability. Accordingly, they reported that broad-sense heritability for all traits showed that number of rows per ear, ear leaves area and grain yield had the highest heritability with values of 89%, 89% and 86%, respectively. Accordingly, they suggested the presence of high genetic expression and low environmental effect for these studied traits.

Bikal *et al.* (2015) reported high heritability (>60%) for grain yield/ha (67%), moderate heritability (30% to 60%) for number of kernel per row (34%), ear weight (45%), number of kernel row per ear (38%) and low heritability (<30%) for 500 kernel weight. Accordingly,

the authors suggested that visual selection for improvement of grain yield may be applicable using traits that possessed good level of heritability.

Pandey *et al*. (2017) found heritability ranging from 72 to 98% for traits considered with the highest heritability (98%) obtained for grain yield per plant. Following this, they reported that grain yield per plant and 100 seed weight showed high heritability with high genotypic variances suggesting the involvement of additive gene action. However, they noted that days to 50% tasseling and silking showed the highest heritability with low genotypic variance suggesting the preponderance of non-additive gene action.

2.7   Correlation and Path Coefficient

Grain yield is a complex trait which is highly influenced by environment and is the result of interrelationships of its various yield components (Grafius, 1960). Thus, breeders have to rely upon some other traits which are relatively simpler and correlated to yield at genetic level. Indirect selection for correlated traits helps in yield enhancement in population (Barua *et al*., 2017). Likewise, path analysis provides an effective measure of direct and indirect causes of association which depicts the relative importance of each factor involved in contributing to the final product (Jakhar *et al*., 2017). Phenotypic and genotypic correlation are the two type of correlations and measure the extent to which degree the same genes or closely linked genes cause co-variation in two different characters(Hallauer and Miranda, 1988). The same scholars pointed out that phenotypic correlation could be directly observed from measurements of the two characters in a number of individuals. Falconer (1989) also described that genetic correlation is the association of breeding values of the two characters.

Pavan *et al*. (2011) studied correlation and path coefficient analysis of grain yield and yield contributing traits for 87 maize single crosses developed by line x tester mating strategy. Accordingly, they reported that plant height, ear length, ear circumference, number of kernel rows per ear, number of kernels per row and 100-grain weight showed significant positive and genetic correlation with grain yield. Similarly, they stated that path coefficient analysis revealed the highest direct effect for days to 50% silking, plant height, number of kernel rows per ear, number of kernels per row and 100-grain weight on grain yield.

Zeeshan *et al*. (2013) reported that grain yield is positively and significantly correlated with flag leaf area, ear diameter, number of kernel rows per ear, number of kernels per ear and

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100 grain weight at both correlation levels. Additionally, they noted that path coefficient analysis for traits like flag leaf area, ear diameter, number of kernel rows per ear, number of kernels per ear row and 100-grain weight showed positive direct effects on the grain yield.

Hailegebrial *et al*. (2015) found positive and significant phenotypic correlation between grain yield and anthesis date, plant height, ear height, ear length, number of ears per plant, ear length and ear weight. Besides, they noted that path coefficient analysis for traits like, days to tasseling, anthesis silking interval, ear diameter, ear length, number of ears per plant and plant height showed highest positive direct effect on seed yield.

Satyanvesh (2016) observed that grain yield per plant was positively correlated with ear length, number of kernels per row, plant height, ear height, ear girth, number of kernel rows per ear while negatively correlated with days to 50% tasseling and silking. He also stated that ear length exhibited highest direct effect on grain yield followed by days to 50% tasseling, number of kernels per row, number of kernel rows per ear, ear girth, plant height, ear height and days to 50% tasseling.

Pandey *et al*. (2017) stated that yield was positively and strongly correlated with cob length, plant height, number of kernels per row and kernel rows per cob. The scholars also mentioned that path coefficient analysis of days to 50% silking, physiological maturity and 100 seed weight showed positive and direct effect on grain yield.

3 MATERIALS AND METHOD

3.1 Description of Study Site

The experiment was conducted at Ambo and Holeta Agricultural Research Centers of the Ethiopian Institute of Agricultural Research (EIAR) during the main cropping season of 2017. Holeta Agricultural research center (HARC) is located in West Showa zone of the Oromia region, 33 km west of Addis Ababa at 09°04'12"N latitude and 38°29'45"E longitudes and an elevation of 2400 m.a.s.l. The center receives an average rainfall of 1102 mm per annum. The maximum and minimum temperatures of this site are 6°C and 22°C, respectively. The center has nitosols and vertisols soil types with pH of 6.0 (Tamene *et al*., 2015).

Ambo Agricultural Research Center (AARC) is located in West Showa zone of the Oromia region, 114 km west of Addis Ababa at 8°57' N latitude and 37° 51' E longitudes with an altitude of 2225 m.a.s.l. The site receives an average rainfall of 1115mm. The maximum and minimum temperatures of this site are 11.7°C and 25.4°C, respectively. The soil type of Ambo is clay (heavy vertisols) with a pH of 7.8 (Demissew, 2014).

3.2 Experimental Materials

The experiment consisted of 50 maize entries which include 48 testcrosses and two hybrid checks (AMH853-Kolba and AMH851-Jibat). The testcrosses (48) were generated from crossing of 24 inbred lines (female parents) with two testers (male parents) in line x tester mating design during 2015/2016 cropping season at AARC. The inbred lines were developed at Ambo Agricultural Research Center from CYMMYT materials using ear-to-row selection and subsequent selfing until they attain homozygosity. The inbred line testers used for the formation of the testcrosses were FS59 (Tester 1) and FS67 (Tester 2) (Table 1). The first tester was from heterotic group "B", while the second was from heterotic group "A". Ambo maize breeding program commonly uses these testers in the identification of promising inbred lines. The hybrid checks are commercial maize hybrids released for highland and sub-humid agro ecologies of Ethiopia. AMH851 (Jibat) and AMH853 (Kolba) are three-way cross hybrid varieties released by Ambo Agricultural Research Center, highland maize breeding program in 2011 and 2015, respectively. They take about 178 days

for grain mature at Ambo and similar environments. Besides, hybrid checks are high yielding, tolerant/resistance to major maize disease in the country and well adapted to the altitude ranging from 1800-2600m in the highland sub-humid agro-ecological conditions of the country (MoANR, 2016).

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

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

Source: *Ambo plant protection research center, highland maize breeding program (2017)*

3.3 Experimental Design and Procedure

The experimental materials along with two hybrid checks were grown during the 2016/2017 main cropping season using alpha lattice design (Patterson and Williams, 1976) with two

replications, 10 incomplete blocks and 5 plots per the incomplete blocks at both locations. Each entry was planted in a single row plot of 5.25m length with a spacing of 75cm between rows and 25cm between plants. Seeds were planted with two seeds per hill and later thinned to one plant at four leaf stage. All agronomic practices were done as per the recommendation of the locations.

3.4 Data Collection

Plot and plant based data collection was performed to meet the objectives of the study as follows;

3.4.1 Plot based data

Days to anthesise (DA): The number of days from planting to the date when 50% of the plants in a plot have tassels shedding pollen.

Days to silking (DS): The number of days from planting date to the date on which 50% of plants in the plot emerged 2-3cm long silk.

Anthesise–Silking interval (ASI): Obtained by subtracting days to 50% anthesise from days to 50% silking.

Ear aspect (EA): It was recorded on general appearance of all ears in the plot using 1–5 rating scale. Factors considered include ear size, grain filling, disease and insect damage, and uniformity and color.

Plant aspect (PA): It was recorded on general appearance of all plant in the plot using 1-5 rating scale.

Grain yield (GY): Yield of total ears unshelled per plot measured in kg/plot and converted to ton per. Conversion made using moisture adjustment of 12.5% which measured in digital moisture tester and fresh ear weight as follow:

$$GY = \frac{\text{fresh ear weight (kg/plot) x (100-MC) x shelling\% x 10}}{(100-12.5) \text{ x area harvested}}$$

Fresh ear weight = unshelled ear weight using balanced weight in kg

MC= moisture content

Number of ears per plant (EPP): It was obtained by dividing the total number of ears to the number of plants in the row.

Thousand kernel weight (TKW): 1000 randomly taken kernels were weighed from each plot using sensitive balance and was adjusted to 12.5 % moisture content.

3.4.2 Plant based data

Plant height (PH):Average height of five randomly selected plants measured in centimeters (cm) from ground level to the point where the tassel starts branching three weeks after flowering is completed.

Ear height (EH):Average ear height of five randomly selected plants measured from the ground to the upper most ear-bearing nodethree weeks after flowering is completed.

Ear position(EPO): It was calculated from the ratio of ear height to plant height for five randomly selected plants.

Ear length (EL):Length of randomly taken five ears from the base to tip will be measured in centimeter. Data recorded represents the average length of ears from each experimental unit.

Ear diameter (ED): It was measured at the mid-section along the ear length using caliper for five randomly taken ears and averaged.

Number of kernel rows per ear (KRPE): Total number of kernel rows per ear and obtained by counting the number of kernels of five representative ears and averaged them.

Number of kernels per row (KPR): Counted for five randomly taken ears and averaged.

3.5 Data Analysis

General analysis of variance and correlation coefficient analysis was conducted using SAS software v9.3. Path coefficient analysis, standard heterosis and heritability estimates were carried out using their respective procedure. AGD-R version 3.0 software was used for line x tester analysis (Francisco, 2015). Mean separation was done using least significant difference (LSD).

3.5.1 Analysis of variance

Analysis of variance for each location and combined analysis were performed using the procedure of general linear model (PROC GLM) in SAS v9.3 (SAS, 20011) by considering location, replication and blocks as random and entry/genotype as fixed factors with statement of RONDOM and TEST option. Data from both locations were pooled after testing homogeneity of variances (Gomez and Gomez, 1984). However, before analysis was carried out, anthesis-silking interval values were transformed using $\ln\sqrt{(ASI + 10)}$, log transformation method as suggested by Bolanos and Edmeades (1996). The significance of mean squares for entries, crosses, and location in combined analysis were tested against the mean squares for their corresponding interaction with location as error term, while their interaction with location were tested against their corresponding pooled error. Here below the linear model and ANOVA Table of alpha lattice design used for combined analysis is given.

$Yijke = \mu + Ti + Le + (TL)ie + Rk (L)e + Bj(RL)ke + \varepsilon ijke$

where, *Yijke* value of the observed trait for i^{th} treatment received in the jth block within k^{th} replicate (superblock) across *e* location, Ti is the fixed effect of the ith treatment; *Le* effect of e-th location; *TL(ie)* interaction effect of ith treatment and e^{th} locationR*je* is the effect of the jth replicate nested under e^{th} location; B*jke* is the effect of the jth incomplete block nested under k^{th} replicate and e^{th} location and $\varepsilon ijke$ is an experimental error.

3.5.2 Line x tester analysis

Based on general analysis of variance, traits that showed significant differences among the entries were further analyzed on the bases of line x tester analysis to partition the mean square due to entries into crosses and then into lines, testers and line by tester interaction

effects (Kempthorne, 1957; Singh and Chaudary, 1985) using analysis of genetic designs with R (AGD-R) version 3.0 procedure for individual and combined data (Francisco *et al.*, 2015). Here below the linear model and ANOVA Table of line x tester analysis used across location is given.

$Y_{ijke} = \mu + L_e + R(L)_{ke} + V_{ij} + (LV)_{ije} + \mathcal{E}_{ijke}$

Where, Y_{ijke} = observed value from each experimental unit; μ = grand mean; L_e = location effect; R_{ke} = replication effect within each location V_{ij} = F_1 hybrid effect = $g_i+g_j+s_{ij}$, where, g_i = general combining ability of ith lines; g_j = general combining ability of jth tester; s_{ij} = specific combining ability of ij^{th} F_1 hybrids; $(LV)_{ije}$ = interaction effect of ij^{th} F_1 hybrid and e^{th} location $\mathcal{E}_{ijke}$ = residual effect

The proportional contributions of line GCA, tester GCA, and SCA of line x tester sum of squares were calculated as the ratio between sum of squares of each component and the cross sum of squares as given by Singh and Chaudary (1985).

Contribution of lines = (SSlines/SScrosses) x100
Contribution of testers = (SStester/SScrosses) x100
Contribution of line x tester = (SSlxt/SScrosses) x100

3.5.3 Estimation of general and specific combining ability effects

After confirmation of the significance line, tester and their interaction mean square significance for studied yield and yield related traits in line x tester analysis, general and specific combining ability effects of individual lines and testers as well as specific combining ability effects for each cross were computed using AGD-R version 3.0 procedure.

The standard error of mean and difference for general and specific combining ability were calculated using the following procedure presented by Dabholkar (1999).

❖ **Standard error of *GCA* and *SCA* effects**

a. SE(GCA for lines) = $\sqrt{\dfrac{MSe}{r \times t \times loc}}$

b. SE(GCA for testers) = $\sqrt{\dfrac{MS\,e}{r \times l \times loc}}$

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c. SE (SCA effect for crosses) = $\sqrt{\dfrac{MS\,e}{r \times loc}}$

❖ **Standard error of the difference for line and tester GCA and SCA of line x tester**

a. SE (gi-gj) lines = $\sqrt{\dfrac{2MSe}{r \times t \times loc}}$

b. SE (gi-gj) testers = $\sqrt{\dfrac{2MS}{r \times l \times loc}}$

c. SE(Sji-Skl) = $\sqrt{\dfrac{2Mse}{r \times loc}}$, where, r = replication l= line, t= testers, loc= location

The significant difference of GCA (for line and tester) and specific combing ability (for crosses) was determined by dividing the corresponding GCA and SCA to their respective value of standard error of mean which gives t-value and compared with t-value of Tabular using error degree freedom.

3.5.4 Estimation of heritability

Dabholkar (1999) described that heritability could be expressed as percentage form of variance due to hereditary differences (s^2g) to the total phenotypic variance (s^2p). He also pointed out that broad sense heritability could be useful if the interest is in relative importance of genotype and environment in the determination of phenotypic values but, fail to indicate the progress which might made via selection. Heritability in broad sense (h^2_b) was estimated using formula suggested by Falconer (1989). Genotypic and phenotypic variances were calculated following the formulae suggested by Singh and Chaundhary (1979) and Allard (1960).

Broad sense heritability, $h^2_b = \dfrac{s^2_g}{s^2_p}$

a. Genotypic Variance, $s^2_g = \dfrac{MSg - MSg*l}{lr}$

b. Genotype by environment interaction variance $s^2_{g*loc} = \dfrac{MSg*loc - MSe}{r}$

c. Phenotypic Variance , $s^2_p = s^2_g + \dfrac{s^2_{g*loc}}{l} + \dfrac{s^2_e}{lr}$, where, h^2_b=broad sense heritability, s^2g=genetic variance, s^2e=error variance, s^2p=phenotypic variance, Mse=error mean square, MSg=mean square of genotype, MSg*l=mean square due to genotype by environment interaction, r=replication, l=location.

After the estimation of heritability for studied significant yield and yield related traits the values were compared to the standard value described by different scholars. The heritability values are categorized according to Robinson *et al*. (1949): 0-30% low, 31-60% moderate and over 60% high.

