HETEROSIS AND COMBINING ABILITY OF ELITE HIGHLAND ADAPTED MAIZE (*Zea mays. L)* INBRED LINES FOR DESIRABLE AGRONOMIC TRAITS.

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ZELEKE KEIMESO LANGO

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HETEROSIS AND COMBINING ABILITY OF ELITE HIGHLAND ADAPTED MAIZE (*Zea mays. L)* INBRED LINES FOR DESIRABLE AGRONOMIC TRAITS.

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ZELEKE KEIMESO LANGO

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Demissew Abakemal (PhD) ________________ ________________
Major AdvisorSignatureDate

Wosene Gebreselassie (Asso. Prof)________________________________
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NameSentayew Alameraw (Prof.)Signature_____________Date_________________

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DEDICATION

I dedicated this thesis to myfriend,**ZinashYilma**and to my grandmother,late**HibseMolore**.

STATEMENT OF THE AUTHOR

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Date of Submission: October, 2018

BIOGRAPHICAL SKETCH

The author was born on April8, 1991 at Damboya district of KembataTambaroZone, Ethiopia from his father Keimeso Lango and his mother Fatuma Anjajo. He attended his Elementary education at Hego primary School and Secondary education at Damboya secondary school. He completed his high school study at Durame Preparatory and Secondary School in2009. After passing the Ethiopian Higher Education Qualification Certificate Examination, he joined Hawassa University and graduated with BSc degree in Plant Science in 2012. After his graduation, he was employed by Southern nations, nationalities and peoples Agriculture and Rural Development Office from January 9, 2013 to June 18, 2013 as job opportunity creator expert in Damboya district of KembataTambaroZone. In June 18, 2013, he joined the Southern Agricultural Research Institute (SARI) and served as junior researcher at Arbaminch Agricultural Research Center and after one-yearof service atArbaminch he joined Ethiopian Institute of Agricultural Research in June, 2014. After three years of service in 2016, he joined Jimma University to pursue his MSc study in Plant Breeding.

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ACRONYMS AND ABBREVIATIONS

ANOVA	Analyses of variance
CIMMYT	International Center for Maize and Wheat Improvement
CSA	Central Statistics Authority
FAO	Food and Agricultural Organization
GCA	General Combining Ability
H^2	Heritability in broad sense
SAS	Statistical Analyses System
SCA	Specific combining ability
SSD	Single seed descent

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ABSTRACT

Maize (Zea mays L.) is one of the cereals that provide calorie requirements in the Ethiopian diet. The national average maize yield in Ethiopia is low and thus, knowledge of combining ability and heterosis is a prerequisite to develop high yielding maize varieties. The objective of the present study was to estimate combining ability of elite maize inbred lines for grain yield and related agronomic traits, to identify crosses with higher yield than the standard check and to determine the relationship existing between grain yield andyield related traits. A total of 36 diallel crosses generated by crossing 9 elite maize inbred lines using half diallel mating scheme and four standard checks were studied for different agronomic and yield traits during the 2017 cropping season at Ambo and Kulumsa Agricultural Research Centers. The genotypes were evaluated in alpha lattice design replicated twice in both locations. Analyses of variances showed significant mean squares due to crosses were observed for most traits studied.The highest grain yield was obtained from crosses L1 x L3, L3 x L8, L4 x L8 and L8 x L9.GCA mean squares were significant for all studied traits whereas, SCA mean squares were significant for grain yield, days to anthesis, ear per plant and ear diameter. Relatively larger GCA over SCA variances were observed in the current study for most studied traits revealed the predominance of additive gene action in controlling these traits. Inbred lines L3 and L8 were the best general combiners for grain yield, and hence are promising parents for hybrid development program. Inbred lines L2, L4, L6, L7 and L8 had negative and significant GCA effects for days to anthesis and silking. Whereas, L1, L2 and L6 showed negative and significant GCA effects for plant and ear height. Based on mean grain yield, standard heterosis and specific combining ability effects, L1 x L3, L1 x L5, L2 x L4, L2 x L7, L3 x L8, L7 x L9 and L8 x L9 are promising crosses that could be promoted for further use in maize breeding program. Grain yield revealed positive and highly significant (P<0.01) phenotypic and genotypic correlation with number of ears per plant, ear length, number of kernels per row and thousand kernel weight. The information generated from this study shall have important implications in the development of maize varieties with desirable traits' composition for highland sub-humid agro-ecology of Ethiopia.

***Key words:**Combining ability, Correlation, General combining ability, Heterosis, Specific combining ability.*

1 INTRODUCTION

Maize (*Zea mays* L.*)* is a diploid (2*n*=20) crop and one of the oldest food grains in the world. It is a member of order *Poales,* family *Poaceae* and tribe*maydeae* (Eubanks, 1995; Acquaah, 2009). It is suggested that domestication of maize began at least 6000 years ago in regions of the southwestern United States, Mexico, and Central America (Mangelsdorf, 1974). It is believed that the crop is originated in Mexico and introduced to West Africa in the early 1500s by the Portuguese traders (Galinat, 1988). It was introduced to Ethiopia in the 16th or 17th century (Haffangel, 1961; Benti and Ransom, 1993). Maize is predominantly a cross-pollinating species, a feature that has contributed to its broad morphological variability and geographical adaptability. It contains approximately 72% starch, 10% protein, and 4% fat, supplying an energy density of 365 Kcal/100 g (Ranum*et al.,* 2014).

Maize is the basic staple cereal grain for inhabitants of Africa, Latin America, and parts of Asia, where it provides more than half of the daily calorie and protein intakes (Musila *et al*., 2010). Several million people in the developing world consume maize as an important staple food and derive their protein and calories requirement from it. In sub-Saharan Africa, it accounts up to 60% of the daily human protein supply.Currently, it is one of the most important field crops to fulfill food security in Ethiopia. It contributes the greatest share of production and consumption along with other major cereal crops, such as tef, wheat and sorghum (CSA, 2017). It has a significant importance in the diets of rural Ethiopia and has gradually penetrated into urban centers. This is particularly evidenced by green maize being sold at road sides throughout the country as a hunger-breaking food (Twumasi *et al.,* 2012).

Maize has an extensive geographical distribution, growing from sea level to elevations exceeding 3,000 meters above sea level and grows from 58°N to 40°S in areas with rainfall ranging from 250 mm to more than 5000 mm per year (Dowswell*et al*., 1996). It is the second most popular crop grown in the world after wheat. It is the first crop in Africa both in cultivated area and total grain production. In terms of dietary intake, it is the third main food crop following rice and wheat.In East Africa, maize is planted onmore than 15 million hectares and is the staple food of millions of poor families andits importance is growing with time(FOSTAT, 2016).

In Ethiopia, maize grows from moisture deficit semi-arid lowlands, mid-altitudes and highlands to moisture surplus areas in the humid lowlands, mid-altitudes and highlands (Legesse *et al.*, 2012).Based on area of production of major cereals, maize ranks second following teff. Whereas it ranks first in total grain production followed by teff, sorghum and wheat (CSA, 2017). Ethiopia's current national maize yield is 3.67 metric tons per hectare.The average yield in ton per hectare at national level was increased by 8.5% between 2015/16 and 2016/17. In 2016/17 cropping season, out of the total grain crop area, 81.27% (10219443.46 hectares) was under cereals of which 16.98% (2135571.85 hectares) was occupied by maize. Cereals contributed 87.42% (253847239.63 quintals) of the grain production from which maize made up 27.02% (78471746.57 quintals) (CSA, 2017).

The high altitude sub-humid areas including the highland transition and true highland of Ethiopia, is next to mid-altitude in maize area and production. In highland areas, maize is the first crop grown and is a popular hunger breaking crop when it is harvested and consumed green (Twumasi *et al*., 2001). It is estimated that the highland sub-humid agro-ecology covers 20% of the land devoted annually to maize cultivation and 30% of small-scale farmers in the area depend on maize production for their livelihood (Mosisa*et al*., 2012).In this agro-ecology maize production is characterized by low yields owing to unimproved varieties coupled with biotic constraints such as turcicum leaf blight, common leaf rust, stalk lodging, stalk borers, and storage pests and abiotic stresses such as frost, hail and low soil fertility (Twumasi *et al*., 2001). Because of these constraints, the highland areas have been facing great challenges in maize production which occasionally lead to food insecurity, malnutrition, reduced income and widespread poverty (Demissew, 2014). Therefore, to ensure these,it remains important to develop high yielding, nutritionally enhanced and stress tolerant maize varieties which fit the diverse highland agro-ecologies of the country.

Combining ability studies are ofprimary importance in maize hybrid development since itprovide information for the selection of parents, identification of promising hybrids and on the nature and magnitude of gene actions. The two types of combining ability estimates, i.e., general (GCA) and specific combining abilities (SCA) have been recognized in genetic studies. General combining ability relates to additive gene effects, while specific combining ability reflects the non-additive gene actions (Sprague and Tatum, 1942).

Heterosis may be defined as the increase in size, vigor, fertility, and overall productivity of a hybrid plant, over the mid parent value (average performance of the two parents), over the performance of best parent or standard checks.Heterosis occurs when two inbred lines of out bred species are crossed, as much as when crosses are made between pure lines.It is practically exploited to develop hybrid varieties (George, 2007).

So far in Ethiopia, several studies on combining ability and heterosis of maize inbred lines for grain yield andyield related traits were conducted fordifferent sets of locally developed/introduced inbred lines (Hadji, 2004; Dagne *et al.,*2010;Demissew *et al.,* 2011; Yoseph*et al*., 2011;Shushay*et al*., 2013; Umar *et al*., 2014; Girma*et al*., 2015; Beyene, 2016;Tolera*et al.,* 2017 and Dufera*et al.,* 2018). However, it is always mandatory for any breeding program to generate suchinformation for any new batch of inbred lines generated or received outside of the program.Understanding the relative importance of general and specific combing ability effects fordifferent traits for newly developed inbred lines is of supreme importance to design futurebreeding strategies for the development of hybrid and/or synthetic varieties. Currently, at Ambo highlandmaize research program there are a number of new batches of inbred lines generated through different methods of inbred line development. So far, little or no information is available on these particular set of new inbred lines used for this study on their specific and general combing ability effects(Demissew Abakemal, personal communication, 2017).

In the current study, therefore, an attempt was made to generate information on nine elite maize inbred lines crossed usinghalf diallel mating schemefollowing Griffing (1956) and evaluated with the following specific objectives:

1. To identify best inbred lines and cross combinations with good general and specific combining ability effects, respectively, for yield and yield related traits for further breeding and/or cultivar development.
2. To determine the magnitude of standard heterosis for yield and yield related traits.
3. To determine the relationship between yield and yield related traitsin selected highland adapted maize inbred lines.

2 LITERATURE REVIEW

2.1 Importance of Maize

Maize is an important source of food and nutritional security for millions of people in the developing world, especially in Africa and Latin America.The role of maize for human consumption, expressed in terms of the share of calories from all staple cereals, varies significantly across regions. This ranges from 61% in Mesoamerica, 45% in Eastern and Southern Africa, 29% in the Andean region, 21% in West and Central Africa to 4% in South Asia. Its use as a source of food accounts for 25% and 15% of the total maize demand in the developing countries and globally, respectively (Tripathi *et al*., 2011).

In South Asia 46% of maize is used as food mainly for poor households who cannot afford other staples such as rice and wheat. The demand for food is also high in Mesoamerica (44%), North Africa (39%) and the Andean region (36%) as well as South East Asia (29%). In sub-Saharan Africa, maize is mainly a food crop accounting for 73% and 64% of the total demand in eastern and southern Africa and west and central Africa. This makes maize particularly important to thepoor in many developing regions of Africa, Latin America and Asia as a means of overcoming hunger and improving food security. The industrial demand for maize is mainly related to its growing use in the bio-energy sector. Investment in maize based bioethanol is increasing. Around 50 developing countries have established targets for blending ethanol with gasoline. However,given the importance of maize for human/animal consumption and for biofuel production, it is also important to analyze the potential trade-offs around using maize to produce ethanol (Headey and Fan 2010).It is also an important component of feed for the meat industry, especially in Asia where maize consumption has advanced, driven by the growing demand for maize aspoultry and pig feed (Bekele*et al*., 2011).

In Ethiopia, maize is increasingly an important component of diets across the country. It is used as a staple food and feed for livestock, and is one of the main sources of calorie in the major maize producing regions (Tsedeke*et al*., 2015). It is an excellent fodder for both milk cattle and draft cattle and used asfodder at various stages of plant growth, particularly from tasselling onwards. The maizeplant does not have toxicity or anti-nutritional problems such as prussic acid orhydrocyanic acid and therefore it can be used as fodder even before flowering or in dryweather (Berhanu, 2009).Maize production, processing and utilization serve as very important employment and income generation activities for a large cross-section of the population including men, women and children (Mandefro*et al*., 2002).

2.2 Maize Production and its Constraints in Ethiopia

In Ethiopia, maize (*Zea mays L.*) exceeds all other cereal crops in terms of annual production and productivity. It is, however, tef (*Eragrostis tef* (*Zucc*)) that leads in terms of area of production and importance as the basic staple (CSA, 2017).It is cultivated in all of the major agro-ecological zones up to altitudes of 2400 m.a.s.l. The mid-altitude sub-humid agro-ecology is the high potential area for maize production and contributes the largest proportion of maize produce in the country (Benti and Ransom, 1993; Mandefro*et al.,* 2002). However, production and productivity of maize in this agro-ecology is constrained by several factors. These include inadequacy of improved varieties, shortage of improved seeds, diseases including gray leaf spot, turcicum leaf blight, and common rust, losses from field and storage insect pests such as, maize stalk borers and the maize weevil, as well as low soil fertility (Abera *et al.,* 2013).

The lowland moisture stress agro-ecology is the other maize producing agro-ecology of Ethiopia.This agro-ecology encompasses drought stressed areas occupying over 40% of area in thecountry and contributes to 20% of the total maize production (Mandefro *et al.,* 2002). In this agro-ecology of the country,droughtis considered as one of the most important stresses threatening maize production in these areas. In addition to regular drought, other constraints such as limited availability of drought tolerant varieties and their seeds, depleted soil fertility, insect pests (stalk borers and the maize weevil) and plant diseases (common leaf rust and turcicum leaf blight) limit maize production in this agro-ecology (Mandefro*et al.,* 2002; Gezahegn*et al.,* 2012).