3.5.5   Estimation of standard heterosis

Standard heterosis was calculated for traits that showed statistically significant differences among genotype based on the procedure suggested by Falconer (1996). Standard Heterosis (SH) = $\left(\frac{F1-SC}{SC}\right) x \ 100$ where; SH = standard Heterosis, F1 = mean value of the crosses, SC = mean value of standard checks. The significant difference for percentage of standard heterosis was tested by t-test. Standard error of difference for heterosis and t-value will be computed as follows; SE (d) for SE (d) = $\sqrt{\frac{2MSe}{r*loc}}$, t = $\frac{F1-SC}{SE(d)}$ where, SE (d) is standard error of the difference, MSe =error mean (Paschal and Wilcox, 1975).

3.5.6   Correlation coefficients

Phenotypic and genotypic correlations were estimated for the characters from variance of each character and the covariance components for each pair of characters (Comstock and Robinson, 1952 and Miller *et al*., 1958). The analysis was performed using SAS 9.3 software package and test of significance of correlation coefficients were carried out comparing the computed values against table 'r' values at 5% and 1% probability levels at n-2 degree of freedom (Fisher and Yates, 1963)

3.5.7   Path coefficient analysis

Path coefficient analysis carried using the model and the formula which was adopted by Dewey and Lu (1959) the path and residual effect were computed. Retherford and Choe (2011) stated that residual effect should be computed to determine how best the casual variables account for the variability of the dependent variables.U =$\sqrt{1-R^2}$, R^2 = $\sum$ pij rij , rij = pij+ Σrikpkj, where, rij = mutual association between the independent character (i) and dependent character (j) as measured by the correlation coefficient, pij = component of direct effects of the independent character (i) on dependent character (j) as measured by the path coefficient and, $\sum$rikpkj = summation of components of indirect effect.

4   RESULTS AND DISCUSSION

The analysis of variance, genotype mean performance, line x tester analysis, general and specific combining ability effects, standard heterosis, heterotic grouping, correlation and path coefficient analysis were conducted and the results are discussed below.

4.1   Analysis of Variance and Mean Performance

The analysis of variances for yield and yield related traits for individual and combined location are presented in Appendix I, II and Table 2, respectively. Significant differences were detected between the two locations for all of the studied traits except for ear length, indicating that the two locations differed in the environmental conditions to cause variation which agreed with the finding of Aly *et al.* (2011). Entry mean squares were significant ($p<0.01$ or $p<0.05$) for all traits except for plant aspect (Table 2).

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

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

**highly significant ($p<0.01$), *significant ($p<0.05$) L=location, Re=replication, Ent=entry, SE= standard error, CV= coefficient of variation, R^2=coefficient of determination

The significance differences obtained among the entries for almost all studied traits, indicating the presence of high degree of genetic variation and had potential of making high yielding hybrids. Similarly, Dagne *et al.* (2010), Amiruzzaman *et al.* (2010), Amare *et al.*

(2016) and Ziggiju *et al.* (2017) reported significant difference among genotypes for grain yield and yield related traits of different sets of maize genotypes. Mean squares of entry x location interaction for most of the studied traits were non-significant, suggesting the consistence in performance of genotypes from one location to another regarding these traits (Table 4). On the other hand, variables like grain yield, plant and ear height, ear diameter and 1000 kernels weight showed significant entry x location interaction mean squares, disclosing entries differed in their performance from one location to another for these traits. Similar to the current finding, Gudeta *et al.* (2015) found significant entry x location interaction for grain yield, 1000 kernels weight and ear height for different maize genotypes. Alake *et al.* (2008), Beyene*et al.* (2011) and Murtadha *et al.* (2016) also reported significant entry x location interaction effect for certain traits and referred to the presence of wide variability with regard to tested entry and locations. The result showed the location played significant role in the variation of these traits. If significant genotype x location interaction mean squares existed, different genes were involved in controlling the traits showing the inconsistency of the genes over locations (Dagne, 2008). The interaction of entry with location suggests further evaluation of the genotypes across more number of locations to remove environmental effect from computation genetic variance. Variation among locations, and single cross hybrids which interact more with environment would be responsible for the interaction of entry by location.

Mean performances for yield and yield related traits for individual location are presented in Appendix III and IV. The mean performance of 50 entries which include 48 crosses and 2 standard checks evaluated across location for grain yield and yield related traits presented in Table 5. Mean grain yield at Holetta ranged from 5.22 (L8 x T2) to 10.51 t ha^{-1} (L23 x T1) with overall mean value of 7.33 t ha^{-1}, while at Ambo it ranged from 3.3(L13 x T1) to 9.87 t ha^{-1} (L11 x T1) with an overall mean value of 7.74 t ha^{-1}. At Ambo grain yield of about ten crosses were significantly higher than the best hybrid checks, while none of the crosses had significantly higher grain yield the best check at Holetta (Appendix III and IV). Across location, overall mean of grain yield was 7.54 t ha^{-1} ranging from 4.64 (L13 x T1) to 10.17 t ha^{-1} (L23 x T1). Out of 48 crosses, two crosses such as L23 x T1 (10.17 t ha^{-1}) and L11 x T1 (9.50 t ha^{-1}) significantly out yielded the hybrid checks AMH853 (Kolba, 7.78t ha^{-1}) and AMH851 (Jibat, 7.68t ha^{-1}). Most of the crosses with highest grain yield involved FS59 as one of the parents thereby indicating that FS59 and inbred lines could be from different heterotic group for this trait.

Table 3a. Mean performances of 48 testcrosses and two hybrid checks of maize for yield and yield related traits for combined data, 2017.

SN	ENTRY	GY t/ha	AD days	SD days	ASI days	PH cm	EH cm	EPO ratio	EPP no	EA 1-5 scale
1	L1xT1	8.16	102.75	103.75	1.00	278.25	159.75	0.57	1.96	2.88
2	L1xT2	7.77	102.50	102.25	-0.25	243.50	128.75	0.53	1.95	2.88
3	L2xT1	8.59	105.00	105.25	0.25	254.75	133.50	0.53	1.83	3.63
4	L2xT2	5.85	102.25	103.25	1.00	214.75	116.00	0.54	1.82	3.75
5	L3xT1	5.48	107.25	109.25	2.00	260.25	143.75	0.55	1.69	3.13
6	L3xT2	6.90	107.00	108.00	1.25	231.00	122.00	0.53	1.64	3.25
7	L4xT1	7.64	102.50	104.25	1.75	274.75	151.25	0.55	1.70	2.75
8	L4xT2	7.20	102.00	103.00	1.00	248.25	126.00	0.51	1.42	2.75
9	L5xT1	8.96	103.00	103.50	0.50	292.50	162.00	0.55	1.77	2.38
10	L5xT2	7.49	101.75	102.25	0.50	262.50	134.75	0.51	1.84	3.25
11	L6xT1	7.79	104.25	103.75	-0.50	264.25	147.00	0.56	1.79	2.63
12	L6xT2	6.02	103.75	103.75	0.00	232.75	129.50	0.56	1.73	2.50
13	L7xT1	6.38	106.75	108.75	2.00	265.25	152.50	0.58	1.59	3.75
14	L7xT2	6.94	108.00	108.00	-0.25	223.50	130.00	0.58	1.79	3.63
15	L8xT1	9.00	104.75	106.75	2.00	266.00	144.00	0.54	1.84	2.88
16	L8xT2	6.08	104.25	105.00	0.75	214.00	111.50	0.52	1.25	3.38
17	L9xT1	8.47	101.75	103.00	1.25	260.00	131.50	0.51	1.96	3.63
18	L9xT2	7.45	103.00	101.75	-1.25	243.25	123.50	0.51	1.82	3.25
19	L10xT1	7.79	107.25	108.50	1.25	289.25	166.25	0.57	1.66	2.75
20	L10xT2	8.55	105.25	105.25	0.00	241.25	124.25	0.52	1.66	2.63
21	L11xT1	9.50	106.50	107.75	1.25	277.00	161.25	0.58	1.81	4.00
22	L11xT2	8.56	106.00	105.25	-0.75	232.50	129.75	0.56	1.72	3.50
23	L12xT1	8.53	107.50	107.50	0.00	280.75	183.75	0.66	1.81	3.75
24	L12xT2	7.21	105.75	104.25	-1.50	239.00	131.50	0.55	1.69	2.88
25	L13xT1	4.64	108.75	110.00	1.25	243.50	130.75	0.54	1.51	3.13
26	L13xT2	7.24	104.50	104.75	0.25	229.25	115.50	0.50	1.54	3.25
27	L14xT1	8.78	107.00	108.25	1.25	286.25	159.25	0.56	1.84	2.88
28	L14xT2	6.96	107.00	107.75	0.75	241.25	125.75	0.52	1.63	3.13
29	L15xT1	9.05	106.00	107.00	1.00	275.00	157.25	0.57	1.70	2.75
30	L15xT2	8.48	104.00	105.25	1.25	236.25	125.50	0.53	1.77	2.88
31	L16xT1	8.86	102.25	103.00	0.75	290.00	170.75	0.59	1.75	3.25
32	L16xT2	6.22	105.75	105.75	0.00	222.50	125.00	0.56	1.78	3.50
33	L17xT1	7.06	103.50	104.50	1.00	281.25	156.00	0.55	1.66	3.13
34	L17xT2	7.83	103.50	110.75	-0.25	234.75	129.25	0.55	1.87	3.25
35	L18xT1	7.59	102.50	104.75	2.25	262.00	143.50	0.55	1.40	2.75
36	L18xT2	5.86	103.75	102.50	-1.25	207.50	112.25	0.54	1.31	2.75
37	L19xT1	6.72	103.75	104.75	0.75	266.75	142.00	0.53	1.65	3.13
38	L19xT2	6.09	105.00	105.50	0.50	217.25	125.25	0.58	1.52	3.13
39	L20xT1	8.39	103.50	104.75	1.25	272.50	150.50	0.55	1.66	2.88
40	L20xT2	7.15	104.75	105.00	0.75	220.50	120.00	0.55	1.39	3.50
41	L21xT1	6.12	106.75	107.75	1.00	261.75	147.00	0.56	1.44	3.25
42	L21xT2	6.59	103.00	102.00	-1.00	251.25	136.50	0.54	1.59	3.13
43	L22xT1	7.51	107.50	108.50	1.00	262.00	132.00	0.50	1.92	3.13
44	L22xT2	7.23	105.00	105.50	0.50	218.75	116.00	0.53	1.66	3.38
45	L23xT1	10.17	103.50	104.00	0.50	260.00	138.25	0.53	2.20	3.13
46	L23xT2	8.20	103.75	104.25	0.50	231.50	109.75	0.48	2.11	3.13
47	L24xT1	7.56	103.50	105.00	1.50	260.25	131.50	0.51	1.81	3.13
48	L24xT2	8.56	104.75	104.25	-0.25	238.75	109.75	0.46	1.92	2.88
49	Kolba	7.78	101.75	103.00	1.25	259.25	144.75	0.56	1.54	2.88
50	Jibat	7.68	100.00	101.75	1.75	258.50	135.00	0.52	1.48	2.88
	Mean	**7.54**	**104.53**	**105.29**	**0.63**	**251.56**	**136.66**	**0.54**	**1.71**	**3.12**
	Cross	**7.53**	**104.68**	**105.41**	**1.50**	**251.25**	**136.53**	**0.54**	**1.72**	**3.13**
	Maximu	**10.18**	**108.75**	**110.75**	**2.25**	**292.50**	**183.75**	**0.66**	**2.20**	**4.00**
	Minimu	**4.64**	**100.00**	**101.75**	**-1.50**	**207.50**	**109.75**	**0.46**	**1.25**	**2.38**
	LSD **(5%)**	**1.48**	**2.52**	**2.57**	**1.82**	**16.67**	**10.45**	**0.06**	**0.25**	**0.51**

Table 3b. Mean performances of 48 testcrosses and two hybrid checks of maize for yield and yield related traits for combined data, 2017.

S/N	ENTRY	EPP	EA	EL	ED	KRPE	KPR	TKW
		no	1-5scale	cm	cm	no	no	gm
1	L1xT1	1.96	2.88	13.50	4.25	12.50	28.40	283.48
2	L1xT2	1.95	2.88	14.25	4.12	12.67	29.75	298.90
3	L2xT1	1.83	3.63	15.25	4.31	12.67	33.00	244.20
4	L2xT2	1.82	3.75	14.46	4.17	12.83	31.85	315.28
5	L3xT1	1.69	3.13	15.29	4.12	13.17	31.33	287.83
6	L3xT2	1.64	3.25	14.58	4.31	13.34	29.08	311.68
7	L4xT1	1.70	2.75	16.21	4.64	13.83	34.35	305.70
8	L4xT2	1.42	2.75	16.38	4.31	12.67	34.08	311.63
9	L5xT1	1.77	2.38	15.79	4.34	12.34	32.93	312.13
10	L5xT2	1.84	3.25	15.75	4.35	12.17	31.93	299.40
11	L6xT1	1.79	2.63	15.17	4.43	13.17	32.00	283.05
12	L6xT2	1.73	2.50	14.92	4.39	13.33	31.83	306.70
13	L7xT1	1.59	3.75	16.75	4.20	13.33	32.25	248.35
14	L7xT2	1.79	3.63	16.25	3.96	12.50	33.75	267.60
15	L8xT1	1.84	2.88	16.50	4.33	13.83	33.70	294.20
16	L8xT2	1.25	3.38	16.38	4.34	12.83	32.65	349.50
17	L9xT1	1.96	3.63	15.13	4.30	13.17	31.83	251.70
18	L9xT2	1.82	3.25	12.50	4.39	13.00	27.58	302.00
19	L10xT1	1.66	2.75	15.42	4.67	13.50	33.08	313.70
20	L10xT2	1.66	2.63	17.29	4.50	13.17	33.58	308.05
21	L11xT1	1.81	4.00	13.33	4.58	14.00	29.48	317.73
22	L11xT2	1.72	3.50	14.88	4.45	12.67	33.68	352.73
23	L12xT1	1.81	3.75	16.00	4.56	13.50	33.18	328.80
24	L12xT2	1.69	2.88	16.38	4.30	12.17	34.25	336.90
25	L13xT1	1.51	3.13	13.38	4.50	13.17	32.08	254.83
26	L13xT2	1.54	3.25	14.09	4.34	12.33	31.08	310.40
27	L14xT1	1.84	2.88	17.50	4.46	13.50	34.65	266.50
28	L14xT2	1.63	3.13	15.29	4.41	13.17	30.75	315.90
29	L15xT1	1.70	2.75	16.79	4.36	13.67	34.75	263.38
30	L15xT2	1.77	2.88	18.25	4.38	12.84	33.90	301.33
31	L16xT1	1.75	3.25	15.37	4.31	12.67	32.25	297.30
32	L16xT2	1.78	3.50	14.71	4.13	11.84	30.85	279.38
33	L17xT1	1.66	3.13	16.13	4.15	12.50	32.23	293.98
34	L17xT2	1.87	3.25	14.54	4.16	12.00	30.08	338.38
35	L18xT1	1.40	2.75	15.84	4.52	13.00	34.10	290.05
36	L18xT2	1.31	2.75	15.42	4.32	12.67	31.23	310.70
37	L19xT1	1.65	3.13	14.71	4.22	13.17	33.75	241.13
38	L19xT2	1.52	3.13	14.46	4.01	12.67	29.90	296.50
39	L20xT1	1.66	2.88	15.71	4.49	13.84	34.23	302.88
40	L20xT2	1.39	3.50	16.04	4.53	13.50	32.43	333.73
41	L21xT1	1.44	3.25	14.96	4.57	13.00	29.65	375.28
42	L21xT2	1.59	3.13	16.04	4.31	11.50	32.65	387.08
43	L22xT1	1.92	3.13	15.63	4.13	13.00	30.93	321.43
44	L22xT2	1.66	3.38	15.63	4.08	11.67	32.15	331.65
45	L23xT1	2.20	3.13	15.42	4.19	12.50	32.10	301.90
46	L23xT2	2.11	3.13	15.08	4.16	13.00	34.10	311.85
47	L24xT1	1.81	3.13	16.67	4.04	12.17	33.18	292.08
48	L24xT2	1.92	2.88	15.88	4.25	13.00	34.08	334.15
49	Kolba	1.54	2.88	16.33	4.58	12.34	33.25	364.03
50	Jibat	1.48	2.88	15.08	4.27	12.50	32.93	303.25
	Mean	**1.71**	**3.12**	**15.47**	**4.32**	**12.87**	**32.26**	**305.01**
	Cross mean	**1.72**	**3.13**	**15.46**	**4.43**	**12.89**	**33.09**	**303.81**
	Maximum	**2.20**	**4.00**	**18.25**	**4.67**	**14.00**	**34.75**	**387.08**
	Minimum	**1.25**	**2.38**	**12.50**	**3.96**	**11.50**	**27.58**	**241.13**
	LSD (5%)	**0.25**	**0.51**	**1.27**	**0.23**	**0.86**	**2.90**	**43.50**

GY=grain yield, AD=anthesis days, AD= silking days ASI= anthesis silking interval, plant height, ear height, EPO= ear position, EPP=ear per plant, EA=ear aspect, PA=plant aspect, EL=ear length, ED=ear diameter, KRPE=kernel row per ear, KPR=kernel per row, TKW=thousand kernel weight.