The high altitude sub-humid area is next to mid-altitude in maize area and production in Ethiopia. Research and variety development of highland maize hasgenerally lagged behind when compared to other agro-ecologies before the launch of thebreeding program. In the past years of research achievements, only a few improved normal maize varieties were released for wide production in the highland agro-ecology of Ethiopia (Twumasi *et al.*, 2002). In thisagro-ecology, maize production is characterized by low yields which resulted fromgrowingunimproved local varieties for production which coupled with biotic constraints such as turcicum leaf blight, common leaf rust, stalk lodging, stalk borers, and storage pests, and abiotic stresses such as frost, hail, and low soil fertility (Demissew *et al.*, 2013).

2.3 Historical Account of Maize Research in Ethiopia

Maize research in Ethiopia started in 1950's with the evaluation of introduced materials focusing mainly on grain yield, early maturity, decreased plant height, lower ear placement and resistance to major biotic and abiotic stresses (Benti and Ransom, 1993). In the 1970s and 1980s, locally developed improved open pollinated varieties (OPVs) were released for wide area production at different agroecologies of the country. In the late 1980s, the first locally developed non-conventional hybrid was released for the mid-altitude sub-humid maize growing areas. Since then, the research system has developed and releasednumber of improved varieties with their accompanying agronomic practices and plant protection technologies for all maize growing agro-ecologies of the country; namely mid-altitude sub-humid, highland, low moisture stress and lowland sub-humid agro-ecologies. This has contributed to the current increasing trend in maize production and productivity in the country(Benti and Ransom, 1993).

The current maize research system in Ethiopiaoriginates from the Ethiopian Agricultural Research System (EARS). Presently, EARS is mainly composed of the Ethiopian institute of agricultural research (EIAR), the seven regional agricultural research institutes (RARIs), higher learning institutions, and public and private companies that participate directly or indirectly in agricultural research activities. The main objectives of the research on maize targeting the four major maize agro-ecologies are: To develop and promote high yielding, stress tolerant and widely adapted hybrids/open pollinated maize varieties with desirable agronomic and quality protein attributes for the different agroecologies; to develop improved maize protection technologies for the four major maize agro-ecologies;to introduce finished maize technologies from abroad and evaluatethem for yield and adaptability and then recommend forproduction in a short period of time; to renew and conserve breeding materials, to increase and maintain true to type breeder seeds of released maize parents and make them available for pre-basic and basic seed production; and todemonstrate and promote improved maize technologies(Dawit *et al*., 2014).

The national maize research was coordinated by different centers and institutions at different times until 1986 (Benti and Ransom, 1993). Since then Bakooperates as the national coordinating center for maize research in Ethiopia and is responsible for germplasm development for mid-altitude areas. However, other research centers also have responsibility to develop maize technologies and co-ordinate research activities in the agro-ecology for which they work. For example, Melkassa is responsible for germplasm development for moisture stress/drought areas while Ambo is responsible for the highland areas(Dawit*et al*., 2014). In addition, the regional research institutes undertake maize research program funded by their respective regional governments. In recent years, the role of public and private seed companies in maize research has considerably increased showing the emerging role of seed companies in maize research.Maize considerably attracts private sector engagement in the seed sector, which is mainly associated with the development of hybrid maize varieties since 1988 when the first hybrid (BH 140) was released (Benti and Ransom, 1993). The support from the International Maize and Wheat Improvement Center (CIMMYT) has been vital for the achievements of the Ethiopian maize research system (Berhanu, 2009).

2.4 Maize Inbred Lineand Hybrid Development

An inbred is a nearly homozygous line obtained through continuous selfing of cross pollinated species with selection accompanying selfing (Singh, 2005). Shull (1909) outlined the pure line method in maize breeding, suggesting the use of self-fertilization to develop homozygous lines that would be of use in hybrid production. This combination of inbreeding and hybridization constitutes the basis of maize improvement. The general process to develop maize hybrids starts with the creation of a source segregating breeding population that it is used to develop inbred lines through inbreeding and selection(Betran *et al.,* 2004). Development of inbred parents can follow different breeding methods, such as pedigree breeding, backcross, bulk, single seed descent, double haploids, and so on.

Pedigree Breeding is the most widely used breeding system to develop maize inbreds (Hallauer *et al.,* 2010). Typically, specific crosses are made between inbred lines and self-pollination is then applied to the F1 and subsequent generations to develop inbred lines that are superior to either parent through genetic segregation and recombination (Singh, 2005). Selection is applied among progeny rows and among plants within S1 families. This process of selfing and selection is repeated in successive generations until homozygous elite inbreds are developed. Effective phenotypic selection and greater selection intensity can be applied in initial inbreeding stages for traits with high heritability, such as pest resistance, maturity, morphological traits, and so on (Hallauer *et al*., 2010).

The Backcross Breeding method is used widely in maize breeding to transfer one or a few traits/genes from the donor parent to the recurrent and most desirable parent. With the beginning of genetically modified organisms, major emphasis is devoted to accelerate backcrosses to transfer the transgenes to elite inbreds. The use of DNA molecular markers has facilitated both the speed and accurate recovery of the recurrent parent and the reduction of linkage drag.The Bulk method, where the seed for each selfing generation are harvested in bulk, and single seed descent, where one or a few seeds from each genotype are advanced each generation until approximate fixation is reached, is also used because of itssimplicity and low space requirements(Acquaah, 2009 and Hallauer *et al*., 2010). Double haploids derived from maternal or paternal gametes have been used to arise homozygous inbred lines rapidly (Birchler, 1994).

If two inbreds are crossed, heterosis is a function of the dominance in those loci with different alleles in the inbreds. Increasing degrees of heterosis are observed after several cycles of hybrid selection, due to increasing divergence of allele frequencies and selection of complementary alleles in the heterotic groups. In line recycling and in the development of source breeding populations, crosses among elite lines from the same heterotic group are preferred. Heterotic response is heritable and inbreds have heterotic reactions similar to their parents(Troyer, 2001).

Hybrid varieties are the first filial generations (F1) from crosses between two or more purelines, inbreds, openpollinated varieties, clones or other populations that are geneticallydissimilar (Singh, 2005). In maize, hybrid breeding remains the method of choice for attaining maximum genetic gain from the effect of heterosis. According to Singh (2005), most of the commercial hybrid varieties are F1’s from two or more inbreds. The success of hybrid maize development depends on the ability of the breeding program to rapidly isolate lines that combine well in hybrid combinations and ability to identify appropriate heterotic combinations to maximize the vigour of the hybrid (Kim and Ajala, 1996). Selected inbred lines are then evaluated in hybrid combinations across locations to select superior hybrids and to estimate their combining ability (Bernardo, 1999; Acquaah, 2009).

2.5 Combining Ability

Combining ability or productivity in crosses is defined as the cultivars or parents’ ability to combine among each other during hybridization process such that desirable genes or characters are transmitted to their progenies(Hallauer and Miranda Filho, 1988). Combining ability has also been described as the ability of a parent to produce inferior or superior combinations in one or a series of crosses (Chaudhary, 1982). It is an especially powerful tool for studying and comparing the performance of inbred lines in hybrid combinations (Griffing, 1956). Information on combining ability among maize germplasm is essential for maximizing the effectiveness of hybrid development, and combining ability analysis is one of the powerful genetic tools in identifying the best combiners that may be used in crosses either to exploit heterosis or to accumulate productive genes.

There are two types of combining abilities, *i.e.*, general combining ability (GCA) and specific combining ability (SCA). General combining ability (GCA) is defined as the mean performance of an inbred line in all its cross combinations and is recognized as primarily as a measure of additive gene action (Sprague and Tatum, 1942). It is measured based on the average value of all crosses having this inbred line as one of the parents, the values being expressed as deviation from overall mean of the crosses (Falconer and Mackay, 1996). Specific combining ability (SCA) is a measure for cases where some hybrid combinations are better or worse than expected based on mean performance of the lines involved.Specific combining ability is most important in hybrid breeding and indicatesthe minimum and maximum genetic gain of hybrids from certain inbred lines. It describes those cases in which certain hybrid combination do relatively better or worse than would be expected on the basis of the average performance of the parents and is regarded as an estimate effect of non-additive gene action such as dominance and epistasis (Sprague and Tatum, 1942).

Information on combining ability of maize germplasm is of great value to maize breeders. It is necessary for selection of suitable parents in hybridization and identification of promising hybrids for development of improved varieties for diverse agro-ecological conditions (Betran *et al.,*2003).In addition to provision of information on the nature of gene action, it also enables classification of selected parental materials with respect to breeding behavior. The choice of the method to be used for the purpose of genetic improvement of crop plants is dependent on the type of gene actions of each gene that controls quantitative characters (Falconer and Mackay, 1996).

Several studies have investigated the relative importance of GCA and SCA in maize, using materials of various genetic structures tested under different environmental conditions. GCA/SCA ratio greater than unity was reported for ear length and grain yield indicating the importance of additive gene actions in the inheritance of these traits, whereas GCA/SCA ratio less than unity was reported for plant height, ear height, ear diameter and number of rows/ear indicating the importance of non-additive gene actions in these traits (Chandel and Mankotia, 2014 and Kamara *et al.,* 2014).Generally, it was found that estimates of additive genetic variance were two to four times greater than estimates of variance due to dominance deviation in maize (Hallauer and Miranda Filho, 1988).

Kanagarasu*et al.* (2010) done combining ability analysis for yield and yield related traits using the line x tester analysis and reported significant line x tester interaction, which indicated the importance of SCA as compared to GCA. Their study also showed that the magnitude of SCA variances was much greater than that of GCA for grain yield, ear length, 1000 kernel weight, days to tasseling, days to silking and number of kernels per row, indicating the preponderance of non-additive gene action in the inheritance of these traits. In contrast to this finding, Tessema*et al.* (2014) evaluated a line x tester cross among thirty-six lines and two testers and reported significant GCA mean squares and non-significant SCA mean squares for grain yield, ear length, 1000 kernel weight, days to tasseling, days to silking and number of kernels per row.

Tolera*et al.* (2017) studied Combining ability and heterotic orientation of mid-altitude sub-humid tropical maize inbred lines for grain yield and related traits in a line by tester among 10 lines and 7 testers and observed significance of both GCA (lines and testers) and SCA of LxT for days to anthesis, days to silking, plant height, ear height,ear aspect and grain yield showed that both additive and non-additive gene actions are important in controlling these traits. Furthermore, they observed that the proportion of GCA sum of squares were greater than the SCA sum of squares for days to anthesis, days to silking, plant height, ear height, and ear aspect indicating the predominance of additive gene actions in controlling these traits. For grain yield, the ratio of GCA to SCA sum of squares was near to unity indicating both additive and non-additive gene actions were equally important.

Bitew*et al.* (2017)studiedcombining ability analyses of quality protein maize (QPM) inbred lines for grain yield, agronomic traits and reaction to grey leaf spot in mid-altitude areas of Ethiopiain diallel crossesamongten quality protein maize (QPM) inbred lines with varying level of resistance to GLSand observed significant mean squares due to GCA and SCA effectsfor most traits and this suggested that both additive and non-additive gene actions have the contribution in the expression of the traits. However, they observed that the ratio of General combining ability (GCA) to specific combining ability (SCA) sum of squares were greater than unity, this revealed that there was preponderance of additive gene action in the expression of all the traits under study.

In a combining ability study of highland maize inbred lines, Bayisa *et al*. (2008) reported a significant meansquare due to GCA of inbred lines for ear height and grain yield, while the GCA oftesters was significant for ear height, ear lengthand grain yield. They observed a significant SCA effect for grain yield.

In a study of heterosis and combining ability for grain yield and yield components of maize in eastern Ethiopia, Habtamu (2015) reported a significant meansquare due to GCA of inbred lines for days to maturity, ear diameter, number of kernels per row, 1000 kernel weight and grain yield, indicating the importance of additive genetic variance in controlling these traits.However,he observed significantmean squares due to SCA for days to maturity, ear length, number of kernels per row and 1000 kernel weight indicating the importance of non-additive genetic variance in controlling these traits.

Abiy(2017) studied the combining ability of highland maize (*Zea mays L.*) inbred lines using line x tester analyses and observed GCA of lines was significant for all 14 traits except for grain yield, plant height, ear aspect and thousand seed weight at Kulumsa. SCA was also significant for all 14 traits except for number of kernel rows per ear. SCA contributed higher proportion for plant height (67%), ear height (61%), harvest index (60%) and ear diameter (79%). He revealed additive gene action was the more important for days to anthesis (61%), husk cover (67.5%), number of kernel row per ear (71%) and ear length (67%). Both additive and non-additive genetic variances were important at Ambo for husk cover, ear aspect, harvest index and ear diameter. For thousand kernel weight (60%), non-additive gene action predominated while for ear length (64%) additive gene action was the most important at Ambo.

In a study of heterosis and combining ability of mid altitude quality protein maize inbred lines at bako western Ethiopia,Beyene (2016)reported significantmean squares due to general and specific combining ability for all the traits except for days to silking, harvest index and total above ground biomass which shows the importance of additive and non-additive gene action in the inheritance of the character. In about 60% of the traits, including yield, however, relative importance of general to specific combining ability was lower than unity denoting the predominance of non-additive gene effects.These studies and other studies on combining ability reported the relative contribution of additive and non-additive gene effects on grain yield and related traits.

2.5.1 Diallel Mating Design

Mating design refers to the procedure of producing the progenies.In plant breeding, plant breeders and geneticists, theoretically and practically, use different form of mating designs and arrangements for targeted purpose (Nduwumuremyi*et al* 2013). However, the choice of a mating design for estimating genetic variances should be dictated by the objectives of the study, time, space, cost and other biological limitations. Thus, several studies (Griffing, 1956; Kearsey and Pooni,1996; Hallauer *et al*., 2010; Acquaah, 2012) described and contrasted different mating designs and six types of mating designs have been described so far: bi-parental progenies (BIP), polycross,topcross, North Carolina (I, II, III), Diallels (I, II, III, IV) and Line × tester design. In all mating designs, the individuals are taken randomly and crossed to produce progenies which are related to each other as half-sibs or full-sibs (Nduwumuremyi*et al* 2013).