Across locations, mean values of days to 50% anthesis, days to 50% silking and anthesis-silking interval ranged from 100 (Jibat) to 108.75 d (L13 x T1), 101.75 (Jibat) to 110.75 d (L17 x T1) and -1.50 d (L12 x T2) to 2.25 (L18 x T1) with overall mean of 104.53, 105.29 and 0.63d, respectively (Table 3). However, all crosses were not significantly earlier to the hybrid checks which are in agreement with the findings of Elmyhum (2013) andDemissew (2014). Crosses L9 x T2, L11 x T2, L12 x T2, L18 x T2 and L21 x T2 had narrower ASI than hybrid checks. Due to frost problem and climate change, breeder should emphasis on developing early flowering maize varieties with high yielding.

Overall means for plant and ear height were 251.25 and 136.66 cm ranging from 207.5 (L18 x T2) to 292.5 cm (L5 x T1) and 109.75 (L24 x T2) to 183.75 cm (L12 x T1), respectively. Twenty (20) and eight (8) crosses showed significantly shorter and taller plant height over Kolba (259.25 cm) and Jibat (258.50 cm). Twenty six (26) and eleven (11) crosses had significantly lower ear placement compared to Kolba (144.75cm) and Jibat (135cm), respectively. Most of the lines crossed with FS67 had shorter plant and ear height which indicates that FS67 had the tendency to reduce plant stature. Furthermore, high yielding crosses were taller in plant and ear height. Al-Tabbal *et al.* (2012) suggested that tall genotypes excelled in capacity to support kernel growth through stem reserve mobilization. In contrary, Abadassi (2015) reported that reduced plant and ear height could be important in decreasing problem of lodging, increase physiological efficiency and facilitate harvesting activity. As the result, variety with medium plant height and ear placement could be affordable.

The overall mean values of number of ears per plant, ear length and ear diameter were 1.7, 15.47cm and 4.32cm ranging from 1.25cm (L8 x T2) to 2.20cm (L23 x T1), 12.50 (L9 x T2) to 18.25cm (L15 x T2), and 4.67 (L10 x T1) to 3.96 (L7 x T2), respectively. Seventeen crosses and one cross (L15 x T1) showed significantly higher ears per plant and longer ear length over Kolba (AMH854), respectively. The crosses that had higher grain yield also were prolific, which indicates increasing number of ear per plant might improve grain yield. Eight crosses revealed significantly wider ear diameter than Jibat (4.24), but none of the crosses had better ear diameter than Kolba (4.58). The mean value of number of kernel rows per ear ranged from 11.5 (L21 x T2) to 14 (L11 x T1) with overall mean value of 12.87. Nine crosses such as L11 x T1, L20 x T1, L18 x T1, L4 x T1, L15 x T1, L10 x T1, L14 x T1, L20 x T2 and L12 x T1 exhibited significantly larger number of kernel rows per ear than the

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hybrid checks (Table 3). Number of kernels per rows and 1000 kernel weigh ranged from 27.58 (L9 x T2) to 34.75 (L15 x T1) and 241.13 (L19 x T1) to 387.08gm (Kolba) with overall mean values of 32.26 and 305.01gm, respectively.

Crosses such as L11 x T1 and L23 x T1 showed better performance over hybrid checks for more than one trait. Higher performance of certain crosses over hybrid checks regarding a number of traits probably caused by using inbred lines from genetically diverse material. Crosses that revealed higher grain yield could be used for across location breeding program to improve grain yield and other traits of interest. Hence, hybrids that exhibited narrow anthesis silking interval, medium plant and ear height, more prolifically, higher number of kernel rows per ear and ear length could be used as sources of favorable genes for improvement of these traits. Several authors (Dagne *et al*., 2010; Zerihun, 2011; Girma *et al*., 2015; Amare *et al*., 2016) also reported that crosses showed better performance than the best hybrid check in their studied materials.

4.2   Line x Tester Analysis

Following the confirmation of significant differences among genotypes for yield and yield related traits, the cross variations were partitioned into variation due to line, tester and line x tester variation using line x tester analysis procedure (Kempthorne, 1957; Singh and Chaudhary, 1985; Dabholkar, 1999). Beside, cross x loc mean squares were partitioned into line x loc, tester x loc and line x tester x loc mean squares.Significant differences ($p<0.01$, or $p<0.05$) were observed among the crosses for all traits except for anthesis-silking interval at Holetta and for number of kernels per row at Ambo (Appendix V and VI). At Ambo, GCA mean squares due to lines were significant ($p<0.01$, or $p<0.05$) for most of the studied traits except for ear position and ear aspect, while tester GCA mean squares were significant ($p<0.01$, or $p<0.05$) for days to 50% silking, anthesis- silking interval, plant and ear height, ear aspect and 1000 kernels weight (Appendix V). Similarly, SCA mean squares for line x tester were significant for grain yield, ear height, ear position and ear aspect.

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Table 4a. Analysis of variance and heritability for yield and yield related traits of 48 testcrosses and two commercial hybrid checks evaluated at Ambo and Holeta, 2017.

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

Table 4b. Analysis of variance and heritability for yield and yield related traits of 48 testcrosses and two commercial hybrid checks evaluated at Ambo and Holeta, 2017.

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

**Highly significant (p<0.01), *significant (p<0.05), Pro.cont (%) = proportional contribution, h^2_b = broad sense heritability

At Holetta, GCA mean squares of lines and testers were significant (p<0.01, p<0.05) for all traits except for ear length, anthesis silking interval and number of kernels per row and GCA of tester for days to 50% anthesis, number of kernels per row and 1000 kernels weight. The mean squares of SCA line x testers were also significant (p<0.01, or p<0.05) for seven traits and non-significant for other seven studied traits (Appendix VI).

This indicates both additive and non-additive gene actions with different level from location to location were involved in the inheritance of these traits. The observed differences in the level of significance of GCA and SCA mean squares with changing locations were an indication of environmental effect on the preponderance of additive and non-additive gene action. Several authors (Zare *et al.,* 2012; Dange *et al.*, 2014; Abdallah, 2014; Sentayehu and Warsi, 2015) reported different level of GCA and SCA mean square for different testing environment. In contrast, Haddadi *et al.* (2015) found no environmental effect on the preponderance of additive and non-additive gene action. The significance of mean squares due to lines and testers indicated inbred lines variation among the lines and tester in their performance. Meanwhile, significant line x tester interaction suggests that inbred lines performed differently according to the testers to which they were crossed.

Combined analysis of line x tester showed highly significant (p<0.01) difference among cross for all studied traits (Table 4). Cross x environment interaction mean squares were significant (p<0.01, or p<0.05) for most traits except for days to 50% anthesis, anthesis silking interval and ear position. This indicates the presence of wide genetic variations among the studied materials that could be influenced due to changing environment. These findings are in agreement with those reported by Aly and Hassan (2011), Aly and Khalil (2013) and Mousa (2014). The significance of cross x environment interaction infers that we shouldevaluate materials in a number of locations to removeenvironmental effects from the estimates of genetic variances. The mean squares of GCA lines and testers and SCA were significant (p<0.01, or p<0.05) for all traits except GCA of testers for days to 50% anthesis, number of ear per plant and ears aspect, and SCA for anthesis silking interval, number of ears per plant, number of kernel rows per ear and ear diameter, which confirms to the finding of Amiruzzaman *et al.* (2013) and Dar *et al.* (2015). Significant GCA and SCA mean squares indicate that both additive and non-additive gene effects were contributed to the variation of crosses through all of the studied traits. However, higher GCA proportional contribution and GCA/SCA ratio greater than unit were obtained for all studied traits. This indicates that variations among crosses through all the studied traits were mainly due to additive gene effect which was in accordance with the findings of Wende (2013) and Amare *et al.* (2016). Several authors (Bhavana *et al.*, 2011; Abdallah, 2014; Adebayo and Menkir, 2015; Hailegebrial *et al.*, 2015; Satyanvesh, 2016; Panda *et al.*, 2017; Tolera *et al.*, 2017; Dar *et al.*, 2018) have earlier reported that additive gene actions were more important than non-additive gene actions for inheritance of grain yield and yield related traits. However,

Shams *et al.* (2010), Abuali *et al.* (2012), Aminu *et al*. (2014), Arsode *et al.* (2017) and Prasad and Shivani (2017) reported that non-additive gene action was predominated in the inheritance of these traits. Based on current findings, the inheritance of all traits was governed by additive gene effect, suggesting selection would be effective in improving yield and yield related traits.

Furthermore, mean squares GCA line x location interaction were significant (p<0.01, or p<0.05) for traits such as grain yield, ear height, number of ears per plant, ear length and number of kernels row per ear, while GCA tester x location interaction effect showed significant for all studied traits except for days to 50% anthesis and silking, ear position and ear length (Table 4). These suggest that the lines and testers were depended on the location in which they were grown and limited number of testing location would be insufficient. Comparable results were reported by Birhanu (2009), Mousa and Aly (2011), Aly (2014), Fan *et al.* (2016) and Noelle *et al.* (2017) for the materials they studied. On the contrary, non-significant GCA x location interaction mean squares were reported by Alemeshet (2014). Nzuve *et al.* (2014) also found non-significant GCA x location for plant and ear height. Significant GCA x location interaction implies that the trend of variation of GCA of lines and testers were different across location and selection for good combining lines would be effective if based on hybrid performance across a range of environment. This also suggests the need for selecting inbred lines at specific locations. However, mean squares of SCA x location interaction were non-significant for all investigated traits which were in agreement with the finding of Dagne *et al.* (2010), Adebayo and Menkir (2015) and Fan *et al.* (2016). But, Dufera *et al*. (2018) for grain yield and ear per plant, Noelle (2017) for days to 50% silking and ear aspect and Mosa *et al.* (2016) for ear length, number of rows per ear and number of kernels per row found significant SCA x location interaction. Non-significant interaction effect of SCA x location for all studied traits indicates that similar trend of SCA variation across locations and selection of best performing hybrids across locations was possible. The GCA x location mean squares were higher than that of SCA x location for all studied traits, indicating additive gene action was more affected by location than non-additive, and selection would be effective if based on more locations.

Regarding broad sense heritability estimates, days to 50% anthesis, days to 50% silking, plant height, ear height, ear position and ear length revealed higher heritability (Table 4). Nzuve *et al.* (2014) and Noor *et al.* (2017) also reported comparable results for days to 50%

anthesis and silking, and plant and ear height. On the other hand, number of ear per plant (58.43%), anthesis silking interval (34.45), ear aspect (50.85%), ear diameter (53.85%) and number of kernels row per ear (48.34%) and 1000 kernel weight (39.72%) showed medium broad sense heritability.Similarly, Aminu *et al.* (2014) found medium broad sense heritability estimate for anthesis silking interval, 1000 kernel weight and ear per plant. Grain yield and number of kernels per row had low broad sense heritability with values of 28.19% and 26.49%. On contrary, Nzuve *et al.* (2014), Bikal *et al.* (2015), Noelle (2017) and Pandey *et al.* (2017) reported high broad sense heritability estimate for grain yield. Medium to high heritability values indicates higher genetic expression and minimum location influence which could be important for successful selection of superior crosses. However, traits with low heritability imply higher location influence and low genetic expression which might be difficult for phenotypicalselection. Particularly, for grain yield considering secondary traits during selection would be effective in improving grain yield. Medium to high broad sense heritability estimate coupled with greater proportional contribution of additive gene action indicates variations were transmitted to the progeny and possibility of improving trait of interest through selection.

4.3   Estimate of general and specific combining ability effects

Following the significance of line, tester and line x tester mean squares for studied traits the general and specific combining ability were computed.

4.3.1 General combining ability effect

Estimates of *gca* effects of 24 inbred lines and two testers for combined data of yield and yield related traits are presented in Table 5. Significant variation was observed among twenty four inbred lines and two testers for *gca* effects of traits evaluated across locations. Out of 24 lines, three of them had positive and highly significant *gca* effects and six lines exhibited negative and significant ($p<0.01$, or $p<0.05$) *gca* effects for grain yield. Line L23 showed maximum *gca* effect (1.64t ha^{-1}) followed by L11 (1.50t ha^{-1}), whereas L13 revealed lowest *gca* effect (-1.57t ha^{-1}) followed by L3 (-1.31t ha^{-1}). This depicts the presence of best and poorest general combiners in the group of the studied inbred lines. L23, L11 and L15 found to be good general combiners suggesting their ability to transmit additive genes in desirable direction for grain yield. L3, L7, L13, L21, L18 and L19 found to be poor general

combiners as they had tendency to reduce grain yield. Among the testers, FS59 revealed significantly positive *gca* effect. Several researchers (Melkamu, 2013; Tessema *et al.*, 2014; Girma *et al.,* 2015; Natol, 2017) reported both positive and negative significant *gca* effects for maize grain yield in different set of materials. High GCA effects are attributed to additive or additive x additive gene effects which denote the fixable genetic components of variance (Griffing, 1956). The inbred lines with good general combining ability can make complementary single cross which can be used as seed parent for three-way or double cross hybrid development.

Table 5a.Estimates of general combining ability (*gca*) effect of lines and testers for yield and yield related traits across two locations, 2017.

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

Table 5b. Estimates of general combining ability (*gca*) effect of lines and testers for yield and yield related traits across two locations, 2017.