A diallel cross is a set of all possible mating among several genotypes, which may be individuals, clones or homozygous lines. It estimates the genetic components of total variance of quantitative characters, general and specific combining abilities of inbreed lines involved in the crosses (Narain, 1990). The diallel analyses was developed in order to generate information on the genetic mechanisms controlling the inheritance of various characters in first filial generation.

Griffing (1956) proposed practical methods of diallel analyses depending on the material involved in the analyses. These are: method 1, which includes parents (n), n (n-1)/2 crossesand reciprocals; method 2, involves parents and F1's only; method 3, includes F1's and reciprocals and method 4, F1's only. Griffing (1956) has also described the method of analyses of combining ability as model I (fixed effect) and model II (random effect) from which one can choose the best fitting as model and method depending on the nature of the study and materials employed. In most cases, a random sample is unlikely, since breeders usually select parental lines to fit the specific breeding objectives. In addition, he suggested that the parents need not be used unless maternal effects are suspected. Thus, among biometrical genetic methods available to obtain information concerning the inheritance of quantitative traits, diallel analyses developed by Griffing (1956) is one of the most commonly used one. It has proven informative in determining the inheritance of quantitative traits of interests to plant breeders (Hallauer and Miranda, 1988; Hill *et al*., 2001).

2.6 Heterosis

Shull (1952)defined heterosis as increase in vigor, size, fruitfulness, speed of development, resistance to disease and pest, or to climatic changes, manifested by cross bred organisms as compared with corresponding inbred. Heterosis is usually described in terms of the superiority of F1 hybrid over some measure of parental performance. It is measured as improvement of F1 over the mean of both parents (mid parent heterosis) (Stuber, 1999); over the mean of the better parent (better parent heterosis) (Surendran*et al.,* 1994). From a commercial point of view, heterosis may also be measured as the degree of hybrid performance over the best available variety, and this is called standard heterosis or economic heterosis (Virmani and Edwards, 1983).Heterosis is important in maize breedingand is dependent on level of dominance and differences in gene frequency. The manifestation of heterosis depends on genetic divergence of the two parental varieties (Hallauer and Miranda, 1988).

Heterosis was first exploited in the 1930s: with large scale production of maize hybrid in USA. Even if exploitation of heterosis has contributed to the increased production of food crops globally, little is known on the genetic basis of heterosis. Classically, two hypotheses are suggested as genetic explanations for the phenomenon of heterosis in hybrids.These are dominance and over-dominance hypotheses. According to the dominance hypothesis, heterosis develops due to accumulation of dominant and superior alleles masking deleterious recessive alleles at multiple sites, resulting in superior manifestation of the trait in the hybrid progenies to any of the parents, whereas the over dominance hypothesis describes the phenomena of heterosis to superiority of heterozygous combination of alleles to any of the homozygous alleles in the parental inbred lines; therefore, increased vigor is proportional to the amount of heterozygosity across the genome (Lamkey and Edwards, 1999). Krivanek*et al*. (2007) declared that heterosis and combining ability are prerequisites for developing economically viable hybrid maize varieties.

Heterosis is an important trait used by breeders to evaluate the performance of offspring in relation to their parents. It estimates the enhanced performance of hybrids compared to their parents. Generally, heterosis is manifested as an increase in vigor, size, growth rate, yield or some other characteristics. But in some cases, the hybrid may be lower than in performance than the weaker parent, which is also considered as heterosis. That means heterosis can be positive or negative. The interpretation of heterosis depends on the nature of trait under study and the way it is measured. For example, a positive heterosis is preferred in yield studies because it shows inclination towards high yield (Beyene, 2016). On the other hand, a negative heterosis is preferred in disease resistance and days to maturity. A negative heterosis in disease parameters shows that, breeding materials could lead towards resistance direction while a positive heterosis would take towards susceptibility of the genotypes, and negative heterosis in days to maturity parameter shows the earliness of the inbred lines.

The knowledge of gene action and hybrid vigor or heterosis helps in identification of superior F1 hybrids in order to use further in future breeding programs (Radhika*et al*., 2001). Gudeta (2007) reported both positive and negative heterosis over better parent heterosis ranging from -14.33% to 331.65% at Ambo, -33.39% to 183.69% at Haramaya and -23.5% to 412.9 % at Holeta for grain yield in line by tester crosses of highland maize materials. He also reported significant better parent heterosis for other agronomic traits such as plant and ear height, days to anthesis and silking, kernel rows per ear, kernels per row, thousand kernel weights in each of the locations. Legesse *et al*. (2009) and Mossisa*et al*. (2009) also reported positive and negative standard heterosis over checks for mid altitude maize growing areas of Ethiopia. Similarly, Koppad (2007) reported significant heterosis over the standard checks in plant height, ear height, ear girth, number of kernels per row, number of kernel row per ear, hundred grain weight, shelling percentage and grain yield per hectare in his study on identification of superior parental combinations based on three way cross hybrid performance comprised of hybridsinvolving twenty eight parents along with four checks in maize.

Ziggiju and Legesse(2016) studied the standard heterosis of eleven pipeline maize hybrids with two checks and theyindicated that, the estimates of standard heterois over the best standard checks showed significant difference among genotypes for grain yield.In their study, nine hybrids exhibited significant andnegative standard heterosis over the best check, while two hybrids showedsignificant and positive standard heterosis over standard check. Standard heterosis over the standard checksfor this trait ranged from -38.72% to 8.62%.

In study of heterosis and combining ability of mid altitude quality protein maize inbred lines at Bako western Ethiopia, Beyene (2016)reported that highest positive mid and better parents heterosis was observed for grain yield and yield related traits, indicating the possibility of increasing grain yield and yield related characters via hybridization. He also reported negative heterosis was observed for phenology and growth traits, and diseases parameters as well.

Natol*et al*.(2017) studied standard heterosis of sixty four hybrids of maize with two checks for yield and yield related traits and reported considerable amount of positive and negative heterosis for the studied traits. They identified three crosses that had positive and significant standard heterosis for grain yield over the two checks.

In a study of combining ability, heterosis and heterotic grouping of quality protein maize inbred lines at Bako western Ethiopia, Dufera*et al.* (2018) reported that three crosses exhibited the highest mid and better parent heterosis for grain yield.They also identified three crosses that had negative and significant mid and better parent heterosis for disease parameters.

2.7 Correlation

Correlation measures the degree ofassociation, geneticor non-genetic, between two or more characters and is measured by a correlation coefficient(Hallauer and Miranda, 1988).In genetics there are two main causes of correlation between characters, genetic and environmental. The genetic cause of correlation is mainly pleiotropy, though linkage is a cause of transient correlation, particularly in population derived from crosses between divergent strains (Falconer and Mackay, 1996). It has established in classical genetics that many genes have various effects; i.e., some genes seem to affect traits that are unrelated. Genes that have diverse effects are pleiotropic, i.e., the same gene affects different traits in a complementary way. The existence of pleiotropic effects of genes in different classical genetic studies showed the presence of pleiotropy in different quantitatively inherited traits. Then it is possible that selection may be exerted on secondary traits that have greater heritability than the primary trait. Indirect selection will be effective if the heritability of the secondary trait is greater than that of the primary trait and the genetic correlation between them is substantial (Hallauer and Miranda, 1988).

Genetic correlation is of interest to determine the degree of association between traits and how they may enhance selection. Genetic correlation is useful whether indirect selection gives greater response than direct selection for the same trait. This depends on estimates of heritability for each trait and genetic correlation between them. Indirect selection for a trait as complex as yield, however, is not credible (Berhanu, 2009). One of the reasons is that the genetic correlation of traits with grain yield is frequently too small to compensate for greater heritability. Another important reason is that grain yield is an expression of fitness and drastic changes in one component of yield are accompanied by adjustments in other components. The association between two characters that can be directly observed is the correlation of phenotypic values, or the phenotypic correlation. This is determined from measurements of the two characters in a number of individuals of the population (Hallauer and Miranda, 1988).

In maize, both genetic and environmental correlations have been extensively studied by various researchers and their importance with respect to a particular trait has been well documented. Mohammad *et al*. (2003); Saleem *et al*. (2008); Beyene (2016) observed genotypic and phenotypic correlations for grain yield and its components. The results revealed that ear length was positively and highly significantly correlated with grain yield per plant, plant height, number of kernel rows per ears, days to anthesis and days to silking. Similarly, Yousuf and Saleem (2001) evaluated seventy-four S1 families of maize population. In their study, grain yieldshowed significant genotypic correlation with plant height, number of kernel rows per ear and number of kernels per row. Both reports suggested the possibility of selection for grain yield through selection for the traits that showed positive and significant correlation. Hadji (2004) reported that grain yield showed significant and positive correlation with days to maturity, ear height, number of ears per plant and ear diameter at phenotypic level. While, days to anthesis, days tosilking and number of diseased ear exhibited significant and negative phenotypic correlation with grain yield. At both phenotypic and genotypic level; plant height, ear length, number of kernel per row and thousand kernel weight revealed significant and positive correlation with grain yield.

In correlation studies for grain yield and yield attributes in maize, Nagarajan and Nallathambi(2017)revealed that cob length (0.794), hundred grain weight (0.762), cob diameter (0.751), number of kernels per row (0.704), number of leaves above the cob (0.555), plant height (0.529), shelling percentage (0.506), number of kernel rows per cob (0.428), fodder yield per plant (0.323), ear height (0.284) and days to maturity (0.008) showed significant positive association with grain yield per plant. Days to anthesis (-0.060)and days to silking (-0.086) showed significant negative association with grain yield per plant.

Asima*et al.* (2018) inferred that genotypic and phenotypic correlations among ten morpho-physiological and yield traits in maize lines were significant. They reported that grain yield per plotwas positively correlated with hundred-seed weight, ears per plot, chlorophyll content, plant height, ear height and number of kernels per row indicating the importance of these traits in selection for yield.

3 MATERIALS AND METHODS

3.1 Descriptions of Experimental Sites

The experimental sites used for this experiment were two representative sites of highland sub-humid agro-ecologyin Ethiopia, *viz*., Ambo Agricultural Research Centre and Kulumsa Agricultural Research Centers. The former is the main breeding station for highland maize germplasm development(Dawit *et al*., 2014). This center is situated at 114 km west of Addis Ababaandlocated at $8^o57'$N latitude, $38^o7'$E longitude with an altitude of 2225 meters above sea level. The center receives an average annual rainfall of 1050 mm with average minimum and maximum temperatures of 10.4°C and 26.3°C, respectively, and relative humidity of 64.4%. The major soil type is heavy vertisolwithtextureof18% silt, 15% sand, 1.5% organic contentand with P^H of 7.8 for the most top soil (0–30 cm). Kulumsa is located 165 km south-east of Addis Ababa in the highlands of Arsi zone. Geographically, Kulumsa lies at $8^05'$N latitude,$39^o10'$Elongitude with an altitude of 2200 m.a.s.l and is located in a tepid to cool, moist plain agro-ecological zone. The average annual rainfall at the research center is 830mm per annum. The mean maximum and minimum temperatures are 23.2^oc and 10^oc, respectively. The soils are luvisol/eutric nitosols with P^H of 6.8 at 0-30 cm of soil depth.

3.2 Experimental Materials

Nine inbred lines obtained from Ambo highland maize breeding program were crossed using diallel mating design during the main cropping season of 2016 and thirty-six single cross hybrids were generated. The list of inbred lines and their origin is presented in Table 1. The inbred lines used in the crosses were DH (double haploid) lineswhich were originally obtained from CIMMYT-Zimbabwe and were locally selected based on previous field performances of the inbred lines in testcross evaluations for adaptation, disease reaction and general combining abilityby the highland maize breeding program. The thirty-six F_1crosses together with four commercial hybrid checks: Argane, Kolba, Jibat and Wench were used in the hybrid trial evaluation in 2017.

Table 1.The list of inbred lines used to make the diallel crosses for the study

Entry	Pedigree	Seed Source
1	(INTA-F2-192-2-1-1-1-B*9/CML505-B)DH-3060-B-B-#	AHMBP*
2	(LPSC7-C7-F64-2-6-2-1-B/CML488)DH-3033-B-B-#	-do-
3	(CML444/CML539)DH-3091-B-B-#	-do-
4	(CML144/CML159)DH-3049-B-B-#	-do-
5	([LZ956441/LZ966205]-B-3-4-4-B-5-B*7-B/DTPWC9-F109-2-6-1-1-B)DH-3001-B-B-#	-do-
6	(CML545/CML505)DH-10-B-#	-do-
7	(CML545/CML505)DH-44-B-#	-do-
8	([CML312/[TUXPSEQ]C1F2/P49-SR]F2-45-3-2-1-BB//INTA-F2-192-2-1-1-1-B*4]-1-5-1-2-1-B*6/CML505)DH-11-B-#	-do-
9	(CML312/CML442)DH-3002-B-B-#	-do-

*AHMBP = Ambo Highland Maize Breeding Program

3.3 Experimental Design and Trial Management

The 36 F_1 crosses plus four hybrid commercial checks adapted to the highland agro-ecology of Ethiopia were planted using alpha lattice design (Patterson and Williams, 1976) with two replications each of which have eight blocks with five entries in each of the blocks. Design and randomization of the trials were generated using CIMMYT’s Field book software(Bindiganavile*et al*. (2007)).

At the experimental sites, the trials were hand planted with two seeds per hill, which later thinned to one plant per hill at the 2-4 leaf stage to get a total plant population of 53,333 per hectare. Reliable moisture level of the soil was assured before planting so as to insure good germination and seedling development. Pre-emergence herbicide, Premagram Gold 660 at the rate of 5lt ha^{-1}, was applied at planting to control weeds followed by hand weeding at a later stage of crop emergence. Each entry (both single crosses and standard checks) were placed in a one-row plot of 5.25 m long and 0.75 m apart. Distance between plants was 0.25 m.

The recommended rate of inorganic fertilizers, i.e., 150 and 200 kg ha^{-1}ofDAP and urea, respectively,wereused.Urea was applied in two splits, *viz*., half of it was applied when plantshadeight leaves or reached knee height, and the rest was applied at flag leaf emergencebefore flowering at both Kulumsa and Ambo. Other standard cultural and agronomic practices were followed in trial management as per recommendations for the areas.