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

**Significant (p<0.01), *significant (p<0.05) using t-table, L=line, T=tester, SE= standard error, GY=grain yield, AD=anthesis days, SD=silking days, ASI=anthesis silking interval, PH=plant height, EH=ear height, EPO=ear position.EPP=ear per plant EA=ear aspect EL=ear length ED=ear diameter, KRPE=kernel rows per ear, KPR=kernels per rows, TKW=thousand kernels weight.

For days to 50% anthesis and silking, *gca* effects of inbred lines ranged from -2.81 to 2.70 days and -2.89 to 3.49 days (Table 5), respectively. L3, L7, L10, L13, L14 and L22 showed positive *gca* effects, while lines L1, L4, L5, L9 and L18 had negative *gca* effects for both traits. Similarly, Shushay *et al.* (2013), Praveen *et al.* (2014) and Yazachew *et al.* (2017)

found significant and positive, and negative lines *gca* effects. Lines *gca* effect for anthesis-silking interval ranged from -1.41 (L12) to 1.06 (L3) and tester *gca* effects for anthesis-silking interval were -0.5 d (T2) to 0.5 d (T1). Despite the importance of negative *gca* effects for anthesis-silking interval, only L12 was found to be good general combiner. Similarly, Sentayehu and Warsi (2015) reported significant positive and negative lines *gca* effects for anthesis-silking interval. In contrast, Ali *et al.* (2012) reported that none of the parents used in their study had desirable general combining ability for anthesis-silking interval. Negative and significant line *gca* affects for days to 50% anthesis and silking, and anthesis silking interval suggests the possibility of exploiting favorable genes for earliness to maturity and narrower anthesis silking interval in future breeding work. Similarly, Sundararajan and Kumar (2011) and Demissew (2014) suggested the importance of the negative *gca* effects for days to 50% anthesis and silking to develop early maturing varieties.

For plant and ear height, L1, L5, L10, L12, and L14 revealed positive and significant lines *gca* effect, while L2, L8, L13, L18 and L22 showed negative and significant *gca* effects. Inbred lines with negative *gca* effects were good general combiners for plant and ear height, while positive *gca* effects evinced poor general combiners.Similarly, Kamara *et al.* (2014), Praveen *et al.* (2014), Girma *et al.*, (2015), Ahmed *et al.* (2017) found positive and negative significant *gca* effects of inbred lines for plant and ear height; and concluded that shorter plant height with lower ear placement was desirable. Inbred lines with negative *gca* effect had tendency to reduce plant and ear height, hence genotypes with shorter plant height with lower ear placement can be good for lodging resistance. Ji *et al.* (2006) also noted that cultivars with high ear positions are prone to root and stalk lodging and suggested that negative significant lines *gca* effects were desirable for plant and ear height towards shorter stature and lower ear placement.

Significant *gca* effects of inbred lines ranged from -0.37 (L18) to 0.40 (L23) for number of ear per plant, -1.71 (L13) to 2.06 (L15) for ear length, -0.24 (L7) to 0.27 (L10) for ear diameter, -0.83 (L17) to 0.73 (L20) for number of kernel rows per ear and -3.02 (L1) to 2.27 (L4) for number of kernels per rows (Table 5). L1, L9, L23 and L24 for number of ears per plant, L4, L7, L8, L10, L12, L14, L15 and L24 for ear length, L4, L10, L11, L12, L14, L20 and L21 for ear diameter and L8, L10, L11, L14, L20 for number of kernel rows per ear and L4 and L15 for number of kernels per rows showed positive and significant *gca* effects. On the other hand, L4, L8, L13, L18, L20 and L21 for number of ears per plant, L1, L9, L11,

L13 and L19 for ear length, L1, L7, L16, L17, L19, L22, L23 and L24 for ear diameter, L2, L5, L16, L17, L21 and L22 for number of kernel rows per ear and L1, L3 and L9 for number of kernels per row revealed negative and significant line *gca* effect. Similarly, EL-Gazzar *et al.* (2013), Tessema *et al.* (2014), Mohamed *et al.* (2014) and Yazachew *et al.* (2017) also reported that certain inbred lines with good general combing ability and suggested the possibility of improving these traits through selection. The present study also identified inbred lines with good general combing ability which could be used for the improvement of traits of interest as these lines had potential to transfer favorable genes to their progenies.

The range of lines *gca* effect for 1000 kernels weight varied from -45.84 gm (L7) to 77.36 gm (L21). Inbred lines L11, L14, L21 and L22 had positive and significant line *gca* effects, while L2, L7, L9, L13, L15 and L19 showed negative and significant line *gca* effects. Hence, L11, L14, L21 and L22 were good general combinersand had favorable allele frequency for developing varieties with heavy grain weight. Similar to the current finding, Wali *et al.* (2010) and Ahmed *et al.* (2017) found positive and negative and significant line *gca* effect for 1000 kernel weight.

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

4.3.2   Specific combining ability effect

Estimates of specific combining ability (*sca*) effects for grain yield and yield related traits for all hybrids computed across locations are presented in Table 6. SCA effect was computed for traits that showed significant difference in line x tester analysis (Table 6). Crosses L2 x T1 (1.03), L3 x T1 (1.04), L8 x T1 (1.10), L11 x T1 (1.14), L13 x T2 (1.64) and L23 x T1 (1.64) were exhibited significant positive *sca* effects for grain yield. Crosses like L2 x T2 (-1.03), L3 x T2 (-1.04), L8 x T2 (-1.10), L11 x T2 (-1.14), L13 x T1 (-1.64) and L23 x T2 (-1.64) found to be poor specific combiners which could be due to the presence of unfavorable gene combinations in the parents.

Table 6a. Estimates of specific combining abilities of line x tester for yield and yield related traits across two location, 2017

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

Table 6b. Estimates of specific combining abilities of line x tester for yield and yield related traits across two location, 2017

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

**highly significant (p<0.01) using t-table, SE=standard error of difference, **highly significant (p<0.01),*significant (p<0.05), using t-table, SE = standard error of difference, GY=grain yield, AD=anthesis days, SD=silking days, PH=plant height EH=ear height, EP =ear position, EPP=ear per plant , EA=ear aspect, EL=ear length, ED=ear diameter, KRPE=kernel rows per ear, KPR=kernels per rows, TKW=thousand kernels weight.

The results were in agreement with the findings of Girma *et al.* (2015), Ahamed *et al.* (2017) and Natol (2017) who reported both positive and negative and significant specific combining ability (*sca*) for grain yield. The positive *sca* effects indicate lines were from opposite heterotic group, while negative sca affects refer lines were from the same heterotic group. The crosses with positive and significant *sca* effects found to be good specific combiners for developing high yielding hybrids. However, high *sca* effects for grain yield were not consistent with high yield performance which was in agreement with the finding of Gichuru *et al.* (2011). For instance, cross L2 x T1 showed significant positive *sca* effect, but

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had lower grain yield than standard checks. The high positive and significant *sca* effects were manifested by crosses of low x low (L13 x T2 and L3 x T2), low x high (L2 x T1 and L8 x T1) and high x high (L23 x T1, L11 x T1), indicating the presence of complementary gene action for grain yield. Inbred lines L3, L2, L13 and T2 had poor general combining ability, but resulted in hybrids with higher *sca* effects for grain yield. This signifies that inbred lines with poor general combining ability might produce better hybrids depending on the other parent with which it combines.

The *sca* effects of days to 50% anthesis (AD) and silking (AD) ranged from -1.98 (L16 x T1) to 1.98 (L16 x T1) and -2.14 (L21 x T2) to 2.14 (L22 x T1), respectively. Crosses such as L13 x T2, L16 x T1 and L21 x T2 revealed negative and significant *sca* effects for days to 50% anthesis and silking, while L13 x T1, L16 x T2 and L21 x T1 showed positive *sca* effects. Dange *et al*. (2010), Izhar and Chakraborty (2013) and Kage *et al*. (2013) and Girma *et al*. (2015) also found positive and negative *sca* effects for days to 50% anthesis and silking in different set of materials. Crosses with negative and significant *sca* effects for these traits are considered as good specific combiners, which indicate the earliness of the hybrids. On the other hand, crosses with positive and significant *sca* effects were found to be poor specific combiners, mainly for highland condition due to lateness. Inbred lines with negative and significant *gca* effects did not necessarily produced crosses with negative and significant *sca* effects. But, tester FS59 had negative and significant *gca* effect and interacted well with L21 and L13 in cross combination thereby resulted in crosses with negative and significant *sca* effects. The interactions involved in the crosses were poor x good general combiners (L13 x T1 and L21 x T1) and poor x poor (T16 x T2).

Crosses L9 x T1, L16 x T2 and L21 x T1 had negative and significant *sca* effects for plant and ear height considered as good specific combinations. These crosses involved parents with general combiners of good x poor, poor x good and poor x poor *gca* effects. L13 x T2, L16 x T1 and L21 x T2 for plant height and L9 x T2, L10 x T1, L12 x T2, L16 x T2 and L21 x T1 for ear height showed positive and significant *sca* effects, indicating that these crosses were poor specific combination for these traits. Similarly, Ali *et al*. (2012), Aly (2013), Shushay (2014) and Tolera *et al*. (2017) reported both positive and negative and significant *sca* effects in maize crosses for plant height and ear height. Accordingly, good specific combination could be utilized in developing lodging resistance hybrids. Positive *sca* effects for plant and ear height indicates crosses had tendency to increase height in undesirable

direction. Besides, too lower ear placement may expose to animal attack there by affect the quantity and quality of final grain yield.

Crosses L8 x T1 for number of ears per plant, L9 x T1, L10 x T2 and L14 x T1 for ear length and L11 x T2 for number of kernels per row had significant and positive *sca* effects. The crosses involved parent interaction of poor x poor, good x poor and good x poor based on their *gca* effects. L8 x T2 for number of ears per plant, L9 x T2, L10 x T1 and L14 x T2 for ear length and L11 x T1 for number of kernels per row showed significant and negative *sca* effects. This indicates the crosses were poor specific combiners which could be due to the presence of unfavorable gene combinations in the parents. Contrarily, Dufera *et al.* (2018) found non-significant *sca* effect for number of ear per plant using different set of genotypes. The crosses exhibiting significant and positive *sca* effects were considered as good specific combiners. On other hand, crosses that showed significant and negative *sca* effects found to be poor specific combiners. Moreover, crosses with positive and significant *sca* effects also had inbred lines with positive (L10 and L14) and negative (L9) *gca* effect. The results were in agreement to the findings ofIzhar and Chakraborty (2013), Praveen *et al.* (2014) and Liaqat *et al.* (2015) who reported positive and negative significant *sca* effects for ear length and number of kernels per row.

Finally, based on the *gca* effects of parents, and *sca* effects hybrids for different traits, it is evident that high specific combinations involved, Inbred lines with high x high, high x low and low x low *gca* effects. The *sca* effects of crosses combinations exhibited no specific trends in cross combinations between parents having good and poor *gca* effects. This indicates high specific combiners were not only obtained from the combination of good x good general combiners, but also resulted from good x poor and poor x poor general combiners. The superiority of hybrids resulted from the crosses of high x low combiners could be due to interactions between positive alleles and negative alleles from good and poor combiners, respectively. The best performance of these combination may be caused by additive x additive (high x high), additive x dominance (high x low), or dominance x dominance (low x low) gene interactions (Milic *et al.*, 2011; Dey *et al.*, 2014; Chigeza *et al.*, 2014; Talukder *et al.*, 2016). Zhang *et al.* (2015) suggested that hybrids with high *sca* effects from parents with low *gca* effects might be primarily due to non-additive gene action which includes dominance and epistasis. For some of the studied traits, high *gca* effect parents resulted from hybrids with low *sca* effect which might be due to the lack of complementary

of gene action. On the other hand, low *gca* effect parents produced hybrids with high *sca* effects which might be caused by complementation of gene actions. Generally, the crosses identified were best specific combiners for yield and yield related traits which can be used in the heterosis breeding.

4.4   Heterotic Grouping

Heterotic grouping of twenty four (24) inbred lines based on their grain yield *sca* effects across location are presented in Table 7. 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). Inbred lines showing positive *sca* effects with FS59 and exhibiting negative SCA effects with FS67 were assigned into heterotic groups "B". Inbred lines showing positive SCA effects with FS67 and negative effects with FS59 were grouped into heterotic group "A". Hence, based on *sca* effects for grain yield inbred lines were separated in to two heterotic groups.

Table 7. Heterotic grouping of 24 inbred lines corresponding to testers

Lines	FS59 (Group ''A'')	*sca* effects	FS67 (Group ''B'')	*sca* effects	Heterotic Grouping	lines *gca* effects
L1	8.17	-0.14	7.77	0.13	A	0.45
L2	8.59	1.03*	5.86	-1.03*	B	-0.30
L3	5.51	-1.04*	6.91	1.04*	A	-1.31**
L4	7.61	-0.17	7.28	0.17	A	-0.08
L5	8.89	0.30	7.60	-0.31	B	0.72
L6	7.79	0.56	5.99	-0.56	B	-0.64
L7	6.42	-0.58	6.91	0.58	A	-0.86*
L8	8.89	1.10*	6.02	-1.10*	B	-0.07
L9	8.43	0.18	7.40	-0.18	B	0.39
L10	7.82	-0.72	8.59	0.72	A	0.68
L11	9.51	1.14*	8.55	-1.14	B	1.50**
L12	8.58	0.34	7.22	-0.34	A	0.37
L13	4.65	-1.64**	7.25	1.64**	A	-1.57**
L14	8.72	0.55	6.95	-0.55	B	0.31
L15	9.08	-0.04	8.49	0.04	A	1.26**
L16	8.85	0.94	6.30	-0.94	B	0.05
L17	7.05	-0.73	7.83	0.72	A	-0.08
L18	7.60	0.53	5.87	-0.53	B	-0.78*
L19	6.76	0.03	6.03	-0.03	A	-1.13**
L20	8.37	0.29	7.11	-0.30	B	0.22
L21	6.15	-0.56	6.60	0.56	A	-1.15**
L22	7.53	-0.17	7.19	0.17	B	-0.16
L23	10.13	1.64**	8.19	-1.64**	B	1.64**
L24	7.56	-0.87	8.63	0.87	A	0.57
Mean	**7.86**		**7.19**			

*significant (p<0.05), **highly significant (p<0.01), *sca*= specific combining ability, *gca*=general specific combining ability

Lines such as L2, L5, L6, L8, L9, L11, L14, L16, L18, L19, L20 and L23 exhibited negative SCA effects with FS67 and belonged to heterotic group ''B''. Inbred lines L1, L3, L4, L7, L10, L12, L13, L15, L17, L21, L22 and L24 exhibited negative SCA effects with FS59 and belonged to heterotic group''A''. Likewise, Tolera *et al.* (2017) and Girma *et al.* (2015) classified different set of inbred lines into different heterotic groups on the basis of grain yield SCA values. Classification of inbred lines into heterotic groups would facilitate exploitation of heterosis and lead to development of high yielding maize hybrids. Heterosis can be maximized by crossing the above inbred lines belonging to different heterotic groups. On the other hand, inbred lines in same heterotic group could be used for development of synthetic varieties. Besides, lines in different heterotic group could assist breeders to avoid development and evaluation of crosses that should be discarded.

4.5   Estimate of Standard Heterosis

The estimates of standard heterosis over the standard checks were computed for combined data of grain yield and yield related traits that showed significant difference among genotypes (Appendix VII). The magnitude of standard heterosis over Kolba and Jibat for grain yield and the values ranged from -40.31 (L13 x T1) to 32.44% (L23 x T1). The cross L23 x T1 (32.44%) exhibited maximum standard heterosis for grain yield followed by L11 x T1 (22.18%). Nine crosses showed negative significant standard heterosis over the best hybrid check (Kolba) for grain yield, while two crosses revealed positive and significant standard heterosis. Several scholars (Amiruzzaman *et al.,* 2010; Kustanto *et al.*, 2012; Hiremath *et al.*, 2013; Melkamu *et al.*, 2013; Habtamu, 2015; Bitew, 2016; Gemechu *et al.*, 2017; Ziggiju *et al.*, 2017) reported positive and negative significant standard heterosis for grain yield. High level of heterosis observed in the current study could be mainly because of the involvement of more distant related inbred lines. Fato (2010) and Hallauer and Miranda (1988) also suggested that full exploitation of heterosis requires crossing of distantly related materials. The crosses with higher grain yield standard heterosis also had positive significant *sca* effects (Table 5 and 6). Natol (2017) also found that crosses with high standard heterosis also had good specific combining ability. In contrast, Kumar and Babu (2016) reported crosses with good specific combining ability effects, but non-significant standard heterosis for grain yield. The difference in these findings might be due to the influence of environmental factors and tested materials.

The standard heterosis for days to 50% anthesis, days to 50% silking and anthesis silking interval ranged from 0 to 8.75%, -1.21 to 8.11% and 1.68 to -13.14% (Appendix VII), respectively. The current study found none of crosses with significant standard heterosis for days to 50% anthesis and silking towards the desirable direction, which was in agreement to the findings of Dufera *et al.* (2017). This states the lack of genetic divergence among crosses for selection of early flowering materials. However, Ram *et al.* (2015), Patil *et al.* (2017) and Natol *et al.* (2017) found negative and significant standard heterosis for days to 50% anthesis and suggested that earliness is a desirable character. For anthesis-silking interval, crosses L6 x T1, L9 x T2, L11 x T2, L12 x T2, L19 x T2 and L22 x T1 revealed negative and significant standard heterosis with respective values of -6.99%, -10.38%, -8.09%, -11.58, -10.38 and -9.22.Negative heterosis for anthesis-silking interval is desirable as it is indicates in pollen shedding and silk receptive synchronization, thereby increase seed set.

The magnitude of standard heterosis for plant height ranged from -19.96 (L18 x T2) to 13.15% (L5 x T1) and for ear height ranged from -24.18 (L23 x T2 and L24 x T2) to 36.78% (L12 x T2) (Appendix VII). Ten (10) crosses had positive and significant heterosis, while twenty two (22) crosses showed negative and significant standard heterosis for plant height over the best standard checks, respectively.For ear height, 9 and 27 crosseshad positive and negative and significant standard heterosis over the best standard check, respectively. Various workers (Melkamu *et al.,* 2013; Melkamu, 2014; Hailegebrial *et al.,* 2015; Natol, 2017) also found positive and negative significant standard heterosis for plant and ear height. So, crosses with shorter plant and ear height over the standard checks are desirable for lodging resistance and mechanical harvesting. Natol *et al.* (2017) and Yazachew*et al.* (2017) also suggested negative standard heterosis for plant and ear height is in desirable. However, Sharma *et al.* (2017) reported the desirability of for ear height negative standard heterosis, while for plant height either negative or positive. Hence, the negative heterosis for plant and ear height is desirable enable the selection of effective shorter plant, with reduction of lodging.

Estimate of standard heterosis ranged from -18.80 (L8 x T2) to 48.57% (L23 x T1) for number of ear per plant, -23.47(L9 x T2) to 21% (L15 x T2) for ear length and -13.54 (L7 x T2) to 9.36% (L10 x T1) for ear diameter. The positive standard heterosis for these traits is in a desirable direction. For number of ears per plant, 26 crosses showed positive and significant standard heterosis over hybrid standard checks. Regarding ear length, only L15 x

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T1 cross showed positive and significant standard heterosis over Kolba. Shushay (2014) and Arsode *et al.* (2017) for number of ear per plant, Raghu *et al.* (2012) and Asif *et al.* (2014) for ear length found comparable results to the current findings. Though ear diameter revealed significantly positive and negative standard heterosis, none of the crosses had wider ear diameter than the best standard checks (Kolba). The positive standard heterosis, *sca* and *gca* effects for number of ear per plant and ear length indicates possibilities of breeding maize for increasing number of ears per plant and ear length thereby improve grain yield.

Standard heterosis for number of kernel rows per ear, number of kernels per row and 1000 kernels weight varied from -8.02 (L21 x T2) to 13.52% (L11 x T1), -17.04 (L9 x T2) to 5.77% (L15 x T1) and -33.76 (L19 x T1) to 27.64% (L21 x T2), respectively. For number of kernels row per ear, twelve crosses exhibited positive and significant standard heterosis over best hybrid check (Kolb). Maximum positive standard heterosis for number of kernels row per ear was recorded for cross L11 x T1 (13.52%) followed by L20 x T1 (12.16%). This indicates increased number of kernels row per ear as compared to the standard checks would be increase grain yield. As to the number of kernels per row and 1000 kernel weight, none of the crosses had positive and significant standard heterosis over the standard checks. This signifies the non-availability of variation among genotypes investigated for these traits. But, Reddy *et al.* (2011), Gemechu *et al.* (2017) and Patil *et al.* (2017) found positive and negative and significant standard heterosis for number of kernels per row and 1000 kernel weight and indicated the possibility of exploitation of the crosses for commercial release.

According to Singh (2015) heterosis was positively correlated with genetic distance and specific combining ability. In line with this, crosses with higher standard heterosis for certain traits could be the result of divergent inbred lines and higher *sca* effects. Heterosis over standard checks helps in either a hybrid variety would be accepted or rejected for commercial cultivation. Ram *et al.* (2015) suggested that over 20% of standard heterosis has high commercial value. L23 x T1 and L11 x T1 crosses proved to be outstanding in grain yield over the best hybrid check (Kolba) with standard heterosis value of 30.70% and 22.18%, respectively. Devi and Singh (2011) suggested that appearance of crosses could be predicted based on the relationship between mean of grain yield, heterosis and specific combining ability. The best performing crosses might indicate the recovery of vigor that was lost during inbreeding as functional gene often absent. These crosses also had high per se performance and positive *sca* effects. Hence, they are ready for further evaluation in

different location and commercial use. Furthermore, for traits with inferior performance in these crosses breeders may improve via accumulation of favorable alleles from other good performing crosses for the trait of interest.

4.6   Correlation and Path Coefficients

Genotypic and phenotypic correlations among significant traits for F_1 hybrids analyzed from the combined data over the two locations shown in table 8. Ratner (2009) categorized the Pearson correlation coefficient as weak, moderate and strong for values ranging from 0 to ±0.29,±0.3 to ±0.69 and ±0.7 to ±1.0, respectively. Grain yield exhibited positive and significant genotypic and phenotypic correlations with plant height, ear height, ears per plant and number of kernels per row (Table 10). The results are in accordance to the finding of Pavan *et al.* (2011), Kumer *et al.*, (2014), Hailegebrial *et al.* (2015), and Pandey *et al.* (2017). In contrast, Zorana *et al.* (2011) and Silva *et al.* (2016) reported negative of correlations for grain yield with plant and ear height.

Tall plant with higher ear placement increases grain yield due to high number of leaves possessed and stem reserve mobilization which is in agreement to the findings of Zeeshan *et al.* (2013) and Al-Tabbal *et al.* (2012). Moreover, ear length, ear diameter and number of kernel rows per ear showed positive significant genotypic and phenotypic correlation with grain yield, which is in conformity to the findings of Izzam *et al.* (2017) and Wuhaib*et al.* (2017). Positive genotypic correlations for these traits imply the presence of moderate inherent relationship, thereby discloses the improvement of maize grain yield was linked with the selection for these traits. Grain yield exhibited negative and significant genotypic and phenotypic correlation with days to 50% anthesis and silking, anthesis silking interval which is analogous to the findings of Raghu *et al.* (2011), Munawar *et al.* (2013), Kumer *et al.* (2014) and Pandey *et al.* (2017). On the contrary, Dagne (2008) and Dar *et al.* (2015) found positive and significant phenotypic correlations for grain yield with days to 50% anthesis and silking. The negative genotypic association of days to flowering with grain yield implies that these traits are not co-inherited together with grain yield. Narrow anthesis silking interval period would increase grain yield due to the synchronization of pollen shedding and silking emergence.

Highly significant positive genotypic and phenotypic correlations observed between days to 50% anthesis and silking (rg=0.91**, rp=0.99**) which are in conformity to the findings of Nataraj *et al*. (2014),Hailegebrial *et al.* (2015) and Hussain *et al*. (2015). This infers jointly improvement of these traits could be possible due to positive genotypic correlation. Negative and significant genotypic and phenotypic correlations obtained between days to 50% silking and 1000 kernel weight which are in agreement with the finding of Kumar *et al*. (2015). In contrast, Nataraj *et al*. (2014) and Varaprasad *et al*. (2016) found positive and significant genotypic and phenotypic correlation for days to 50% silking with 1000 kernel weight. Such differences might be attributed to the differences in locationsused and the genetic make-up of studied materials (Iqbal*et al.*, 2011). Based on the current findings, early silking could be responsible for timely pollination and grain filling thereby increase weight of the kernels.Zhou *et al*. (2017) confirmed that climate variation from silking to maturity were the main factors affecting kernel weight.

Plant and ear height had positive and significant genotypic correlation with ear position, ear diameter and number of kernel rows per ear, which indicates that increase in plant and ear height would simultaneously increase these traits. These results support the findings of Mathew (2015), Singh *et al*. (2017) and Prasad and Shivani (2017). Number of ear per plant had negatively significant genotypic and phenotypic correlation with ear diameter, number of kernel rows per row and 1000 kernel weight which confirms the finding of Ziggiju *et al.* (2015). Eleweanya *et al*. (2005) suggested that positive associations among traits indicate positive responses in the levels of one character when the other is selected, while the negative signify the reverse situation. Magnitudes of genotypic correlations were relatively higher than phenotypic one for most of studied traits which indicates presence of greater inherent relationship among the traits which allows simultaneous improvement of these traits. Hallauer *et al*. (2010) noted the more importance of genetic correlation as it represents the heritable fraction of parent characters to progeny.

Table 8. Genotype and phenotype correlation coefficients for yield and yield related traits of 48 hybrids evaluated across two locations, 2017.

Traits	GY	AD	SD	ASI	PH	EH	EPO	EPP	EL	ED	KRPE	KPR	TKW
GY	**1.00**	-0.21**	-0.14*	0.25**	0.48**	0.37**	0.02	0.56**	0.24**	0.20**	0.22**	0.38**	-0.03
AD	-0.17*	**1.00**	0.91**	-0.19*	-0.07	0.08	0.30**	-0.06	0.04	0.08	0.33**	-0.06	-0.08
SD	-0.18*	0.99**	**1.00**	0.49	0.08	0.20**	0.31**	-0.01	0.05	0.04	0.33**	-0.06	-0.14*
ASI	-0.14*	0.59**	0.58**	**1.00**	0.26**	0.23**	0.09	0.07	0.04	-0.05	0.08	-0.02	-0.12
PH	0.40**	-0.08	-0.07	-0.01	**1.00**	0.90**	0.34**	0.26**	0.14*	0.35**	0.33	0.15*	-0.23**
EH	0.32**	-0.24**	-0.23**	-0.17*	0.81**	**1.00**	0.72**	0.13	0.11	0.38**	0.33**	0.09	-0.01
EPO	0.04	-0.33**	-0.34**	-0.29**	0.16*	0.65**	**1.00**	-0.12	0.03	0.25**	0.19**	-0.03	-0.03
EPP	0.44**	0.29**	0.27**	0.20**	0.20**	0.05	-0.18*	**1.00**	-0.12	-0.30**	-0.01	-0.05	-0.24*
EL	0.17*	0.06	0.07	0.09	0.08	0.03	-0.04	-0.07	**1.00**	0.06	0.04	0.72**	0.05
ED	0.20**	-0.34**	-0.33**	-0.33**	0.23**	0.33**	0.25**	-0.31**	-0.23**	**1.00**	0.52	0.15*	0.25**
KRPE	0.21**	0.30**	0.27**	0.12	0.18*	0.15*	0.02	0.08	-0.21**	0.28**	**1.00**	0.14*	-0.28**
KPR	0.33**	-0.10	-0.12	-0.05	0.08	0.11	0.09	-0.14*	0.02	0.09	0.38**	**1.00**	-0.08
TKW	0.18*	-0.58**	-0.58**	0.1	-0.05	0.05	0.14	-0.29**	-0.14*	0.43**	-0.25**	0.04	**1.00**

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

Estimates of direct and indirect effects towards grain yield for individual traits with significant correlation are presented in Table 9. Lenka and Mishra (1973) categorized the path coefficient into negligible (0.00-0.09), low (0.1-0.19), moderate (0.2-0.29), high (0.3-1) and very high (>1). Based on this, days to 50% silking, number of ears per plant, ear diameter, number of kernels per row and number of kernel rows per ear exerted higher positive direct effect towards grain yield. Similar findings were reported by Rafiq *et al.* (2010) and Raghu *et al.* (2011) for number of kernels per row and ear diameter, Pavan *et al.* (2011) for days to 50% silking and number of kernel rows per ear and Reddy *et al.* (2013) for number of ear per plant.

Table 9. Direct (diagonal) and indirect effect of genotypic path coefficient among yield and yield related traits of 50 maize hybrids evaluated at two locations, 2017.