3.4 Data Collected

The procedure of data collection followed CIMMYT'S manual for managing trials and reporting data(CIMMYT, 1985):

3.4.1 Data collected on plot base:

- **Days to 50% anthesis (DA):**It was recorded as the number of days from emergence to when 50% of the plants in a plot shed pollen.
- **Days to 50% silking (DS):**It was recorded as the number of days from plant emergence to when 50% of the plants in a plot emerge 2-3 cm long silk.
- **Anthesis-silking interval (ASI):**it was calculated asthe difference between days to silking and anthesis (ASI = DS – DA).
- **Grain yield (GY) (t -ha^{-1}):** The total grain yield from all the ears of each experimental unit was recorded. This was adjusted to 12.5% moisture level to estimate grain yield per hectare. Which was calculated by the following formula:

$$\mathrm{GY} = \frac{\text{Ear weight}(100 - \text{moisture})(\text{shelling }\%)\text{number of plants/plot} \times 10}{(100 - 12.5)(\text{area harvested})}$$

- **Thousand kernel weight (TKW) (g):** After shelling, random kernels from the bulk of each experimental unit were counted using a photoelectric seed counter and weighed in grams after the moisture adjusted to 12.5%.

3.4.2 Datacollected on plant base

- **Ear height (EH) (cm):** The average height of five randomly taken plants measured from the ground level to the upper most ear bearing node. The measurement was made two weeks after pollen shedding has ceased.
- **Plant height (PH) (cm):**It was measured as the height from the soil surface to the base of the tassel branch. Like ear height, this was also measured two weeks after pollen shedding has ceased from the same plants used for ear height.
- **Ear length (EL) (cm):**It was measured from the base of the ear to tip by ruler. It was measured as the average length of five randomly taken ears from each experimental unit.
- **Ear diameter (ED) (cm):** This was measured at the mid-way along ear length byusing the instrument called caliper. It was measured as the average diameter of fiverandomly taken ears from each experimental plot.
- **Number of ears per plant (EPP):** The total number of ears harvested from a plot divided by the number of plants in that particular plot.
- **Number of rows per ear (RPE):** This was recorded as the average number of kernel rows per ear from five randomly taken ears.
- **Number of kernels per row (KPR):** This was recorded as the average number of kernels per row from five randomly taken ears.

3.5 Statistical Analyses

3.5.1 Analyses of variance (ANOVA)

Before data analyses, anthesis-silking interval (ASI) was normalized using $\ln\sqrt{ASI + 10}$assuggested by Bolanos and Edmeades (1996). Analysis of variance (ANOVA) per individual and across locations was carried out using PROC MIXEDmethod = type3 procedure in SAS (2003)by considering genotypes as fixed effects and replications and blocks within replications as random effects. Furthermore, environments, replications within environments and blocks within replications by environment interaction were considered as random and genotypes as fixed effects in combined analysis following Moore and Dixon (2015) procedure. Combinedanalyses were performed for the traits that showed significant genotypic mean squares forindividual location analyses and after testing homogeneityof error variance using Bartlett's test (Gomez and Gomez, 1984). In combined analyses, entries and location effects were tested using themean squares ofentry xlocation interactionas an error term,whileentry x location interaction mean squares were tested against pooled error.

3.5.2 Combining ability analyses

Combining ability analyseswas done for traits that showed significant differences among genotypes using a modification of the DIALLEL-SASprogram (Zhang *et al.*,2005). TheGriffing's Method IV (crosses only) and Model I (fixed) of diallelanalyses (Griffing, 1956) was used to estimate combining ability effects(Table 2).The significance of GCA and SCA effects were tested against the respective standard errors of GCA and SCA effects, respectively using t-test (Griffing, 1956; Singhand Chaudhary, 1985).In combined combining ability analyses, the significance of GCA and SCA sources of variations were determined using the corresponding interactions with location as error term.The mean squares attributableto all the interactions with locations were tested against pooled error.

The basic genetic model (a linear mathematical model) developed by Griffing (1956) for an observation made on the genotype for Method IV and model I wasused as follows:
Combining ability for individual location was analyzed using the mathematical model:

$$X_{ij} = \mu + g_i + g_j + s_{ij} + \frac{1}{bc}\sum_k \sum_l e_{ijkl} \quad \begin{cases} i, j = 1, \ldots, p, \\ k = 1, \ldots, b, \\ l = 1, \ldots, c. \end{cases}$$

Where,

X_{ij} = the value of a character measured on cross of ith and jth parents.

μ = Population mean

g_i (g_j) = the general combing ability effect

s_{ij} = the specific combing ability effect

e_{ijkl} = is the error effect

p, b and c = number of parents, blocks and sampled plants, respectively

Combining ability for across locationswasanalyzed using the mathematical modelas follows:

$$\mathbf{Y_{ijk}=m+l_k+r(l_k)+g_i+g_j+s_{ij}+(lg)_{ik}+(lg)_{jk}+(ls)_{ijk}+e_{ijk}.}$$

Where,

Y_{ijk} is the mean over replications and blocks within replications of the single cross (ij) in the k^{th} environment; m is the overall mean; lk is the k^{th} environment effect; $r(l_k)$is is replication effect within environment, g_i, g_j, and s_{ij} are general and specific combining ability effects, $(lg)_{ik}$ and $(lg)_{jk}$ are GCA effects of i and j parents and their interaction with environment, respectively; $(ls)_{ijk}$ is SCA interaction with environment; and $e_{ijk}$is the error term.

3.5.3 Estimation of combing ability effects

For the traits that showed significant mean squares for general and specific combing ability, the GCA effect of parents and SCA effects of ij^{th} crosses was estimated as:

$$g_i = \frac{1}{n(n-2)}[(nYi - 2Y)]$$

$$S_{ij} = Y_{ij} - \frac{1}{n-2}[Yi + Yj] + \frac{2}{(n-1)(n-2)}Y..$$

Where, g_i = estimates of general combing ability (GCA) effects of i^{th} parents

S_{ij} = estimates of specific combining ability (SCA) effects of ij^{th} crosses

Y_i = array total of the crosses involving the i^{th} parent

Yj = array total of the crosses involving the j^{th} parent

Yij = j^{th} parent mean value in the diallel table

Y=grand total of ‘n’ parental lines and n (n-1)/2 progenies

3.5.4 Standard errors for combining ability effects

In order to test the significant difference between any two GCA and SCA effects, the standard errors for both were calculated as follow.

1. Standard error for general combining ability effects

$$\text{SE (gca effects)} = \sqrt{\frac{n-1}{n(n-2)}\sigma^2}$$

2. Standard error for specific combining ability effects

$$\text{SE (sca effects)} = \sqrt{\frac{(n-3)}{(n-1)}\sigma^2}$$

Inorder to test significance of GCA and SCA effects,t-value was calculatedas follows:

$$\text{t-cal(gca)i}=\frac{\text{gca}}{\text{Se(gi)}}\text{ ; t-cal(gca)j}=\frac{\text{gca}}{\text{Se(gj)}}\text{ ; t-cal(sca)ij}=\frac{\text{sca}}{\text{Se(sij)}}$$

Where,

gca(i) and gca(j)= general combining ability of i^{th} and j^{th} parents respectively

sca(ij)= specific combining ability of ij^{th} cross

se(gi) and se(gj)= standard error of gca of i^{th} parent and gca of j^{th} parent, respectively

se(sij)= standard error of sca of ij^{th} cross

t-tabular value was estimated by using excel i.e TINV(prb, Dfe)

t-calculated value is compared with t-table value at error degrees of freedom.

3.5.5 Estimation of standard heterosis

Standard heterosis oreconomic heterosis in percent was calculated for the characters that showed significantdifferences for genotypes following the method suggested by Falconer and Mackay (1996).This was computed as percentage increase or decrease of the cross performances over the beststandard check. Kolba was used as standard check.

$$\text{SH (\%)} = \frac{(F1-SV)}{SV} \times 100$$

F1 ═ Mean value of a cross
SV = Mean value of standard check
SH= Standard heterosis

Variety test of significance for percent heterosis was made using the t-test. The standard errors of the difference for heterosis and t-value were computed as follows (Singh, 1985).

$$\text{t (standard cross)} = \frac{F1-SV}{SE(d)}$$

$$\text{SE (d) for SH} = \sqrt{2MSe/r}$$

Where, SE (d) = standard error of the difference
SH= standardheterosis
Me = error mean square
r = number of replications

The computed t value was tested against the t tabular-value at degree of freedom for error.

3.5.6 Estimation of genotypic and phenotypic correlations

Genotypic and phenotypic correlation coefficients were calculated according to Al-Jibouri*et al.* (1958) from the analyses of variance and covariance as follow:

$$Genotypic\ r = \frac{\sigma_{g12}}{\sqrt{({\sigma^2}_{g1})\ ({\sigma^2}_{g2})}}$$

$$Phenotypic\ r = \frac{\sigma_{p12}}{\sqrt{(\sigma^2{}_{p1})\ (\sigma^2{}_{p2})}}$$

where σ_{p12} is the phenotypic covariance between the two traits, $\sigma^2{}_{p1}$ is the phenotypic variance of the first trait and $\sigma^2{}_{p2}$ is phenotypic variance of the second trait, $\sigma^2{}_{g12}$ is the genotypic covariance between the two traits, $\sigma^2{}_{g1}$ is the genotypic variance of the first trait and $\sigma^2{}_{g2}$ is the genotypic variance of the second traits.

The phenotypic correlation coefficients were tested for traits of significance with 'r' table for sample correlation coefficients at n-2 degree of freedom, as suggested by (Gomez and Gomez, 1984); while the genotypic correlation coefficients were tested for their significance using the formula adopted by (Robertson, 1959).

$$t = \frac{r_{gxy}}{SE_{gxy}}$$

$$SE_{gxy} = \sqrt{\frac{(1 - r^2)^2}{2h^2{}_x h^2{}_y}}$$

The 't' value, calculated using the above formula, was compared with 't' tabulated at (g-2) degree of freedom at 1% and 5% levels of significance; where, r_{gxy} is the genotypic correlation between x and y traits; g = number of genotypes, h^2_x and h^2_y are heritability for traits x and y, respectively.

4 RESULTS AND DISCUSSION

4.1 Analyses of Variance

Analyses of variances were conducted for the two individual locations; namely, Ambo and Kulumsa (Table 2 and 3). Subsequently, combined analyses were performed for the traits that showed significant genotypic mean squares for individual location analyses and had homogenous error variance analyzed using Bartlett's test (Gomez and Gomez, 1984). Analyses of variance (ANOVA) conducted for individual location for the hybrid trial (including 36 hybrids and four standard checks) showed significant differences among genotypes for most of the traits, except for number of kernel rows per ear and number of kernels per row at both locations, Ear length at Ambo and Ear height at Kulumsa (Tables 2 and 3).

The combined analyses of variances revealed highly significant ($P<0.01$) differences among the 40 genotypes including checks for all traits studied under combined analyses (Table 4), indicating the presence of inherent variation among the materials, which makes selection possible. Desirable genes from these genotypes can effectively be utilized to develop high performing hybrids. Similarly, several previous studies reported significant differences among genotypes for grain yield and grain yield related traits in different sets of maize genotypes (Dagne *et al*., 2007; Demissew, 2014; Habtamu *et al*., 2015; Amare *et al.*, 2016;Tolera*et al.*, 2017 and Dufera*et al.*, 2018).

The interaction between genotypes and locations (G x LOC) was significant for grain yield, Anthesis-silking interval and ear diameter, indicating that genotypes performed differently across locations, which means that the relative performances of the genotypes were influenced by the varying environmental conditions for these traits. On the other handdays to anthesis, days to silking, plant height, number of ears per plant and thousand kernel weight showed non-significant difference for genotype by location interaction (Table 4), indicating that the relative performance of the genotypes was not influenced by the varying environmental conditions for these traits. In consistent with the present finding, Gudeta (2007) reported significant G x LOC interaction for grain yield, number of rows per ear and ear diameter and non-significant G x LOC interaction for number of ears per plant.

Table 2. Analyses of variance for grain yield and other agronomic traits of 36 diallel crosses and four hybrid checks evaluated at Ambo in 2017.

Trait	Sources of variation					
	Genotype (DF = 39)	Replication (DF = 1)	Block(Rep) (DF =14)	Error (DF =25)	Grand mean	CV(%)
GY	3.37**	0.0005^{ns}	1.33*	0.61	7.14	10.92
DA	19.75**	0.20^{ns}	2.25*	0.97	92.48	1.07
DS	26.74**	0.45^{ns}	4.23*	1.73	93.60	1.41
ASI	0.0074**	0.00001^{ns}	0.002^{ns}	0.003	1.19	4.32
PH	596.44*	1304.10^{ns}	328.70^{ns}	315.90	231.80	7.67
EH	281.47**	27.61^{ns}	124.10^{ns}	107.80	123.30	8.42
EPP	0.07**	0.00001^{ns}	0.035*	0.02	1.37	9.30
EL	2.89^{ns}	4.05^{ns}	2.22^{ns}	2.16	15.80	9.29
ED	0.08**	0.35**	0.04^{ns}	0.03	4.43	3.62
RPE	0.92^{ns}	2.18^{ns}	0.93^{ns}	0.86	12.96	7.17
KPR	12.42^{ns}	33.80^{ns}	7.19^{ns}	11.42	31.95	10.58
TKW	3288.40*	325.22^{ns}	1197^{ns}	1581	306.60	12.97

** Significant at 0.01 level of probability, * = significant at 0.05 level of probability, ns = non-significant,DF = degrees of freedom, Rep= replication, GY= grain yield, DA= number of days to anthesis, DS= number of days to silking, ASI= anthesis silking interval, PH= plant height, EH= ear height, EPP= number of ears per plant, EL= ear length, ED= ear diameter, RPE= number of kernel rows per ear, KPR= number of kernels per row and TKWT =1000-kernel weight.

Table 3.Analyses of variance for grain yield and other agronomic traits of 36 diallel crosses and four commercial hybrid checks evaluated at Kulumsa in 2017.