TRAIT	AD	SD	ASI	PH	EH	EPP	EL	ED	KRE	KPR	RGY
AD	**-0.50**	0.48	0.01	0.01	0.03	-0.03	0.00	0.07	-0.24	-0.02	-0.19
SD	-0.45	**0.52**	0.00	-0.04	0.06	-0.08	0.00	0.11	-0.33	0.05	-0.16
ASI	0.09	-0.04	**-0.04**	-0.03	0.03	-0.04	-0.01	-0.11	0.06	-0.14	-0.25
PH	0.02	0.07	0.00	**-0.30**	0.22	0.28	-0.01	0.35	-0.25	0.13	0.52
EH	-0.06	0.12	0.00	0.26	**0.25**	0.15	0.00	0.36	-0.25	0.08	0.38
EPP	0.01	-0.04	0.00	-0.08	0.03	**1.08**	0.00	-0.29	0.02	-0.18	0.57
EL	-0.01	0.06	-0.01	-0.05	0.03	-0.14	**-0.04**	0.06	-0.04	0.36	0.22
ED	-0.04	0.06	0.01	-0.11	0.09	-0.32	0.00	**0.95**	-0.38	-0.06	0.20
KRPE	-0.17	0.25	0.00	-0.10	0.09	-0.03	0.00	0.52	**0.70**	0.37	0.22
KPR	0.01	0.03	0.01	-0.04	0.02	-0.21	0.21	-0.06	-0.28	**0.92**	0.38
					Residual Effect(U) = **0.22**						

AD=anthesis days SD=silking days ASI=anthesis silking interval PH=plant height, EH=ear height, EPP=ear per plant, EL=ear length, ED=ear diameter, KRPE=kernel rows per ear, KPR=kernels per rows

Though plant height and ear length had positive genotypic correlation, they exerted negative direct effect towards grain yield. Similar results were reported by Selvaraj and Nagarajan (2011) for plant height, Zarei *et al.* (2012) for days to 50% anthesis and Bullo (2015) for ear length. In contrast, Praveen (2013), Poudel *et al.* (2016) and Varaprasad *et al.* (2016) found that days to 50% anthesis, plant height and ear length with positive direct effect. Positive higher indirect effect on grain yield was obtained from days to 50% silking via days to 50% anthesis, ear diameter via number of kernel rows per ear, plant height, ear height, and number of kernels per row via ear length and number of kernel rows per ear. Satyanvesh (2016) also found positive indirect effect from number of kernels per row through ear length and number of kernel rows per ear. Furthermore, higher, negative indirect effects on grain

yield noted for days to 50% anthesis via days to 50% silking, number of ear per plant through ear diameter, and number of kernels per row via days to 50% silking. The contrasting findings could be due to the difference of materials and environments encountered. Finally, number of ear per plant, ear diameter, number of kernel rows per ear, number of kernels per rows and ear height excreted positive direct effect and they are good indicators in indirect selection for higher grain yield.

Residual effect, determines how best the causal variables (anthesis days, silking days, anthesis silking interval, plant height, ear height, ear per plant, ear length, ear diameter, number of kernel rows per ear and kernels per row). Its estimate of 0.22 indicated that the causal variables explained about 78% of the variability in grain yield and only 22% of the variability remained unexplored.

5 SUMMARY AND CONCLUSION

The study aimed to estimate combining ability, standard heterosis, trait association, heritability, and classify inbred lines to heterotic groups for evaluated maize single cross hybrids. During 2016/2017 cropping season, 48 maize single crosses and two hybrid commercial check hybrids were evaluated in alpha lattice design with two replications at Ambo and Holetta Agricultural Research Centers. Data were collected on days to 50% anthesis and silking, anthesis-silking interval, plant and ear height, ear position, number of ears per plant, ear length, ear diameter, ear aspect, plant aspect, number of kernel rows per ear, number of kernels per row and 1000 kernels weight were subjected to analysis of variance.

Analysis of variance revealed the presence of significant variation among the genotypes for all studied traits except for plant aspect. Mean square of entry x location interaction for most of studied traits showed non-significant, indicating that hybrid performance was consistent across locations. Nevertheless, genotype by location interaction was significant for some traits, suggesting further evaluation of selected genotypes over a number of locations. Mean squares of GCA and SCA were significant for most of studied traits, indicating that both additive and non-additive gene action were involved in the control of the inheritance of these traits. However, the proportional contribution of GCA effect was higher and GCA/SCA ratio was greater than unit for all studied traits, suggesting that additive gene action was more important than non-additive gene action for these traits. Moreover, mean square of GCA line x location and GCA tester x location interaction were significant ($p<0.01$ or $p<0.05$) for most studied traits, while mean square of line x tester x location interaction were non-significant. This indicates that the effects of lines and testers were different under different locations for the traits where their interaction effectswere significant traits, while lines x tester interaction showed similar trends of variations across locations.

Furthermore, all traits had medium to high broad sense heritability estimates except grain yield and number of kernels per row that depicted higher genetic expression which enable breeders to select of superior crosses based on phenotypic performances. The high to medium heritability coupled with higher proportional contribution of GCA effects and GCA/SCA ratio of greater than unit, indicated the preponderance of additive gene action which enable breeders to improve the maize genotypes for these traits via selection. Ears per

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plant, ear height, ear diameter, kernel rows per ear and kernels per row had positive association with grain yield and exerted positive direct and indirect effects on grain yield, thereby suggesting simultaneous improvement of these and grain yield could be possible.

Estimation of *gca* effects identified lines with which were good general combiners for studied traits. Accordingly, inbred lines L23, L11 and L15 for grain yield, L12 for anthesis silking interval, L2, L18 and L19 for plant height, L13, L22, L23 and L24 for ear height, L1, L9, L23 and L24 for number of ears per plant,L7, L8, L14 and L15 for ear length, L4, L10, L11 and L20 for ear diameter, L8, L14 and L20 for number of kernels row per ear, L4 and L15 for number of kernels per row and L11, L12 and L21 for 1000 kernels weight were the top good general combiners. Tester FS59 was a good general combiner for grain yield, ear diameter and number of kernels rows per ear while tester FS67 was a good general combiner for days to 50%, anthesis silking interval, plant height, ear height and 1000 kernels weight. As to estimation of *sca* effects, crosses such as L11xT1, L13xT2 and L23xT1 for grain yield, L13xT1, L16xT2 and L21x T1 for plant height, L12xT2, L16xT2 and L21xT2 for ear height, L6xT2 for number of ear per plant, L9xT1, L10xT2 and L14xT1 for ear length and L11xT2 for number of kernels per row revealed good specific combining ability. Based on the *sca* effects twelve inbred lines were grouped under belonged to heterotic group ''A'' and the other twelve were under heterotic group ''B'', which could be used to exploit maximum heterosis by avoiding weak crosses. The inbred lines with general combining ability and crosses with specific combining ability in the desired direction could be exploited to develop hybrid and synthetic varieties. The level of standard heterosis were high in certain crosses for traits like grain yield, plant and ear height, ear per plant, ear length and number of kernels per ear. Crosses L11xT1 and L23xT1 revealed significant and positive standard heterosis for grain yield and some yield related traits over commercial hybrid checks. Based on the findings of the current study the following conclusions have been drawn;

- L11xT1 and L23xT1 crosses were superior hybrids for grain yield and some yield related components and should be used for single cross hybrids or parents for three ways cross hybrids development after further evaluation across multi-locations.

- Inbred lines with desirable general combining ability effects for traits of interest can be effectively used in maize variety development program.

- Lines belonged to different heterotic groupscould be used to develop superior hybrid or create genetic variability for future breeding activities.

- Population improvement through accumulating the fixable gene could be possible as medium to high heritability and greater proportional contribution of additive gene action as compared to non-additive gene action were identified for most of traits.

- Finally, the information from this study may possibly be useful for researchers who would like to develop high yielding varieties of maize.

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7 APPENDICES

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

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

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

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

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

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

Appendix III. Mean performances of 48 testcrosses and two hybrid checks of maize for yield and yield related traits at Holetta, 2017

ENTRY	GY	AD	SD	ASI	PH	EH	EPO	EPP	EA	EL	ED	KRPE	KPR	TKW
L1xT1	7.48	110.50	112.50	2.00	279.50	151.50	0.54	1.98	2.75	13.95	4.28	12.35	28.65	272.75
L1xT2	6.27	110.50	112.50	2.00	237.50	118.50	0.50	1.93	3.00	14.00	3.91	12.35	29.00	257.85
L2xT1	8.76	114.50	115.00	0.50	246.50	124.50	0.51	1.83	3.75	15.55	4.26	12.70	31.00	233.85
L2xT2	6.40	110.50	112.50	2.00	199.50	102.50	0.52	1.90	4.00	14.55	3.93	12.65	32.50	255.40
L3xT1	6.85	116.50	119.50	3.00	263.00	143.50	0.55	1.97	3.25	16.25	4.21	13.30	30.65	262.65
L3xT2	5.79	114.50	117.00	2.50	226.00	117.50	0.52	1.66	3.50	13.90	4.25	14.35	28.15	278.60
L4xT1	7.10	110.50	112.50	2.00	275.50	147.50	0.54	1.68	2.75	15.65	4.59	13.65	32.70	298.25
L4xT2	6.37	109.50	112.00	2.50	239.50	116.50	0.49	1.60	2.75	16.50	4.17	12.70	33.00	269.75
L5xT1	9.05	113.00	113.00	0.00	291.00	155.00	0.53	1.86	1.75	16.90	4.29	12.35	34.00	304.50
L5xT2	6.66	110.00	112.00	2.00	252.00	120.00	0.48	1.80	3.50	16.75	4.22	12.00	33.15	288.50
L6xT1	8.41	112.50	112.50	0.00	255.50	140.00	0.55	1.79	2.50	16.00	4.57	13.65	34.50	291.20
L6xT2	6.88	111.50	114.00	2.50	226.00	123.50	0.55	1.79	2.50	15.65	4.35	13.35	31.65	294.75
L7xT1	6.96	113.00	116.00	3.00	263.00	146.50	0.56	1.70	4.00	16.75	4.20	13.65	29.65	238.75
L7xT2	6.13	118.00	118.00	0.00	214.50	120.00	0.56	1.85	3.75	16.85	3.77	12.35	35.00	233.10
L8xT1	8.91	113.50	116.50	3.00	266.00	140.50	0.53	2.00	2.75	16.15	4.24	14.00	34.20	265.85
L8xT2	5.22	113.50	116.50	3.00	207.00	103.50	0.50	1.40	3.75	15.70	4.14	13.30	32.15	297.60
L9xT1	7.18	108.00	111.50	3.50	260.00	127.00	0.49	2.01	4.00	15.25	4.28	13.65	29.30	209.40
L9xT2	7.21	112.00	111.50	-0.50	240.00	115.00	0.48	1.86	3.50	12.15	4.23	13.65	28.50	280.00
L10xT1	9.80	116.00	118.00	2.00	294.00	169.50	0.58	2.08	2.50	15.15	4.68	14.70	32.80	295.45
L10xT2	8.56	114.00	115.50	1.50	236.50	120.00	0.51	1.86	2.50	17.75	4.28	13.35	34.00	247.50
L11xT1	9.14	115.50	118.00	2.50	285.50	168.00	0.59	2.00	4.00	12.15	4.35	14.70	26.80	340.65
L11xT2	7.37	115.00	115.50	0.50	230.00	127.50	0.56	1.66	4.00	14.75	4.16	12.00	32.35	282.75
L12xT1	8.29	118.00	118.00	0.00	300.00	186.00	0.62	1.88	3.75	16.20	4.55	13.70	31.65	301.25
L12xT2	6.67	115.00	115.00	0.00	228.00	123.00	0.54	1.79	3.25	16.95	4.05	12.00	35.85	262.45

GY=grain yield, AD=anthesis days, SD=silking days, ASI=anthesis silking interval, PH=plant height, EH=ear height, EPO =ear position, EPP=ear per plant, EA=ear aspect, EL=ear length, ED=ear diameter, KRPE=kernel rows per ear, KPR=kernels per rows, TKW=thousand kernels weight.

Appendix III. (continued)

ENTRY	GY	AD	SD	ASI	PH	EH	EPO	EPP	EA	EL	ED	KRPE	KPR	TKW
L13xT1	5.99	115.00	117.50	2.50	261.50	135.50	0.52	1.68	3.00	14.85	4.31	13.00	32.35	228.6
L13xT2	7.59	112.00	114.00	2.00	226.00	110.50	0.49	1.62	3.25	14.10	4.25	13.00	31.65	270.5
L14xT2	6.07	115.50	117.50	2.00	234.50	124.00	0.53	1.62	3.50	14.50	4.38	13.65	27.65	257.7
L15xT1	8.52	116.00	118.00	2.00	277.50	155.00	0.56	1.84	3.00	16.95	4.34	14.65	35.00	232.7
L15xT2	8.45	112.50	115.00	2.50	247.50	122.50	0.50	1.88	2.50	19.15	4.25	13.35	35.65	243.6
L16xT1	8.94	110.50	112.50	2.00	286.00	163.50	0.57	1.74	3.25	15.65	4.28	13.30	31.50	274.3
L16xT2	5.84	114.50	116.50	2.00	217.00	115.50	0.53	1.69	3.75	14.40	4.00	12.70	31.85	239.9
L17xT1	7.57	111.00	113.00	2.00	290.50	160.50	0.55	1.79	3.00	16.40	4.12	12.65	30.80	280.9
L17xT2	6.43	113.00	115.50	2.50	230.00	119.00	0.52	1.88	3.50	13.60	3.98	11.65	28.30	310.1
L18xT1	7.60	110.50	113.50	3.00	265.00	142.50	0.54	1.55	3.00	16.25	4.50	13.65	34.20	263.3
L18xT2	5.71	111.00	110.50	-0.50	205.50	104.00	0.51	1.41	3.00	15.15	4.04	12.35	30.30	276.1
L19xT1	6.50	111.50	114.00	2.50	261.50	141.00	0.54	1.83	3.50	14.60	4.10	14.00	33.20	199.6
L19xT2	5.76	113.00	115.00	2.00	219.00	119.50	0.55	1.69	3.50	14.10	3.86	13.00	30.80	243.3
L20xT1	7.76	111.50	113.50	2.00	263.50	142.50	0.54	1.74	2.75	15.50	4.40	14.35	33.80	258.8
L20xT2	5.96	113.00	113.50	0.50	217.00	115.00	0.53	1.55	3.75	15.00	4.36	13.65	31.50	260.3
L21xT1	6.37	116.50	118.50	2.00	261.00	144.00	0.55	1.41	3.25	15.00	4.71	14.00	29.65	334.4
L21xT2	7.06	111.00	111.50	0.50	242.50	123.50	0.51	1.73	3.25	16.25	4.14	11.00	33.15	359.2
L22xT1	6.63	117.00	119.00	2.00	263.50	137.00	0.52	2.05	3.00	16.35	4.09	13.00	30.50	275.3
L22xT2	5.49	114.00	116.50	2.50	209.50	107.00	0.51	1.36	3.50	15.40	3.91	11.30	28.80	303.9
L23xT1	10.51	111.00	113.00	2.00	257.00	131.00	0.51	2.46	2.75	16.35	4.17	12.35	34.50	303.2
L23xT2	7.15	111.00	113.00	2.00	230.50	102.00	0.45	2.22	3.25	15.65	4.17	13.35	33.85	250.2
L24xT1	7.10	112.00	114.00	2.00	258.50	127.50	0.50	1.89	3.00	16.60	4.00	12.35	34.20	268.3
L24xT2	7.80	113.00	115.50	2.50	233.50	100.00	0.43	1.85	3.00	16.25	4.30	12.65	34.15	318.0
CHECK1	8.71	109.50	112.00	2.50	268.50	140.50	0.53	1.76	2.50	15.65	4.52	12.00	32.80	315.8
CHECS2L	7.46	108.50	111.50	3.00	241.50	122.50	0.51	1.56	2.75	15.05	4.11	12.70	31.35	289.2
Mean	**7.33**	**112.93**	**114.76**	**1.83**	**249.37**	**131.31**	**0.52**	**1.79**	**3.18**	**15.56**	**4.23**	**13.09**	**31.94**	**273.8**
Maximum	**10.51**	**118.00**	**119.50**	**3.50**	**300.00**	**186.00**	**0.62**	**2.46**	**4.00**	**19.15**	**4.71**	**14.70**	**35.85**	**359.2**
Minimum	**5.22**	**108.00**	**110.50**	**-0.50**	**199.50**	**100.00**	**0.43**	**1.36**	**1.75**	**12.15**	**3.77**	**11.00**	**26.80**	**199.6**
LSD(0.05)	**2.05**	**3.52**	**3.36**	**3.24**	**17.13**	**15.67**	**0.05**	**0.38**	**0.93**	**1.49**	**0.31**	**1.28**	**3.38**	**60.17**

Appendix IV. Mean performances of 48 testcrosses and two hybrid checks of maize for yield and yield related traits at Ambo, 2017

ENTRY	GY	AD	SD	ASI	PH	EH	EPO	EPP	EA	EL	ED	KRPE	KPR	TKW
L1xT1	8.86	95.00	95.00	0.00	277.00	168.00	0.61	1.95	3.00	13.05	4.22	12.65	28.15	294.20
L1xT2	9.26	94.50	92.00	-2.50	249.50	139.00	0.56	1.98	2.75	14.50	4.34	13.00	30.50	339.95
L2xT1	8.42	95.50	95.50	0.00	263.00	142.50	0.55	1.84	3.50	14.90	4.37	12.70	35.00	254.55
L2xT2	5.29	94.00	94.00	0.00	230.00	129.50	0.56	1.73	3.50	14.35	4.41	11.65	31.20	375.15
L3xT1	4.12	98.00	99.00	1.00	257.50	144.00	0.56	1.40	3.00	14.30	4.03	13.00	32.00	313.00
L3xT2	8.01	99.50	99.50	0.00	236.00	126.50	0.54	1.62	3.00	15.25	4.36	12.35	30.00	344.75
L4xT1	8.16	94.50	96.00	1.50	274.00	155.00	0.57	1.71	2.75	16.75	4.69	14.00	36.00	313.15
L4xT2	8.04	94.50	94.00	-0.50	257.00	135.50	0.53	1.31	2.75	16.25	4.46	12.65	35.15	353.50
L5xT1	8.89	93.00	94.00	1.00	294.00	169.00	0.58	1.62	3.00	14.65	4.38	12.35	31.85	319.75
L5xT2	8.29	93.50	92.50	-1.00	273.00	149.50	0.55	1.83	3.00	14.75	4.49	12.35	30.70	310.30
L6xT1	7.16	96.00	95.00	-1.00	273.00	154.00	0.57	1.79	2.75	14.30	4.30	12.70	29.50	274.90
L6xT2	5.17	96.00	93.50	-2.50	239.50	135.50	0.57	1.68	2.50	14.15	4.43	13.30	32.00	318.65
L7xT1	5.81	100.50	101.50	1.00	267.50	158.50	0.60	1.49	3.50	16.75	4.20	13.00	34.85	257.95
L7xT2	7.76	98.00	97.50	-0.50	232.50	140.00	0.61	1.74	3.50	15.65	4.15	12.65	32.50	302.10
L8xT1	9.09	96.00	97.00	1.00	266.00	147.50	0.55	1.68	3.00	16.85	4.42	13.65	33.20	322.55
L8xT2	6.94	95.00	93.50	-1.50	221.00	119.50	0.54	1.11	3.00	17.10	4.54	12.35	33.15	401.40
L9xT1	9.77	95.50	94.50	-1.00	260.00	136.00	0.52	1.91	3.25	15.00	4.33	12.70	34.35	294.00
L9xT2	7.68	94.00	92.00	-2.00	246.50	132.00	0.54	1.73	3.00	12.85	4.54	12.35	26.65	324.00
L10xT1	5.78	98.50	99.00	0.50	284.50	163.00	0.57	1.24	3.00	15.65	4.67	12.35	33.35	331.95
L10xT2	8.54	96.50	95.00	-1.50	246.00	128.50	0.53	1.47	2.75	16.85	4.73	13.00	33.15	368.60
L11xT1	9.87	97.50	97.50	0.00	268.50	154.50	0.58	1.62	4.00	14.50	4.81	13.35	32.15	294.80
L11xT2	9.76	97.00	95.00	-2.00	235.00	132.00	0.57	1.79	3.00	15.00	4.75	13.30	35.00	422.70
L12xT1	8.78	97.00	97.00	0.00	261.50	181.50	0.70	1.74	3.75	15.85	4.58	13.30	34.70	356.35
L12xT2	7.76	96.50	93.50	-3.00	250.00	140.00	0.56	1.60	2.50	15.80	4.55	12.35	32.65	411.35
L13xT1	3.30	102.50	102.50	0.00	225.50	126.00	0.56	1.34	3.25	11.95	4.70	13.35	31.80	281.05
L13xT2	6.90	97.00	95.50	-1.50	232.50	120.50	0.52	1.45	3.25	14.10	4.43	11.65	30.50	350.30

Appendix IV. (continued)

ENTRY	GY	AD	SD	ASI	PH	EH	EPO	EPP	EA	EL	ED	KRPE	KPR	TKW
L14xT1	7.51	97.00	97.50	0.50	288.00	165.50	0.58	1.81	3.00	17.30	4.41	12.70	34.80	260.00
L14xT2	7.85	98.50	98.00	-0.50	248.00	127.50	0.52	1.64	2.75	16.10	4.45	12.70	33.85	374.05
L15xT1	9.58	96.00	96.00	0.00	272.50	159.50	0.59	1.56	2.50	16.65	4.38	12.65	34.50	294.00
L15xT2	8.53	95.50	95.50	0.00	225.00	128.50	0.57	1.63	3.25	17.35	4.51	12.35	32.15	359.05
L16xT1	8.78	94.00	93.50	-0.50	294.00	178.00	0.61	1.76	3.25	15.05	4.35	12.00	33.00	320.25
L16xT2	6.60	97.00	95.00	-2.00	228.00	134.50	0.59	1.88	3.25	15.00	4.27	11.00	29.85	318.80
L17xT1	6.56	96.00	96.00	0.00	272.00	151.50	0.56	1.47	3.25	15.85	4.17	12.35	33.65	307.05
L17xT2	9.22	94.00	91.00	-3.00	239.50	139.50	0.59	1.86	3.00	15.50	4.35	12.35	31.85	366.65
L18xT1	7.58	94.50	96.00	1.50	259.00	144.50	0.56	1.21	2.50	15.45	4.54	12.35	34.00	316.75
L18xT2	6.02	96.50	94.50	-2.00	209.50	120.50	0.58	1.22	2.50	15.70	4.60	13.00	32.15	345.25
L19xT1	6.94	96.00	95.00	-1.00	222.00	143.00	0.69	1.48	2.75	14.85	4.33	12.35	34.30	282.60
L19xT2	6.42	97.00	96.00	-1.00	216.50	131.00	0.61	1.35	2.75	14.85	4.15	12.35	29.00	349.70
L20xT1	9.03	95.50	96.00	0.50	281.50	158.50	0.57	1.59	3.00	15.90	4.58	13.35	34.65	346.95
L20xT2	8.35	96.50	97.50	1.00	224.00	125.00	0.56	1.24	3.25	17.10	4.70	13.35	33.35	407.10
L21xT1	5.88	97.00	97.00	0.00	262.50	150.00	0.57	1.47	3.25	14.95	4.43	12.00	29.65	416.15
L21xT2	6.12	95.00	92.50	-2.50	260.00	149.50	0.58	1.46	3.00	15.85	4.49	12.00	32.15	414.95
L22xT1	8.40	98.00	98.00	0.00	260.50	127.00	0.49	1.75	3.25	14.90	4.18	12.65	31.35	367.55
L22xT2	8.97	96.00	94.50	-1.50	228.00	125.00	0.55	1.95	3.25	15.85	4.26	12.00	35.50	359.35
L23xT1	9.83	96.00	95.00	-1.00	263.00	145.50	0.56	1.95	3.50	14.50	4.21	12.65	29.70	300.60
L23xT2	9.26	96.50	95.50	-1.00	232.50	117.50	0.51	1.83	3.00	14.50	4.16	12.70	34.35	373.45
L24xT1	8.02	95.00	96.00	1.00	262.00	135.50	0.52	1.74	3.25	16.75	4.09	12.00	32.15	315.80
L24xT2	9.33	96.50	93.50	-3.00	244.00	119.50	0.49	1.98	2.75	15.50	4.20	13.30	34.00	350.25
CHECK1	6.85	94.00	94.00	0.00	250.00	149.00	0.60	1.33	3.25	17.00	4.64	12.70	33.70	412.25
CHECK2	7.90	91.50	92.00	0.50	275.50	147.50	0.54	1.41	3.00	15.10	4.44	12.35	34.50	317.25
Mean	**7.74**	**96.10**	**95.53**	**-0.57**	**252.76**	**142.01**	**0.56**	**1.62**	**3.06**	**15.37**	**4.41**	**12.63**	**32.56**	**336.14**
Maximum	**9.87**	**102.50**	**102.50**	**1.50**	**294.00**	**181.50**	**0.70**	**1.98**	**4.00**	**17.35**	**4.81**	**14.00**	**36.00**	**422.70**
Minimum	**3.30**	**91.50**	**91.00**	**-3.00**	**209.50**	**117.50**	**0.49**	**1.11**	**2.50**	**11.95**	**4.03**	**11.00**	**26.65**	**254.55**
LSD(0.05)	**2.22**	**3.75**	**4.03**	**1.79**	**29.39**	**14.46**	**0.11**	**0.34**	**0.48**	**2.13**	**0.36**	**1.20**	**1.86**	**65.27**

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

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

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

Appendix VI. Mean squares, and proportional contribution of lines, tester and line x tester of yield and yield related traits of 48 maizetestcross
Holetta, 2017

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

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

Appendix VII. Standard heterosis of 48 testcrosses and two commercial checks hybrids for yield and yield related traits for combined data, 2017

S/N	ENTRY	GY KOLBA	JIBAT	AD KOLBA	JIBAT	SD KOLBA	JIBAT	ASI KOLBA	JIBAT
1	L1xT1	4.89	6.29	0.98	2.75*	0.73	1.97	-0.93	-2.68
2	L1xT2	-0.16	1.17	0.74	2.50	-0.73	0.49	-5.91*	-7.57**
3	L2xT1	10.41	11.89	3.19*	5.00**	2.18	3.44**	-3.85	-5.54*
4	L2xT2	-24.85*	-23.84*	0.49	2.25	0.24	1.47	-0.93	-2.68
5	L3xT1	-29.51**	-28.57*	5.41**	7.25**	6.07**	7.37**	2.67	0.85
6	L3xT2	-11.31	-10.13	5.41**	7.25**	4.85**	6.14**	-1.88	-3.61
7	L4xT1	-1.74	-0.42	0.74	2.50	1.21	2.46	1.80	0.00
8	L4xT2	-7.39	-6.16	0.98	2.75*	0.00	1.23	-3.85	-5.54*
9	L5xT1	12.86	14.36	0.25	2.00	0.49	1.72	0.91	-0.87
10	L5xT2	-3.76	-2.48	0.00	1.75	-0.73	0.49	-2.85	-4.57
11	L6xT1	0.10	1.43	2.46	4.25**	0.73	1.97	-6.99**	-8.63**
12	L6xT2	-22.60*	-21.56*	1.97	3.75**	0.73	1.97	-4.87*	-6.55*
13	L7xT1	-17.94	-16.84	4.91**	6.75**	5.58**	6.88**	2.67	0.85
14	L7xT2	-10.77	-9.58	6.14**	8.00*	4.85**	6.14**	-4.87*	-6.55*
15	L8xT1	15.69	17.23	2.95	4.75**	3.64**	4.91**	2.67	0.85
16	L8xT2	-21.89*	-20.85*	2.46	4.25**	1.94	3.19*	-1.88	-3.61
17	L9xT1	8.94	10.39	0.00	1.75	0.00	1.23	0.00	-1.76
18	L9xT2	-4.28	-3.00	1.23	3.00*	-1.21	0.00	-10.38**	-11.96**
19	L10xT1	0.10	1.43	5.41**	7.25**	5.34**	6.63**	0.00	-1.76
20	L10xT2	9.93	11.40	3.44**	5.25**	2.18	3.44**	-4.87*	-6.55*
21	L11xT1	22.18*	23.81*	4.67**	6.50**	4.61**	5.90**	0.00	-1.76
22	L11xT2	10.09	11.56	4.18**	6.00**	2.18	3.44**	-8.09**	-9.71**
23	L12xT1	9.71	11.17	5.65**	7.50**	4.37**	5.65**	-4.87*	-6.55*
24	L12xT2	-7.30	-6.06	3.93**	5.75**	1.21	2.46	-11.58**	-13.14**
25	L13xT1	-40.31**	-39.51*	6.88**	8.75**	6.80**	8.11**	0.00	-1.76

Appendix VII. (continued)

S/N	ENTRY	GY KOLBA	JIBAT	AD KOLBA	JIBAT	SD KOLBA	JIBAT	ASI KOLBA	JIBAT
26	L13xT2	-6.88	-5.64	2.70*	4.50**	1.70	2.95*	0.00	-5.54
27	L14xT1	12.83	14.33	5.16**	7.00**	5.10**	6.39**	-3.85	-1.76
28	L14xT2	-10.58	-9.38	5.16**	7.00**	4.61**	5.90**	0.00	-3.61
29	L15xT1	16.36	17.92	4.18**	6.00**	3.88**	5.16**	-1.88	-2.68
30	L15xT2	14.05	15.57	2.21	4.00**	2.18	3.44**	-0.93	-1.76
31	L16xT1	13.85	15.37	0.49	2.25	0.00	1.23	0.00	-3.61
32	L16xT2	-20.06*	-18.99	3.93**	5.75**	2.67*	3.93**	-1.88	-6.55*
33	L17xT1	-9.19	-7.98	1.72	3.50**	1.46	2.70*	-4.87*	-2.68
34	L17xT2	0.61	1.95	1.72	3.50**	7.52**	8.85**	-0.93	-1.76
35	L18xT1	-2.44	-1.14	0.74	2.50	1.70	2.95*	0.00	1.69
36	L18xT2	-22.40*	-21.37*	1.97	3.75**	-0.49	0.74	3.52	-11.96**
37	L19xT1	-13.60	-12.44	1.97	3.75**	1.70	2.95*	-10.38**	-2.68
38	L19xT2	-21.73*	-20.68*	3.19*	5.00**	2.43	3.69**	-0.93	-4.57
39	L20xT1	7.91	9.35	1.72	3.50**	1.70	2.95*	-2.85	-1.76
40	L20xT2	-7.75	-6.51	3.44**	5.25**	1.94	3.19**	0.00	-7.57*
41	L21xT1	-21.28*	-20.23*	4.91**	6.75**	4.61**	5.90**	-5.91*	-2.68
42	L21xT2	-15.33	-14.20	1.23	3.00	-0.97	0.25	-0.93	-10.82**
43	L22xT1	-3.44	-2.15	5.65**	7.50**	5.34**	6.63**	-9.22**	-2.68
44	L22xT2	-7.07	-5.83	3.19*	5.00**	2.43	3.69**	-0.93	-4.57
45	L23xT1	30.70**	32.44**	1.72	3.50**	0.97	2.21	-2.85	-4.57
46	L23xT2	5.46	6.87	1.97	3.75**	1.21	2.46	-2.85	-4.57
47	L24xT1	-2.80	-1.50	1.72	3.50**	1.94	3.19*	-2.85	-0.87
48	L24xT2	10.09	11.56	2.95*	4.75**	1.21	2.70*	0.91	-8.63**
SE(d)		**0.75**		**1.25**		**1.29**		**0.91**	
LSD(0.05)		**1.17**		**1.94**		**2.58**		**1.82**	
LSD(0.01)		**1.41**		**2.34**		**3.43**		**2.41**	