	Sources of variation					
Trait	Genotype (DF = 39)	Replication (DF = 1)	Block(Rep) (DF =14)	Error (DF =25)	Grand mean	CV(%)
GY	3.55**	1.16^{ns}	1.08^{ns}	0.64	9.53	8.40
DA	27.36**	7.20^{ns}	4.02^{ns}	4.26	88.18	2.34
DS	28.10**	12.01^{ns}	4.96^{ns}	3.68	90.90	2.11
ASI	0.0007*	0.00098^{ns}	0.0003^{ns}	0.00035	1.27	1.47
PH	618.10**	84.05^{ns}	123.90*	51.30	197	3.64
EH	162.60^{ns}	485.10^{ns}	105.40^{ns}	132.40	99.54	11.56
EPP	0.08**	0.02^{ns}	0.02^{ns}	0.03	1.48	12.01
EL	1.80**	2.81*	0.59^{ns}	0.62	15.64	5.02
ED	0.07**	0.001^{ns}	0.02^{ns}	0.03	4.63	3.47
RPE	0.96^{ns}	0.00^{ns}	0.61^{ns}	0.82	12.78	7.07
KPR	9.21^{ns}	14.45^{ns}	6.96^{ns}	7.85	36.00	7.78
TKW	3392.30**	1332^{ns}	1090^{ns}	1292	380.30	9.45

** Significant at 0.01 level of probability, * = significant at 0.05 level of probability, ns = non-significant,DF = degrees of freedom, Rep= replication,GY= grain yield, DA= number of days to anthesis, DS= number of days to silking, ASI= anthesis silking interval, PH= plant height, EH= ear height, EPP= number of ears per plant, EL= ear length, ED= ear diameter, RPE= number of kernel rows per ear, KPR= number of kernels per row, and TKWT =1000-kernel weight**.**

Table 4.Combined analyses of variance for grain yield and yield related traits of 36 diallel crosses and four hybrid checks evaluated at Ambo and Kulumsa.

	Sources of variation								
Trait	Loc (DF = 1)	Rep(Loc) (DF = 2)	Blk(Loc,rep) (DF = 28)	Genotype (DF = 39)	Genotype*Loc (DF = 39)	Error (DF =50)	Grand mean	SE(m)	CV(%)
GY	228.90**	0.57^{ns}	1.20*	4.81**	1.89**	0.62	8.34	±0.56	9.48
DA	739.60**	3.70^{ns}	3.13^{ns}	41.56**	3.40^{ns}	2.62	90.32	±1.14	1.79
DS	288.90**	6.23^{ns}	4.59*	47.64**	3.79^{ns}	2.71	92.25	±1.16	1.78
ASI	0.20**	0.0005^{ns}	0.001^{ns}	0.004**	0.003**	0.0015	1.23	±0.03	3.15
PH	48546.05**	694.08*	226.27^{ns}	951.19**	196.36^{ns}	183.59	214.36	±9.58	6.32
EPP	0.48**	0.008^{ns}	0.03^{ns}	0.08**	0.05 ^{ns}	0.02	1.42	±0.1	10.85
ED	1.64**	0.17 ^{ns}	0.03^{ns}	0.11**	0.03**	0.03	4.53	±0.12	3.54
TKW	217378.16 ^{ns}	828.46^{ns}	1143.64^{ns}	4907.65**	1207.44^{ns}	1436.51	343.41	±26.8	11.04

** Significant at 0.01 level of probability, * = significant at 0.05 level of probability, ns = non-significant,Loc= location, Rep= replication, Blk= block, DF= degrees of freedom,SE(m)= standard error of mean, GY= grain yield, DA= number of days to anthesis, DS= number of days to silking, ASI= anthesis silking interval, PH= plant height,EPP= number of ears per plant, ED= ear diameter and TKWT =1000-kernel weight**.**

4.1 Genotypes performances

Mean values of all genotypes evaluated for grain yield and related traits in each location and across locations were presented in Tables 6-8.At ambo, the overall-mean grain yield was7.1t/ha ranging from 4.6 t/ha to 11.24 t/ha (Table5). Cross combination L4 x L8 (9.57 t/ha) showed higher grain yield than the three hybrid checks except Kolba which showed highest grain yield of 11.24 t/ha,while the other cross combinations such as L4 x L7 (8.67 t/ha), L1 x L3 (8.36 t/ha), L6 x L8 (8.27 t/ha) and L3 x L4 (8.00 t/ha) showed higher grain yield than only one check (Argane) and the rest crosses except L4 x L8 were all inferior compared to the checks (Table 6). The least yield was obtained from crosses L5 x L9 (4.6 t/ha), L5 x L6 (4.71 t/ha), L2x L9 (5.49 t/ha), L3 x L5 (5.65 t/ha) and L1 x L6 (5.82 t/ha) (Table 5). The crosses with mean values better than the standard checks indicated the possibility of obtaining good hybrid (s) for future use in breeding program or for direct release. In line with this, Dagne *et al* (2010), Amare *et al*., 2016; Beyene, 2016,Dufera*et al.*, 2018 identified genotypes performing better than check forgrain yield.

The overall mean of days to anthesis and silking for all genotypes at ambo were 92.5 and 93.6 respectively (Table 5)and ranged from 88 to 106 and 87 to 106 days, respectively.Cross L5 x L9 took longer days to both anthesis and silking (106 days); while the shortest number of days were recorded for the standard check Kolba(88) days to anthesis and for the cross L4 x L8 (87) days to silking (Table 5). Most of the crosses showed longest number of days to anthesis and silking.This shows that those crosses could be grouped as late maturing types. Late maturing crosses are important in the breeding programs for development of high yielding hybrids in areas that receive sufficient rain fall (Girma*et al.*, 2015).

Anthesis-silking interval (ASI) ranged from 1.04 days for L2 x L8 to 1.3 days for L3 x L7 (Table 5). In general, all crosses exhibited short ASI or short gaps between anthesis and silking days which is a desired character for good seed setting. Positive ASI observed for all of the genotypes studied is an expected result as maize is a protoandrous plant in which anthesis normally begins 1-3 days before silk emergence (Rahman *et al*., 2013).At same site, plant and ear height ranged from 198.5 to 278 cm and 104.5 to 160.5cm with mean values of 231.8 cm and 123.3 cm, respectively. The lowest mean value for plant height was exhibited for cross L1 x L7 (198.5 cm), while the lowest mean value for ear height was observed from cross L1 x L8 (104.5 cm). The highest mean values for both plant and ear heights were recorded from one of the checks (Kolba) (Table 5). Genotypes with shorter ear and plant heights could be used as sources of genes for the development of shorter statured varieties.Ear position is one of the traits that determine lodging tolerance as well as vulnerability of ears to wild animals' attack in the field. Maize varieties with too high ear placement and height are prone to lodging, while those with too short ear placement are prone to wild animals attack. In line with this result,Beyene (2016), Abiy (2017) and Tolera*et al.*(2017)also identified genotypes with short and long plant and ear heights.

Number of ears per plant ranged from 1.03 (L1 x L7) to 1.7 (L1 x L3), with an overall mean of 1.37. Six crosses exhibited higher number of ears per plant than the best check, Kolba(Table 5).These genotypes can be selected for yield improvement since theyhad significant and positive genotypic and phenotypic correlation with grain yield (Table 14).Desirability of high number of ears for grain yield improvement was suggested by various authors such as Dagne *et al.* (2010), Demissew *et al.* (2011),Girma*et al.* (2015), Ram *et al.* (2015), Amare *et al.* (2016).The means for ear diameter ranged from 4 to 5 cm with a mean of 4.43 cm. Crosses L4 x L8 (4.95 cm), L1 x L4 (4.8 cm) and L1 x L9 (4.75 cm) displayed the wider ear diameter.Cross (L3 x L9) had the narrowest (4 cm) ear diameter.Seven crosses showed wider ear diameter than the best check Wenchin terms of ear diameter (Table 5). Indicates that these crosses with wider ear diameter could be used for grain yield improvement since increasing ear diameter could lead to increase in number of rows per eari.e they are positively correlated with each other and thus, can contribute for yield improvement (Table 14).

Mean thousand kernel weight ranged from 182.6g (L3 x L9) to 408.5g (L6 x L8) with an overall mean of 306.55g. Two crosses showed thousand kernel weight greater than the best standard check Jibat in terms of thousand kernel weight(Table 5). In line with the present findings, Abiy (2017) reported minimum and maximum values of thousand kernel weight402.78 and 469.35 for the hybrids trial at the same location.

Table 5. Mean values and range of grain yield and yield related traits of diallel crosses and four commercial hybrid checks evaluated at Ambo in 2017.

	Traits								
Value	GY	DA	DS	ASI	PH	EH	EPP	ED	TKW
Minimum	4.6	88	87	1.04	198.5	104.5	1.03	4	182.6
Maximum	11	106	106	1.3	278	160.5	1.7	5	408.5
Grand mean	7.1	92.5	93.6	1.19	231.8	123.3	1.37	4.43	306.55
CV (%)	11	1.07	1.41	4.32	7.67	9.29	9.3	3.6	12.97
LSD $_{(0.05)}$	1.61	2.03	2.71	0.11	36.6	21.38	0.26	0.3	81.89

GY= grain yield, DA= number of days to anthesis, DS= number of days to silking, ASI= anthesis silking interval, PH= plant height, EPP= number of ears per plant, ED= ear diameter, TKWT =1000-kernel weight

Based on the analyses carried out for all traits at Kulumsa showed that the mean grain yield (GY) of the hybrids including checks ranged from 7.60 t/ha to 13.1 t/ha with overall mean of 9.53 t/ha (Table6). At this site, Kolba showed the highest value of grain yield (13.1 t/ha). Cross combination L1 x L3 showed the second highest grain yield of 11.93 t/ha next to Kolba. The other cross combinations such as L3 x L8 (11.59 t/ha) and L7 x L9 (10.91 t/ha) showed higher grain yield than Jibat which showed grain yield value of 10.89 t/ha. The least yield was obtained from the crosses L6 x L7 (7.59 t/ha), L5 x L9 (7.73 t/ha), L6x L8 (7.75 t/ha)and L2 x L9 (7.98 t/ha) (Table 6).

Days to anthesis and silking ranged from 78.5 to 99 and 81.5 to 101with overall means of 88.2 and 90.9 days, respectively. The shortest number of days were recorded for cross L4 x L6to both anthesis (78.5 days) and silking (81.5 days), whereas longest number of days were recorded from crossL3 x L9 (99 days) to anthesis and (101 days) to silking (Table 6).Most of the crosses showed longest number of days to anthesis and silking. Anthesis-silking interval ranged from 1.24days for (L6 x L8), (L2 x L9), (L2 x L8), (L1 x L6), (L8 x L9), (L3 x L7) and (L3 x L9) to 1.30 days for (L3 x L8), (L1 x L4), Argane, Wenchi and Kolba(Table 6). In general, all crosses exhibited short anthesis silking interval or short gaps between anthesis and silking days (Table 6). On the other hand, plant height ranged from 162.5 to 224.5 cm with mean value of 197 cm. The lowest mean value for plant height was observed for the cross L6 x L7, while the highest mean value wasexhibited byJibat(Table 6).

Number of ears per plant ranged from 1.17(L1 x L4) to 1.88 (L3 x L8), with an overall mean of 1.48. Two crosses exhibited higher number of ears per plant than the best check Wenchiin terms of number of ears per plant(Table 6). The mean value of ear length for genotypes was 15.6 cm. The highest ear length value was 18 cm which was exhibited by both (L1 x L2 and Argane)and lowest ear length value was 13.5 cm which was exhibited by both L6 x L9 and L4 x L8. The means for ear diameter ranged from 4.1 to 5.15 cm with over all mean of 4.63 cm. The crosses L3 x L9 (4.1 cm), L2 x L9 (4.3 cm) and L3 x L7 (4.35 cm) had the narrowest ear diameter as compared to other hybrids, whilecrosses L4 x L8 (5.15 cm), L4 x L7 (4.95 cm), L1 x L4 (4.95 cm) and L1 x L8 displayed the wider ear diameter.Ten crosses showed wider ear diameter than the best check Jibat in terms of ear diameter which showed ear diameter of 4.7 cm (Table 6).

At the same site (Kulumsa), significant variations were also observed among genotypes forthousand kernel weight. Mean thousand kernel weight ranged from 245.8g (L3 x L9) to 449.9 g (Jibat) with an overall mean of 380.3 g.

Table 6. Mean values and range of grain yield and yield related traits of diallel crosses and four commercial hybrid checks evaluated at Kulumsa in 2017.

	Traits								
Value	GY	DA	DS	ASI	PH	EPP	EL	ED	TKW
Minimum	7.60	78.5	81.5	1.24	162.5	1.17	13.5	4.1	245.8
Maximum	13.1	99	101	1.30	224.5	1.88	18	5.15	449.9
Grand mean	9.53	88.2	90.9	1.27	197	1.48	15.6	4.63	380.3
CV(%)	8.40	2.34	2.11	1.47	3.64	12.00	5.02	3.47	9.45
LSD$_{(0.05)}$	1.65	4.25	3.95	0.038	14.8	0.37	1.62	0.33	74.03

In combined analyses across locations (Table 7), mean grain yield of the genotypes was 8.34 t/ha with a range of 6.16 t/ha to 11.07 t/ha. Kolba (11.07 t/ha) followed by Jibat (10.91 t/ha), Wenchi (10.43 t/ha) and Argane (10.15t/ha) had higher grain yield, while crosses L5 x L9 (6.16 t/ha) and L2 x L9 (6.74 t/ha) showed lower grain yield. Genotypes that had high grain yield could be used in the breeding program to improve the grain yield. The high heritability (0.64) for this trait indicated the trait was not greatly influenced by the environment. Thus, the selection for this character could be more effective (Table 7). Days to anthesis ranged from 84.25 days (L4 x L6) to 102 days (L5 x L9) with overall mean of 90.33 days. Mean number of days to silking was 92.26 with a range of 85.5 (L4 x L6) to 103.5 (L5 x L9). The heritability values for both days to anthesis and silking were very high (0.92 and 0.93 respectively) indicating the traits were not greatly influenced by environment. Thus, it shows selection for these traits could be more effective and easy since the genetic variability was detected clearly because of low environmental influence (Table 7). Anthesis-silking interval ranged from 1.14 days (L2 x L8) to 1.29 days (L4 x L5) with a mean of 1.23 days (Table 7). Plant height ranged from 185.25 cm (L2 x L6) to 251.25 cm (Kolba) with a mean of 214.37 cm. Genotypes that were earlier in anthesis and silking and shorter in plant height could be used as sources of genes for development of early maturing and shorter statured varieties respectively for highland agro-ecology of Ethiopia.