**significant (0.01), *significant (0.05) from t-table, LSD used to compare two heterosis value

Appendix VII. (Continued)

S/N	ENTRY	PH KOLBA	JIBAT	EH KOLBA	JIBAT	EPO KOLBA	JIBAT	EPP KOLBA	JIBAT
1	L1xT1	7.33**	7.64**	10.36**	18.33**	-2.23	-9.57	27.07**	32.21**
2	L1xT2	-6.08	-5.80	-11.05**	-4.63	5.80	-0.96	26.42**	31.53**
3	L2xT1	-1.74	-1.45	-7.77*	-1.11	6.25	-0.48	18.80*	23.61**
4	L2xT2	-17.16**	-16.92**	-19.86**	-14.07**	4.02	-2.87	17.67*	22.43**
5	L3xT1	0.39	0.68	-0.69	6.48	1.34	-5.74	9.24	13.66
6	L3xT2	-10.90**	-10.64**	-15.72**	-9.63*	5.80	-0.96	6.32	10.62
7	L4xT1	5.98	6.29*	4.49	12.04**	1.34	-5.74	9.89	14.33
8	L4xT2	-4.24	-3.97	-12.95**	-6.67	9.82	3.35	-8.10	-4.38
9	L5xT1	12.83**	13.15**	11.92**	20.00**	1.34	-5.74	14.59	19.22*
10	L5xT2	1.25	1.55	-6.91	-0.19	8.93	2.39	19.29*	24.11**
11	L6xT1	1.93	2.22	1.55	8.89*	0.89	-6.22	15.72	20.40*
12	L6xT2	-10.22**	-9.96**	-10.54**	-4.07	0.45	-6.70	12.16	16.69
13	L7xT1	2.31	2.61	5.35	12.96**	-3.12	-10.53	3.24	7.42
14	L7xT2	-13.79**	-13.54**	-10.19**	-3.70	-4.02	-11.48**	16.21	20.91*
15	L8xT1	2.60	2.90	-0.52	6.67	4.02	-2.87	19.29*	24.11**
16	L8xT2	-17.45**	-17.21**	-22.97**	-17.41**	7.14	0.48	-18.80*	-15.51
17	L9xT1	0.29	0.58	-9.15*	-2.59	9.82	3.35	26.74**	31.87**
18	L9xT2	-6.17	-5.90	-14.68**	-8.52*	9.38	2.87	17.67*	22.43**
19	L10xT1	11.57**	11.90**	14.85**	23.15**	-2.23	-9.57	7.29	11.64
20	L10xT2	-6.94**	-6.67*	-14.16**	-7.96*	7.59	0.96	7.62	11.97
21	L11xT1	6.85**	7.16**	11.40**	19.44**	-4.02	-11.48**	17.18*	21.92*
22	L11xT2	-10.32**	-10.06**	-10.36**	-3.89	0.00	-7.18	11.67	16.19
23	L12xT1	8.29**	8.61**	26.94**	36.11**	-17.86**	-26.32**	17.18*	21.92*
24	L12xT2	-7.81**	-7.54**	-9.15*	-2.59	1.79	-5.26	9.72	14.17
25	L13xT1	-6.08	-5.80	-9.67**	-3.15	3.57	-3.35	-2.11	1.85

Appendix VII. (Continued)

S/N	ENTRY	PH		EH		EPO		EPP	
		KOLBA	JIBAT	KOLBA	JIBAT	KOLBA	JIBAT	KOLBA	JIBAT
27	L14xT1	10.41**	10.74**	10.02**	17.96**	0.45	-6.70	19.45*	24.28**
29	L15xT1	6.08	6.38	8.64*	16.48**	-2.23	-9.57	10.05	14.50
30	L15xT2	-8.87**	-8.61**	-13.30**	-7.04	4.91	-1.91	14.75	19.39*
31	L16xT1	11.86**	12.19**	17.96**	26.48**	-4.91	-12.44**	13.13	17.71*
32	L16xT2	-14.18**	-13.93**	-13.64**	-7.41	0.00	-7.18	15.56	20.24*
33	L17xT1	8.49**	8.80**	7.77*	15.56**	1.34	-5.74	7.62	11.97
34	L17xT2	-9.45**	-9.19**	-10.71**	-4.26	1.79	-5.26	20.91*	25.80**
35	L18xT1	1.06	1.35	-0.86	6.30	2.23	-4.78	-9.56	-5.90
36	L18xT2	-19.96**	-19.73**	-22.45**	-16.85**	3.13	-3.83	-15.07	-11.64
37	L19xT1	2.89	3.19	-1.90	5.19	4.91	-1.91	7.13	11.47
38	L19xT2	-16.20**	-15.96**	-13.47**	-7.22	-3.12	-10.53	-1.62	2.36
39	L20xT1	5.11	5.42	3.97	11.48**	1.34	-5.74	7.62	11.97
40	L20xT2	-14.95**	-14.70**	-17.10**	-11.11**	2.68	-4.31	-9.72	-6.07
41	L21xT1	0.96	1.26	1.55	8.89*	0.00	-7.18	-6.65	-2.87
42	L21xT2	-3.09	-2.80	-5.70	1.11	3.13	-3.83	3.24	7.42
43	L22xT1	1.06	1.35	-8.81*	-2.22	10.27	3.83	24.31**	29.34**
44	L22xT2	-15.62**	-15.38**	-19.86**	-14.07**	5.36	-1.44	7.29	11.64
45	L23xT1	0.29	0.58	-4.49	2.41	4.91	-1.91	42.79**	48.57**
46	L23xT2	-10.70**	-10.44**	-24.18**	-18.70**	15.18**	9.09	36.63**	42.16**
47	L24xT1	0.39	0.68	-9.15*	-2.59	9.82	3.35	17.34*	22.09*
48	L24xT2	-7.91**	-7.64**	-24.18**	-18.70**	17.86**	11.96**	24.15**	29.17**
SE(d)		8.34		5.23		0.03		0.13	
LSD(0.05)		16.67		8.13		0.53		0.26	
LSD(0.01)		22.16		9.78		0.70		0.35	

Appendix VII. (Continued)

S/N	ENTRY	EL		ED		KRPE		KPR		TKW	
		KOLBA	JIBAT	KOLBA	JIBAT	KOLBA	JIBAT	KOLBA	JIBAT	KOLBA	JIBAT
1	L1xT1	-17.34**	-10.49*	-7.15**	-0.53	1.34	-0.02	-14.54**	-13.68**	-22.13**	-6.52
2	L1xT2	-12.75**	-5.52	-9.99**	-3.57	2.70	1.32	-10.53*	-9.62*	-17.89**	-1.43
3	L2xT1	-6.64	1.09	-5.79*	0.94	2.72	1.34	-0.75	0.25	-32.92**	-19.47**
4	L2xT2	-11.48**	-4.14	-8.96**	-2.46	4.03	2.64	0.51	1.52	-13.39*	3.97
5	L3xT1	-6.38	1.38	-9.99**	-3.57	6.73	5.30	-5.77	-4.81	-20.93**	-5.08
6	L3xT2	-10.71**	-3.32	-5.95*	0.76	8.11*	6.66	-12.53**	-11.65**	-14.38*	2.78
7	L4xT1	-0.77	7.46	1.26	8.48**	12.14**	10.64**	3.26	4.30	-16.02**	0.81
8	L4xT2	0.26	8.57*	-5.79*	0.94	2.70	1.32	2.51	3.54	-14.39*	2.76
9	L5xT1	-3.32	4.69	-5.30*	1.46	0.00	-1.34	-1.00	0.00	-14.26*	2.93
10	L5xT2	-3.57	4.43	-4.92	1.87	-1.36	-2.68	-4.01	-3.04	-17.75**	-1.27
11	L6xT1	-7.15	0.55	-3.17	3.74	6.75	5.32	-3.76	-2.79	-22.25**	-6.66
12	L6xT2	-8.68*	-1.11	-4.10	2.75	8.09*	6.64	-4.26	-3.30	-15.75**	1.14
13	L7xT1	2.56	11.06*	-8.25**	-1.70	8.09*	6.64	-3.01	-2.03	-31.78**	-18.10*
14	L7xT2	-0.51	7.74	-13.54**	-7.37**	1.34	-0.02	1.50	2.53	-26.49**	-11.76
15	L8xT1	1.03	9.40*	-5.52*	1.23	12.14**	10.64**	1.26	2.28	-19.18**	-2.98
16	L8xT2	0.28	8.59*	-5.30*	1.46	4.03	2.64	-1.76	-0.77	-3.99	15.25*
17	L9xT1	-7.39	0.28	-6.01*	0.70	6.75	5.32	-4.26	-3.30	-30.86**	-17.00**
18	L9xT2	-23.47**	-17.12**	-4.21	2.63	5.39	3.98	-17.04**	-16.21**	-17.04**	-0.41
19	L10xT1	-5.62	2.20	2.08	9.36**	9.46**	8.00*	-0.50	0.50	-13.83*	3.45
20	L10xT2	5.88	14.65**	-1.64	5.38	6.75	5.32	1.00	2.02	-15.38*	1.58
21	L11xT1	-18.37**	-11.60**	0.00	7.14*	13.52**	12.00**	-11.28**	-10.39*	-12.72*	4.77
22	L11xT2	-8.92*	-1.38	-2.73	4.21	2.68	1.30	1.26	2.28	-3.10	16.32*
23	L12xT1	-2.02	6.10	-0.33	6.79*	9.44**	7.98*	-0.25	0.76	-9.68	8.43
24	L12xT2	0.26	8.57*	-6.12*	0.59	-1.36	-2.68	3.01	4.05	-7.45	11.10
25	L13xT1	-18.09**	-11.30**	-1.64	5.38	6.75	5.32	-3.51	-2.54	-30.00**	-15.97*

Appendix VII. (Continued)

S/N	ENTRY	EL		ED		KRPE		KPR		TKW	
		KOLBA	JIBAT	KOLBA	JIBAT	KOLBA	JIBAT	KOLBA	JIBAT	KOLBA	JIBAT
27	L14xT1	7.13	16.01**	-2.68	4.27	9.46**	8.00**	4.26	5.31	-26.79**	-12.12
28	L14xT2	-6.37	1.39	-3.66	3.22	6.75	5.32	-7.52	-6.59	-13.22*	4.17
29	L15xT1	2.82	11.34**	-4.81	1.99	10.78**	9.30**	4.51	5.57	-27.65**	-13.15
30	L15xT2	11.74**	21.00**	-4.31	2.52	4.05	2.66	2.00	3.03	-17.22**	-0.63
31	L16xT1	-5.88	1.92	-5.84*	0.88	2.68	1.30	-3.01	-2.03	-18.33**	-1.96
32	L16xT2	-9.95*	-2.49	-9.72**	-3.28	-4.05	-5.34	-7.26	-6.33	-23.25**	-7.87
33	L17xT1	-1.27	6.91	-9.45**	-2.98	1.34	-0.02	-3.01	-2.04	-19.24**	-3.06
34	L17xT2	-10.96**	-3.58	-9.07**	-2.57	-2.72	-4.02	-9.52*	-8.61*	-7.05	11.58
35	L18xT1	-3.05	4.99	-1.31	5.73*	5.39	3.98	2.51	3.55	-20.32**	-4.35
36	L18xT2	-5.60	2.22	-5.63*	1.11	2.70	1.32	-6.02	-5.07	-14.65*	2.46
37	L19xT1	-9.93*	-2.47	-7.92**	-1.35	6.75	5.32	1.50	2.53	-33.76**	-20.48**
38	L19xT2	-11.46**	-4.13	-12.51**	-6.26*	2.70	1.32	-10.03*	-9.12*	-18.55**	-2.23
39	L20xT1	-3.83	4.14	-1.97	5.03	12.16**	10.66**	3.00	4.04	-16.80**	-0.12
40	L20xT2	-1.78	6.36	-1.04	6.03*	9.44**	7.98*	-2.50	-1.52	-8.32	10.05
41	L21xT1	-8.40*	-0.81	-0.16	6.96*	5.39	3.98	-10.78*	-9.88*	3.09	23.75**
42	L21xT2	-1.78	6.36	-5.79*	0.94	-6.77	-8.02*	-1.76	-0.77	6.33	27.64**
43	L22xT1	-3.31	4.71	-9.72**	-3.28	5.39	3.98	-5.76	-4.81	-11.70	6.00
44	L22xT2	-4.33	3.60	-10.81**	-4.45	-5.43	-6.70*	-3.26	-2.29	-8.89	9.37
45	L23xT1	-5.60	2.22	-8.52**	-1.99	1.34	-0.02	-3.50	-2.53	-17.07**	-0.45
46	L23xT2	-7.65	0.00	-9.07**	-2.57	5.41	4.00	2.51	3.55	-14.33*	2.84
47	L24xT1	2.05	10.51*	-11.74**	-5.44	-1.36	-2.68	-0.25	0.76	-19.76**	-3.68
48	L24xT2	-2.80	5.25	-7.21**	-0.59	5.37	3.96	2.51	3.54	-8.21	10.19
	SE(d)	0.64		0.12		0.42		1.45		21.76	
	LSD(0.05)	1.28		0.24		0.65		2.25		43.51	
	LSD(0.01)	1.70		0.32		0.78		2.71		57.84	

**significant (0.01), *significant (0.05), from t-table, LSD used to compare two heterosis values

Appendix VIII.Mean monthly field temperature, relative humidity and rainfall at Holetta and Ambo during the study period (2017)

Holetta(ARC)						Ambo(PPRC)				
Month	RF(mm)	Air Temperature(ºC)			RH (%)	RF(mm)	Air Temperature(ºC)			RH (%)
		min	max	average			min	max	average	
January	0	-0.6	25.2	12.3	36	5.5	8.3	26.3	17.3	60.6
February	30.2	5.2	25.6	15.4	39	60.9	11	27.1	18.3	56.3
March	24	8.2	26.3	17.25	47	11.9	12	28.4	20.2	47.7
April	56	8.8	26.2	17.5	53	29.3	12.4	28.5	20.5	54.7
May	129.6	10	23.5	16.75	69	145.7	12.1	25.8	19	69.2
June	74.6	8.8	24.2	16.5	77	134.7	11.7	24.7	18.2	72
July	172.8	8.8	22.1	15.45	83	205.8	11.9	22.2	17	79.5
August	311.4	10.4	21.7	16.05	76	144.1	11.5	21.9	16.7	82.1
September	244	8.3	22.6	15.45	71	209.6	10.7	22.8	16.8	76.8
October	29	7.8	24.2	16	61	6.2	9.8	25.2	17.5	60.9
November	0	2.8	24	13.4	46	18.0	8.7	25.4	17.1	54.5
December	0	0.6	23.9	12.25	47	0	7.7	25.4	16.6	46.7
mean	89.3	6.6	24.1	15.35	58.8	81.0	10.7	25.3	17.9	63.4

*RF= rain fall, RH = relative humidity, min= minimum, Max= maximum   (HARC and AARC, 2017)