Mean number of ears per plant of genotypes was 1.42 ranged from 1.18 (L1 x L7) to 1.74 (L1 x L3). The mean for ear diameter ranged from 4.05 to 5.05 cm with over all mean of 4.53 cm. The cross L3 x L9 (4.05 cm) had the narrowest ear diameter as compared to other hybrids, while cross L4 x L8 (5.05 cm) displayed the wider ear diameter. Thousand kernel weight ranged from 214.18 gm for (L3 x L9) to 410.9 gm for (Jibat) with overall mean of 343.41 gm.

Generally, results of individual locations indicated that higher mean grain yield was obtained at Kulumsa (9.53 t/ha) as compared to mean grain yield of Ambo (7.1 t/ha) (Table 5 and 6). None of the crosses performed better than the best commercial check (kolba) at both locations and combined across locations. Suggesting that the crosses were from same heterotic group B. Some cross combinations at both individual locations showed better yield than the other three or two or one commercial checks. Suggests that these hybrids could be used in breeding program to improve the grain yield and other traits of interest. On average, the genotypes evaluated were late in anthesis and silking at Ambo as compared to Kulumsa. This is because Ambo is situated at higher altitudes as compared to Kulumsa (Descriptions of experimental Site page 18 and in addition Appendix Table 3 and 4).

In this study the higher mean for ear diameter and thousand kernel weight were recorded at Kulumsa; while the overall mean of plant height and ear height were maximum at Ambo thanof Kulumsa. Also, hybrids that were earlier in anthesis and silking, shorter in ear and plant heights could be used as sources of genes for development of early maturing and shorter statured varieties respectively. In line with the present results, several researchers identified genotypes performing better than the checks for most yield and yield related traits (Dagne *et al.* 2007; Zerihun, 2011; Shushay, 2014; Beyene, 2016; Ziggiju and Legesse, 2016;Tolera*et al.,* 2017 and Dufera*et al.,* 2018).

Table 7.Mean values of yield and yield related traits of 36 diallel crosses and four commercial checks evaluated at Ambo and Kulumsa in 2017.

	Traits							
Genotypes	**GY**	**DA**	**DS**	**ASI**	**PH**	**EPP**	**ED**	**TKW**
L1*L2	8.80	87.25	88.50	1.21	199.75	1.37	4.53	379.10
L1*L3	10.05	91.75	94.50	1.27	210.75	1.74	4.50	306.48
L1*L4	7.87	88.00	90.25	1.25	198.00	1.22	4.88	363.33
L1*L5	9.03	92.75	95.25	1.26	228.75	1.38	4.58	335.78
L1*L6	7.09	87.00	89.50	1.26	187.50	1.20	4.53	377.33
L1*L7	7.03	88.50	90.50	1.24	192.00	1.18	4.43	358.48
L1*L8	8.25	88.00	89.50	1.21	207.75	1.29	4.83	370.28
L1*L9	7.49	92.75	95.50	1.27	218.75	1.31	4.70	326.03
L2*L3	8.96	91.00	93.25	1.25	219.25	1.62	4.35	329.10
L2*L4	8.85	86.75	88.50	1.23	205.50	1.44	4.60	343.85
L2*L5	7.48	92.75	94.75	1.24	216.75	1.23	4.45	357.15
L2*L6	7.44	86.25	87.25	1.19	185.25	1.48	4.35	350.35
L2*L7	9.06	88.50	90.00	1.22	209.00	1.54	4.40	378.85
L2*L8	8.07	88.50	88.50	1.14	202.25	1.27	4.65	381.90
L2*L9	6.74	94.75	96.00	1.21	212.75	1.41	4.40	276.68
L3*L4	8.55	91.75	94.25	1.26	232.50	1.39	4.48	313.25

Table7(continued)

L3*L5	8.00	96.00	98.25	1.25	237.50	1.44	4.40	290.83
L3*L6	8.75	91.25	92.75	1.22	199.00	1.66	4.33	330.23
L3*L7	7.41	92.00	94.75	1.27	219.50	1.47	4.25	306.90
L3*L8	9.68	92.50	95.50	1.28	224.25	1.71	4.43	328.65
L3*L9	7.34	98.75	100.50	1.23	226.00	1.63	4.05	214.18
L4*L5	8.03	90.50	93.75	1.29	204.50	1.37	4.43	316.20
L4*L6	7.54	84.25	85.50	1.21	194.50	1.23	4.58	312.90
L4*L7	8.78	86.75	89.50	1.27	207.00	1.36	4.75	384.00
L4*L8	9.41	86.50	87.00	1.17	228.50	1.30	5.05	378.73
L4*L9	7.59	91.25	93.50	1.25	213.25	1.41	4.58	312.10
L5*L6	7.29	91.00	92.25	1.21	208.75	1.36	4.48	359.75
L5*L7	7.54	93.50	96.00	1.26	232.25	1.29	4.63	334.38
L5*L8	8.13	93.00	95.00	1.24	240.25	1.49	4.73	308.53
L5*L9	6.16	102.00	103.50	1.22	224.00	1.30	4.58	274.20
L6*L7	7.18	86.25	87.50	1.21	188.25	1.25	4.45	405.68
L6*L8	8.01	85.75	86.25	1.17	191.75	1.42	4.63	399.95
L6*L9	7.62	92.50	94.75	1.25	200.75	1.59	4.43	327.28
L7*L8	8.23	86.50	89.00	1.26	198.25	1.26	4.65	389.18
L7*L9	8.42	92.25	94.75	1.26	226.00	1.55	4.40	327.98
L8*L9	9.26	91.75	93.25	1.22	235.50	1.63	4.70	301.28
Argane	10.15	87.75	89.50	1.23	222.50	1.48	4.50	383.55
Kolba	11.07	87.50	90.00	1.26	251.25	1.57	4.55	408.03

Table 7(continued)

Jibat	10.91	88.75	90.00	1.19	239.75	1.55	4.55	410.90
Wenchi	10.43	88.50	91.50	1.28	235.00	1.54	4.50	383.18
Mean	8.34	90.33	92.26	1.23	214.37	1.42	4.53	343.41
LSD $_{(0.05)}$	1.12	2.30	2.34	0.055	19.24	0.22	0.23	53.83
CV (%)	9.48	1.79	1.78	3.15	6.32	10.9	3.54	11.04
R^2	0.95	0.96	0.96	0.88	0.92	0.86	0.88	0.89
H^2	0.64	0.92	0.93	0.12	0.81	0.37	0.76	0.81
Min	6.16	84.25	85.5	1.14	185.25	1.18	4.05	214.18
Max	11.07	102	103.5	1.29	251.25	1.74	5.05	410.9

GY= grain yield, DA= number of days to anthesis, DS= number of days to silking, ASI= anthesis silking interval, PH= plant height, EH= ear height, EPP= number of ears per plant, EL= ear length, ED= ear diameter, RPE= number of kernel rows per ear, KPR= number of kernels per row, and TKWT =1000-kernel weight, R^2 = Coefficient of determination, H^2= heritability in broad sense, Min= minimum, Max= maximum.

4.2 Standard Heterosis

The estimates of standard heterosis over the best standard check (Kolba) was computed for grain yield and yield related traits that showed significant differences among genotypes and the result is presented in Table 8. Standard heterosis for grain yield over the best check Kolba ranged from -44.35%(L5 x L9) to -8.31%(L1 x L3). Out of the 36 hybrids studied, none of the hybrids had positive and significant as well as negative and significant heterosis over the standard check Kolba (Table 8). All hybrids exhibited non-significant and negative standard heterosis over the best standard check Kolba. This indicates that the check hybrid Kolba was more prolific than all the F1 hybrids and indicating the lack of significant heterosis among the inbred lines used in the current study. The highest negative standard heterosis was manifested by L5 x L9 (-44.35 %) followed by L2 x L9 (-39.11%) and L1 x L7 (-36.49%) over Kolba for grain yield. Positive standard heterosis was considered to be desirable for grain yield as it indicates increased yield over the existing standard check. In contrast to this finding, several other authors reported positive and significant heterosis for grain yield over best standard check indicating the possibility of increasing yield by exploiting heterotic potential of maize genotypes (Tiwari, 2003; Twumasi *et al*., 2003; Amiruzzaman *et al*., 2010; Wali*et al*., 2010; Habtamu *et al*., 2015;Ziggiju and Legesse, 2016; Dufera*et al.*, 2018).

Negative standard heterosis was considered as desirable for days to anthesis and silking as it indicates the earliness of a genotype and the reverse is true for the crosses with positive and significant standard heterosis. Standard heterosis over best check Kolba ranged from -3.71% to 16.57% and -5.00% to 15.00%, respectively,for days to anthesis and silking which was revealed by crosses(L4 x L6) and (L5 x L9), respectively,for both traits. Out of the 36hybrids studied, ten crosses exhibited negative and non-significant standard heterosis for days to anthesis, while twenty of the hybrids showed significant heterosis and the rest six hybrids exhibited positive and non-significant heterosis for days to anthesis in undesired direction. For days to silking, out of 36hybrids, twelve crosses revealed negative heterosis, while only two crosses (L4 x L6) and (L6 x L8) revealed significant heterosis in desired direction over best standard check. Twenty four crosses showed positive heterosis over best standard check. Among them, seventeen of the crosses revealed significant heterosis in undesired direction.

Negative heterosis for these traits indicated earliness as compared to the standard check (Kolba).In line with this study, Natol*et al*. (2017) also reported negative and non-significant, and positive and significant heterosis for days to anthesis and silking in their study on standard heterosis of maize inbred lines for grain yield and yield related traits at southern Ethiopia. In addition, previous investigators reported significant negative and positive standard heterosis for days to anthesis and silking over standard check (Bayisa, 2004; Mahantesh, 2006; Shushay, 2014; Ziggiju and Legesse, 2016; Abiy, 2017).

For anthesis silking interval, standard heterosis ranged from -9.52 %(L2 x L8) to 2.38% (L4 x L5) overKolba. Almost all crosses showed negative standard heterosis over the best check for anthesis silking interval, indicating the tendency of the crosses to have short interval between anthesis and silking dates than Kolba, which is desirable for synchronization of anthesis and silking, and for seed setting. In line with this study, Dufera*et al.*(2018) reported negative standard heterosis over best checks in their study on combining ability, heterosis and heterotic grouping of quality protein maize inbred lines at bako, western Ethiopia.

The magnitude of standard heterosis for plant height ranged from -26.27% (L2 x L6) to -4.38(L5 x L8) (Table 8). For this trait, all of the crosses showed negative and non-significant heterosis over the best check. This implies that all crosses were shorter in plant height than kolba, which is favorable trait for lodging resistance. This result is in agreement with the findings of Shushay (2014).

For number of ears per plant, standard heterosis among hybrids varied from -24.84(L1 x L7) to 10.83% (L1 x L3). Seven hybrids showed positive standard heterosis over the check kolba. This result indicatedthe prolificacy of the new hybrids over the standard check, Kolba. The rest 29 crosses showed negative standard heterosis over best check and are undesirable for high number of ear per plant. Similarly significant positive and negative standard heterosis was observed by Koppad (2007), Shushay (2014) and Ziggiju and Legesse, 2016 for number of ears per plant.

Standard heterosis for ear diameter varied between -10.99 (L3 x L9) and 10.99 % (L4 x L8) over kolba (Table 8). Sixteen crosses showed positive heterosis over best standard check. Among them only one cross (L4 x L8) showed significant and positive standard heterosis over kolba. Among twenty crosses those showed negative standard heterosis, only one hybrid (L3 x L9) had negative and significant standard heterosis over Kolba for ear diameter. Positive standard heterosis shows that the F1 crosses had larger ear diameter than the standard check which is important to increase number of kernel rows per ear and thus important to increase grain yield while negative heterosis depicts that the check hybrids had larger ear diameter than the F1 hybrids. Similar result was previously reported by Beyene (2016).

Standard heterosis for thousand kernel weight varied from -47.51(L3 x L9) to -0.58% (L6 x L7). All of the crosses showed negative and non-significant standard heterosis over the standard check Kolba (Table 8). Similar to the current study, both desirable and undesirable heterosis for thousand kernel weight in maize has been reported by previous investigators (Amiruzzaman. *et al.,* 2010;Shushay, 2014).

Generally, positive standard heterosis is desirable for grain yield and yield components like thousand kernel weight, ear diameter and number of ears per plant. On the other hand, negative standard heterosis is desirable for traits like days to anthesis and silking, anthesis-silking interval and plant height. Negative standard heterosis for these traits is directly contributed for earliness, short number of days between anthesis and silking and short plant stature which is resistant to lodging respectively.

Table 8. Standard heterosis of F1 hybrids over Kolba for grain yield and related traits evaluated at Kulumsa and Ambo in 2017.

Crosses	**GY**	**DA**	**DS**	**ASI**	**PH**	**EPP**	**ED**	**TKW**
L1*L2	-20.51^{ns}	-0.29^{ns}	-1.67^{ns}	-3.97^{ns}	-20.5^{ns}	-12.74^{ns}	-0.44^{ns}	-7.09^{ns}
L1*L3	-8.31^{ns}	4.86*	5.00**	0.79^{ns}	-16.12^{ns}	10.83^{ns}	-1.10^{ns}	-24.89^{ns}
L1*L4	-28.91^{ns}	0.57^{ns}	0.28^{ns}	-0.79^{ns}	-21.19^{ns}	-22.29^{ns}	7.25^{ns}	-10.96^{ns}
L1*L5	-18.43^{ns}	6.00**	5.83**	0.00^{ns}	-8.96^{ns}	-12.10^{ns}	0.66^{ns}	-17.71^{ns}
L1*L6	-35.95^{ns}	-0.57^{ns}	-0.56^{ns}	0.00^{ns}	-25.37^{ns}	-23.57^{ns}	-0.44^{ns}	-7.52^{ns}
L1*L7	-36.49^{ns}	1.14^{ns}	0.56^{ns}	-1.59^{ns}	-23.58^{ns}	-24.84^{ns}	-2.64^{ns}	-12.14^{ns}
L1*L8	-25.47^{ns}	0.57^{ns}	-0.56^{ns}	-3.97^{ns}	-17.31^{ns}	-17.83^{ns}	6.15^{ns}	-9.25^{ns}
L1*L9	-32.34^{ns}	6.00**	6.11**	0.79^{ns}	-12.94^{ns}	-16.56^{ns}	3.30^{ns}	-20.10^{ns}
L2*L3	-19.06^{ns}	4.00*	3.61^{ns}	-0.79^{ns}	-12.74^{ns}	3.18^{ns}	-4.40^{ns}	-19.34^{ns}
L2*L4	-20.05^{ns}	-0.86^{ns}	-1.67^{ns}	-2.38^{ns}	-18.21^{ns}	-8.28^{ns}	1.10^{ns}	-15.73^{ns}
L2*L5	-32.43^{ns}	6.00**	5.28**	-1.59^{ns}	-13.73^{ns}	-21.66^{ns}	-2.20^{ns}	-12.47^{ns}
L2*L6	-32.79^{ns}	-1.43^{ns}	-3.06^{ns}	-5.56^{ns}	-26.27^{ns}	-5.73^{ns}	-4.40^{ns}	-14.14^{ns}
L2*L7	-18.16^{ns}	1.14^{ns}	0.00^{ns}	-3.17^{ns}	-16.82^{ns}	-1.91^{ns}	-3.30^{ns}	-7.15^{ns}
L2*L8	-27.10^{ns}	1.14^{ns}	-1.67^{ns}	-9.52^{ns}	-19.50^{ns}	-19.11^{ns}	2.20^{ns}	-6.40^{ns}
L2*L9	-39.11^{ns}	8.29**	6.67**	-3.97^{ns}	-15.32^{ns}	-10.19^{ns}	-3.30^{ns}	-32.19^{ns}
L3*L4	-22.76^{ns}	4.86*	4.72*	0.00^{ns}	-7.46^{ns}	-11.46^{ns}	-1.54^{ns}	-23.23^{ns}
L3*L5	-27.73^{ns}	9.71**	9.17**	-0.79^{ns}	-5.47^{ns}	-8.28^{ns}	-3.30^{ns}	-28.72^{ns}
L3*L6	-20.96^{ns}	4.29*	3.06^{ns}	-3.17^{ns}	-20.80^{ns}	5.73^{ns}	-4.84^{ns}	-19.07^{ns}
L3*L7	-33.06^{ns}	5.14**	5.28**	0.79^{ns}	-12.64^{ns}	-6.37^{ns}	-6.59^{ns}	-24.78^{ns}
L3*L8	-12.56^{ns}	5.71**	6.11**	1.59^{ns}	-10.75^{ns}	8.92^{ns}	-2.64^{ns}	-19.45^{ns}
L3*L9	-33.69^{ns}	12.86**	11.67**	-2.38^{ns}	-10.05^{ns}	3.82^{ns}	-10.99**	-47.51^{ns}
L4*L5	-27.46^{ns}	3.43^{ns}	4.17*	2.38^{ns}	-18.61^{ns}	-12.74^{ns}	-2.64^{ns}	-22.51^{ns}
L4*L6	-31.89^{ns}	-3.71^{ns}	-5.00**	-3.97^{ns}	-22.59^{ns}	-21.66^{ns}	0.66^{ns}	-23.31^{ns}
L4*L7	-20.69^{ns}	-0.86^{ns}	-0.56^{ns}	0.79^{ns}	-17.61^{ns}	-13.38^{ns}	4.40^{ns}	-5.89^{ns}
L4*L8	-15.00^{ns}	-1.14^{ns}	-3.33^{ns}	-7.14^{ns}	-9.05^{ns}	-17.20^{ns}	10.99**	-7.18^{ns}
L4*L9	-31.44^{ns}	4.29*	3.89*	-0.79^{ns}	-15.12^{ns}	-10.19^{ns}	0.66^{ns}	-23.51^{ns}

Table 8 (contd)

L5*L6	-34.15 ^{ns}	4.00*	2.50 ^{ns}	-3.97 ^{ns}	-16.92 ^{ns}	-13.38 ^{ns}	-1.54 ^{ns}	-11.83 ^{ns}
L5*L7	-31.89 ^{ns}	6.86**	6.67**	0.00 ^{ns}	-7.56 ^{ns}	-17.83 ^{ns}	1.76 ^{ns}	-18.05 ^{ns}
L5*L8	-26.56 ^{ns}	6.29**	5.56**	-1.59 ^{ns}	-4.38 ^{ns}	-5.10 ^{ns}	3.96 ^{ns}	-24.39 ^{ns}
L5*L9	-44.35 ^{ns}	16.57**	15.00**	-3.17 ^{ns}	-10.85 ^{ns}	-17.20 ^{ns}	0.66 ^{ns}	-32.80 ^{ns}
L6*L7	-35.14 ^{ns}	-1.43 ^{ns}	-2.78 ^{ns}	-3.97 ^{ns}	-25.07 ^{ns}	-20.38 ^{ns}	-2.20 ^{ns}	-0.58 ^{ns}
L6*L8	-27.64 ^{ns}	-2.00 ^{ns}	-4.17*	-7.14 ^{ns}	-23.68 ^{ns}	-9.55 ^{ns}	1.76 ^{ns}	-1.98 ^{ns}
L6*L9	-31.17 ^{ns}	5.71**	5.28**	-0.79 ^{ns}	-20.10 ^{ns}	1.27 ^{ns}	-2.64 ^{ns}	-19.79 ^{ns}
L7*L8	-25.65 ^{ns}	-1.14 ^{ns}	-1.11 ^{ns}	0.00 ^{ns}	-21.09 ^{ns}	-19.75 ^{ns}	2.20 ^{ns}	-4.62 ^{ns}
L7*L9	-23.94 ^{ns}	5.43**	5.28**	0.00 ^{ns}	-10.05 ^{ns}	-1.27 ^{ns}	-3.30 ^{ns}	-19.62 ^{ns}
L8*L9	-16.35 ^{ns}	4.86*	3.61 ^{ns}	-3.17 ^{ns}	-6.27 ^{ns}	3.82 ^{ns}	3.30 ^{ns}	-26.16 ^{ns}
Kolba(mean)	11.07	87.50	90.00	2.50	251.25	1.57	4.55	408.03
SE(d)	0.79	1.62	1.65	0.04	13.55	0.14	0.17	37.90

** Significant at 0.01 level of probability, * = significant at 0.05 level of probability, ns = non-significant, SE(d)= standard error of difference, GY= grain yield, DA= number of days to anthesis, DS= number of days to silking, ASI= anthesis silking interval, PH= plant height, EPP= number of ears per plant, ED= ear diameter and TKWT =1000-kernel weight**.**

4.3 Combining Ability Analyses

Diallel analysesfor grain yield and related agronomic traits were computed and are presented in Tables 9 and 10 for Ambo and Kulumsa, respectively.Combining ability analysesacross the two locations is presented in Table 11.The results showed that both general combining ability (GCA) and specific combining ability (SCA) mean squares were significant for days to anthesis, days to silking, anthesis-silking interval and number of ears per plant at Ambo.At Kulumsa GCA and SCA mean squares were significant for grain yield, plant height, number of ears per plant and thousand kernel weight.Mean squares due to GCA and SCA were significant for grain yield, days to anthesis,number of ears per plant and ear diameter across the two locations (Table9, 10 and 11).This indicates that both additive and non-additive gene actions are important in the inheritance of these traits. Reports on similar studies by Dagne *et al*. (2007) showed that both GCA and SCA mean squares were significant for ear height, plant height and days to maturity. Similarly, Yoseph*et al*. (2011) observed significant GCA and SCA for anthesis date, anthesis silking interval, ear height and plant height in elite maize inbred lines developed by CIMMYT for insect resistance.

The contribution of GCA variances were much greater than that of SCA variances for most of the traits except for grain yield at Kulumsa and across locations,number of ears per plant at Ambo and anthesis silking interval at both Ambo and Kulumsa, which showed higher contribution of SCA variance for these traits at these particular locations. This higher percentage relative contribution of SCA over GCA showed the predominant role of non-additive gene action overadditive gene action in the inheritance of thetraits. Thus, genotypes whose traits predominantly controlled by non-additive gene action can be used to develop hybrid varieties. In line with this result, Dagne *et al.* (2008) studied the combining ability of eight elite maize inbred lines for grain yield and reaction to grey leaf spot (GLS) diseaseand reported the preponderance of SCA effects for grain yield than GCA. The higher percentage relative contribution of GCA sum of squares over SCA sum of squares showed the predominant role of additive gene action over non-additive gene action in the inheritance of the traits studied. The breeding implication of this predominance of additive gene action is that the genotypes having this character can be used to develop hybrid and/synthetic varieties. Similar results were reported by other authors in their study on combining ability for yield and yield related traits in maize (Chandel and Mankotia, 2014; Amare *et al*., 2016; Beyene, 2016; Bitew*et al.,* 2017 and Tolera*et al.,* 2017).They reported predominance of additive gene action over non-additive for most of the traits they studied.

GCA mean squares were significant for grain yield at both locations and across the two locations. SCA mean squares were significantly different for grain yield at Kulumsa and across locations. But it was non-significant at Ambo. Significant GCA and SCA mean squares indicated the importance of both additive and non-additive gene actions in governing grain yield. This has breeding implications, since hybridization methods such as reciprocal recurrent selection which utilizes both additive and non-additive gene effects simultaneously, could be useful in genetic improvement of the population characters under consideration.Similar to the present study Hadji (2004) found highly significant mean squares due to GCA and SCA for grain yield in diallel study of quality protein maize inbred lines.In addition,Dagne *et al.,* 2011; Demissew *et al.,*2011;Shushay*et al.*, 2013andBitew*et al.,* 2017 also reported the importance of both additive and non-additive gene actions in governing grain yield in maize.

For number of days to anthesis and silking, mean squares due to GCA were highly significant ($p<0.01$) at both Ambo and Kulumsa as well as across the two locations.Mean square due to SCA was highly significant ($p<0.01$) at Ambo for days to anthesis but non-significant at Kulumsa and significant ($p<0.05$) across the two locations. For days to silking, mean square due to SCA was significant at Ambo but it was non-significant at Kulumsa and across the two locations. In agreement with this study,Tolera*et al.*(2017) found the importance of both additive and non-additive gene effects for both days to anthesis and silking. GCA sum of squares were larger than SCA sum of squares for anthesis and silking dates at both locations and across the two locations. The predominance of GCA sum of squares to SCA sum of squares for these traits indicate the relative importance of additive gene action to non-additive gene action for the inheritance of these traits. This indicates thatgenotypes having this character can be used in the development of hybrid and/synthetic varieties.In line with this study Ahmad and Saleem (2003) reported the preponderance of additive gene action in the inheritance of days to anthesis andsilking.

For Anthesis silking interval, mean squares due to GCA were highly significant ($p<0.01$) at Ambo and significant ($p<0.05$) at Kulumsa,whereas mean squares due to SCA were highly significant ($p<0.01$) at ambo but not significant at Kulumsa (Tables 9and 10). In this study both additive and non-additive gene actions were important in governing this trait. But the relative contribution of SCA is larger than GCA at both individual locations. Indicating its importance in the development of hybrid varieties. The across locations combining ability analyses for anthesis silking interval was not done since it showed non-significant mean squares due to genotypes when genotype by environment interaction is used as an error term.

For plant height, mean squares due to GCA were highly significant ($p<0.01$) at Ambo,Kulumsa and across locations. For ear height, mean squares due to GCA were highly significant ($p < 0.01$) at Ambo. Mean squares due to SCA for plant and ear height were non-significant at Ambowhile plant height at Kulumsa showed highly significant ($p<0.01$) SCA mean square but it showed non-significant SCA mean square across locations (Table 9, 10 and 11).In this study, both additive and non-additive gene actions were important for plant height while additive gene action than non-additive gene action was importantfor ear height. In consistent with this finding, Dagne (2002), Hadji (2004) and Demissew *et al.* (2011) reported the importance of additive and non-additive gene action in the inheritance of plant height. Similarly, Leta *et al.* (1999) found significant GCA effect and non-significant SCA effect for ear height.

Mean squares due to crosses for number of ears per plant were highly significant at both individual locations and across the two locations (Tables9-11). Combining ability analyses revealed highly significant GCA effects for ear per plant at both locations and across the two locations. Meansquare due to SCA for ear per plant was highly significant ($p<0.01$) at Ambo and across the two locations, and significant ($p<0.05$) at Kulumsa. Significant GCA and SCA mean squares indicated the importance of both additive and non-additive gene actions in governing ears per plant. Similar to the present study,Malik*et al.* (2004) reported significant GCA and SCA mean squares for number of ears per plant in a diallel study of nine quality protein maize (QPM) inbred lines.

GCA mean squares were highly significantly ($p < 0.01$) different for ear length at Kulumsa, whereas GCA mean squares for ear diameter were highly significantly ($p<0.01$) different at Ambo, Kulumsa and across the two locations.Mean squares due to SCA for ear length at Kulumsa and ear diameter at both Ambo and Kulumsa were non-significant while ear diameter at across the two locations showed significant ($p<0.05$) SCA meansquare.Combining ability analyses for ear length at ambo and across locations were not estimated as the mean squares due to entries were not significant in the analyses of variance. Similarly, Dufera*et al.*(2018) reported the importance of only additive gene action for ear length. For eardiameter both additive and non-additive gene effects were important in agreement with the study of Dagne (2002), Hadji (2004) and Gudeta (2007).

Mean squares due to GCA for thousand kernel weight were highly significant ($p<0.01$) at individual and across locations (Table 9,10 and 11). Mean squares due to SCA were significant for thousand kernels weight at Kulumsa but not significant at Ambo and across locations. This study showed both additive and non-additive gene actions were important in governing this trait. Similar to this finding, Dagne (2002), Dagne *et al.* (2007),Gudeta (2007) and Beyene (2016)reported the importance of both additive and non-additive gene actions for this trait.

GCA × Loc mean squares were significant for grain yield, days to anthesis and ears per plant indicating that GCA effects associated with parents were not consistent for these traits over the two environments (Table 11). But the interaction was not significant for days to silking, plant height, ear diameter and thousand kernel weight, indicating that GCA effects associated with parents were consistent over the two environments. SCA × Loc mean squares were significant for grain yield and ear per plantshowing that SCA effects of these traits associated with crosses were not consistent over the two environments,while, SCA × Loc showed non-significant mean squares for the rest of traits, indicating that SCA effects associated with crosses were consistent over the two environments. Similar findings were reported by Dagne *et al*. (2007)in their study on heterosis and combining ability for grain yield and its component in selected maize inbred lines.

Table 9.Combining ability analyses for grain yield and other agronomic traits of 36 diallel crosses evaluated at Ambo in 2017.

	Mean squares									
Source of variation	**DF**	**GY**	**DA**	**DS**	**ASI**	**PH**	**EH**	**EPP**	**ED**	**TKW**
Replication	1	0.023^{ns}	0.89 ^{ns}	4.01 ^{ns}	0.0018^{ns}	1334.72*	53.39 ^{ns}	0.00017 ^{ns}	0.33**	347.16 ^{ns}
Crosses	35	2.40**	25.41**	31.73**	0.0079**	565.76*	247.00**	0.067**	0.09**	4058.61**
GCA	8	6.63**	93.15**	124.21**	0.017**	1325.64**	719.93**	0.14**	0.22**	12744.32**
SCA	27	1.15 ^{ns}	5.34**	4.32*	0.0052**	340.61 ^{ns}	106.87 ^{ns}	0.05**	0.05 ^{ns}	1485.07 ^{ns}
Error	35	0.83	1.46	2.36	0.0022	302.78	99.19	0.02	0.03	1583.45
% GCA		63.15	83.8	89.5	48.57	53.55	66.62	47.35	58.00	71.77
% SCA		36.85	16.2	10.5	50.42	46.44	33.38	52.65	42.00	28.23

** Significant at 0.01 level of probability, * = significant at 0.05 level of probability, ns = non-significant, GY= grain yield, DA= number of days to anthesis, DS= number of days to silking, ASI= anthesis silking interval, PH= plant height, EH= ear height, EPP= number of ears per plant, ED= ear diameterand TKWT =1000-kernel weight**.**

Table 10.Combing ability analyses for grain yield and other agronomic traits of 36 diallel crosses evaluated at Kulumsa in 2017.

Source of variation	**DF**	**Mean squares**								
		GY	**DA**	**DS**	**ASI**	**PH**	**EPP**	**EL**	**ED**	**TKW**
Replication	1	1.40 ^{ns}	9.39 ^{ns}	12.50 ^{ns}	0.00036^{ns}	125.35 ^{ns}	0.0082 ^{ns}	1.68 ^{ns}	0.011 ^{ns}	2440.68 ^{ns}
Crosses	35	2.61**	37.29**	37.74**	0.00059*	631.80**	0.081**	1.73**	0.082**	4041.63**
GCA	8	2.48**	150.07**	153.89**	0.00083*	2126.97**	0.18**	3.99**	0.27**	11027.02**
SCA	27	2.65**	3.878 ^{ns}	3.33 ^{ns}	0.00052^{ns}	188.79**	0.05*	1.056 ^{ns}	0.03 ^{ns}	1971.89*
Error	35	0.79	4.27	4.30	0.00031	76.89	0.03	0.62	0.018	1079.30
% GCA		21.72	92	93.19	31.86	76.94	51.55	52.85	75.87	62.36
% SCA		78.28	8	6.81	68.14	53.06	48.45	47.15	24.13	37.64

** Significant at 0.01 level of probability, * = significant at 0.05 level of probability, ns = non-significant, GY= grain yield, DA= number of days to anthesis, DS= number of days to silking, ASI= anthesis silking interval, PH= plant height, EPP= number of ears per plant, EL= ear length, ED= ear diameter and TKWT =1000-kernel weight**.**

Table 11.Across locations combing ability analyses of variance for grain yield and other agronomic traits of 36 diallel crosses evaluated at Ambo and Kulumsa (2017).

Source of variation	**Mean squares**							
	DF	**GY**	**DA**	**DS**	**PH**	**EPP**	**ED**	**TKW**
Location (LOC)	1	201.17**	720.03**	315.06**	43646.17**	0.29**	1.65**	189667.5**
Replication (LOC)	2	0.71 ns	5.14 ns	8.26 ns	730.03*	0.0042 ns	0.17**	1393.92 ns
Crosses	35	3.12**	57.57**	66.16**	952.29**	0.09**	0.14**	6551.29**
GCA	8	5.89*	235.78**	274.24**	3189.48**	0.23**	0.47**	22818.03**
SCA	27	2.30*	4.76*	4.51 ns	289.42 ns	0.05**	0.04*	1731.52 ns
GCA*LOC	8	3.22**	7.40*	3.87 ns	263.14 ns	0.09**	0.03 ns	953.31 ns
SCA*LOC	27	1.50*	4.45 ns	3.14 ns	239.98 ns	0.04*	0.03 ns	1725.43 ns
Error	70	0.81	2.87	3.33	189.83	0.02	0.03	1331.38
% GCA		43.18	93.62	94.74	76.55	55.91	76.54	79.61
% SCA		56.82	6.38	5.26	23.45	44.09	23.46	20.39

** Significant at 0.01 level of probability, * = significant at 0.05 level of probability, ns = non-significant, GY= grain yield, DA= number of days to anthesis, DS= number of days to silking, PH= plant height, EPP= number of ears per plant, ED= ear diameter and TKW=1000-kernel weight.

4.3.1 General combining ability estimates

The general combining ability effects of parental inbred lines were computed for the traits exhibited significant general combining ability (GCA) mean squares in combining ability analyses of variance (Table11). The estimates of GCA effects for parental lines showed significant differences for various traits. General combining ability effects of grain yield and related agronomic traits for across locations analyses are presented in Tables 12.

GCA effects of lines for grain yield ranged between -0.59 t/ha (L9) to 0.61 t/ha (L3) (Table 12). Five inbred lines showed positive GCA effects for grain yield. Two inbred lines L3 (0.61 t/ha) and L8 (0.62 t/ha) showed positive and significant GCA effects, indicating the potential advantage of these inbred lines for the development of high-yielding hybrids and/or synthetic varieties, as the lines can contribute desirable alleles in the synthesis of new varieties. Four inbred lines (L5, L6, L7 and L9) showed negative and non-significant GCA (Table 12), indicating these lines were poor combiners for grain yield. Results of the current study are similarto the findings of several authors(Kanagarasu *et al*., 2010; Yoseph*et al*., 2011;Girma*et al*., 2015; Amare*et al*., 2016; Beyene, 2016; Dufera*et al*., 2018)who reported significant positive and negative GCA effects for grain yield in maize germplasm.

In combined analyses across locations, GCA effects of lines for days to anthesis ranged between -2.90 (L6) to 4.49 (L9), while for days to silking it ranged from -3.44 (6) to 4.56 (L9) (Table 12). Six inbred lines (L1, L2, L4, L6, L7 and L8)showed negative and significant GCA effects for days to anthesis, indicating that these lines were good general combiners for early maturity while three inbred lines (L3, L5 and L9) exhibited significant and positive GCA effects for days to anthesis, indicating that these lines have tendency to increase late maturity.L9 had higher and positive GCA effect for days to silking (4.45) whereas L6 had lower and negative GCA effect (-3.44). All the three inbred lines those showed positive GCA effects had significant GCA effects for days to silking while six inbred lines exhibited significant and negative GCA effects for days to silking. L1 (-0.90), L2(-1.87), L4 (-2.51), L6 (-3.44), L7 (-1.12) and L8 (-2.26) were the best general combiners for early maturity (Table 12).Lines with negative and significant GCA effects for days to anthesis and silking are desirable when the objective is to develop early maturing hybrids, as hybrids generated using these lines tend to flower earlier. Similarly, lines with positive and significant GCA effects for days to flowering are desirable when the objective is to develop late maturing hybrids. Thus, there is possibility of making effective selection for these traits, which could lead to considerable genetic improvement for earliness and lateness. Desirability of negative GCA for days to anthesis and silking for earliness and desirability of positive GCA for these traits for lateness was suggested by various authors such as (Shushay*et al*., 2013; Umar *et al*., 2014; Girma*et al*., 2015; Beyene, 2016 and Abiy, 2017).

Even thoughfive inbred lines showed negative GCA effects for plant height in combined analyses across locations (Table 12), only one inbred line L6 (-19.85) showed significant GCA effect, implying the tendency of this line to reduce plant height,which is very important for development of genotypes resistant to lodging. Allthe four inbred lines those showed positive GCA (L3, L5, L8 and L19) were the poor general combiners for short plant height as they showed positive and significant GCA effects. In line with the present study, Dagne *etal.*(2010), Demissew *et al*. (2011) and Dufera*et al.* (2018)found significant positive and negative GCA effects for plant height.

For number of ears per plant, four inbred lines showed positive GCA effects among them two inbred lines L3 (0.19) and L9 (0.08) had significant GCA effects. L3 had positive and highly significant GCA effect for number of ears per plant, hence, it was the best general combiner for prolificacy.Two inbred lines L1 (-0.09) and L4 (-0.08) showed significantly negative GCA effects for ears per plant, hence are considered as poor combiners for number of ears per plant. L1 had the smallest GCA effect of -0.09 for ears per plant.Similar to the present findings, Dagne *et al*. (2007) reported significant positive and negative GCA effects for number of ears per plant.

In combined analyses across the two locations, four inbred lines showed positive GCA effects for ear diameter among themthree inbred lines had significant GCA effects. L1 (0.1), L4 (0.15) and L8 (0.20) were the best general combiners for ear diameter,i.e the line has the tendency to increase ear diameter as they had highly significant and positive GCA effect (Table 12).On the other hand, three inbred lines had significantly negative GCA effects. L3 was the worst general combiner for this trait at ambo and across locations.The present study is in agreement with Melkamu, 2013; Rahman *et al*., 2013 and Habtamu, 2015 who reported significant positive and negative GCA effects for ear diameter.

Significantly positive and negative GCA effects were obtained for thousand kernel weight across the two locations. From a total of six inbred lines which showed positive GCA effects for thousand-kernel weight, three of the inbred lines L6 (23.33), L7 (26.46) and L8 (22.61) showed significant and positive GCA effects,indicating that the inbred lines were the best general combiners for thousand-kernel weight. On the other hand, L3 (-40.08) and L9 (-48.64) showed negative and significant GCA effects, which are undesirable.In support of this findings, Amiruzzaman *et al*. (2010) and Demissew *et al*. (2011)recorded significant positive and negative GCA effects for thousand kernel weights.

Table 12. Estimates of general combining ability effects (GCA) of nine inbred lines across the two locations (2017).

Line	**GY**	**DA**	**DS**	**PH**	**EPP**	**ED**	**TKW**
L1	0.14^{ns}	-1.22*	-0.90*	-7.35^{ns}	-0.09**	0.10**	16.66^{ns}
L2	0.09^{ns}	-1.26*	-1.87**	-6.32^{ns}	0.01^{ns}	-0.07*	13.82^{ns}
L3	0.61*	2.92**	3.42**	10.58**	0.19**	-0.21**	-40.08**
L4	0.26^{ns}	-2.69**	-2.51**	-1.57^{ns}	-0.08*	0.15**	3.45^{ns}
L5	-0.44^{ns}	3.85**	4.14**	14.00**	-0.06^{ns}	0.0008^{ns}	-17.62^{ns}
L6	-0.54^{ns}	-2.90**	-3.44**	-19.85**	-0.02^{ns}	-0.07*	23.33*
L7	-0.15^{ns}	-1.47**	-1.12**	-3.21^{ns}	-0.06^{ns}	-0.04^{ns}	26.46**
L8	0.62*	-1.72**	-2.26**	4.83^{ns}	0.01^{ns}	0.20**	22.61*
L9	-0.59^{ns}	4.49**	4.56**	8.89*	0.08*	-0.06^{ns}	-48.64**
SE(gi)	0.31	0.57	0.44	4.45	0.034	0.037	10.01

** Significant at 0.01 level of probability, * = significant at 0.05 level of probability, ns = non-significant, SE(gi)= standard error of general combining ability effects, GY= grain yield, DA= number of days to anthesis, DS= number of days to silking, PH= plant height, EPP= number of ears per plant, ED= ear diameter and TKWT =1000-kernel weight**.**

4.3.2 Specific combining ability estimates

Specific combining ability effects for grain yield and related agronomic traits for across location is presented in Table 13. The crosses showed considerable variation in their SCA effects for the different traits.

In combined analyses across the two locations,positive SCA effects were found in seventeen of the crosses for grain yield. The cross L1 x L3 was the only best positive and significant ($p<0.05$) cross combination with SCA value of 1.47. Thus, this cross could be selected for its specific combining ability to improve grain yield. Crosses with higher value of SCA effects also showed higher values of mean grain yield, indicating good correspondence between SCA effects and mean grain yield. Hence such cross combinations could effectively be exploited in hybrid breeding program in maize research. Nineteen crosses showed negative SCA effects for grain yield, (Table 13) which are undesirable as these crosses showed a tendency to reduce grain yield performance.In line with the current finding, Kamara *et al.*, 2014; Girma*et al.*, 2015; Ram *et al.*, 2015; Bullo and Dagne (2016)reported significant positive and negative SCA for grain yield. They suggested that, when high yielding specific combinations are desired, especially in hybrid maize development, SCA effects could help in the selection of parental material for hybridization.

For days to anthesis, only one cross L5 x L9 (3.09) showed positive and significant SCA effect (Table 13).Thus, this cross could be used for late maturity for the locations with sufficient rain fall. In agreement with this finding several researchers reported significant positiveandnegative SCA effects for days to anthesis (Kanagarasu *et al.*,2010, Dagne *et al.*,2011, Aminu and Izge (2013) and Aminu *et al.*,2014).

Positive SCA effects were found in eighteen of the crosses for ear per plant. The crosses L1 x L3 and L2 x L7 were the two best positive and significantcross combinations with SCA values of 0.22 and 0.17, respectively. Thus, these crosses could be selected for their specific combining ability to improve number of ears per plant. Eighteen crosses showed negative SCA effects in undesired direction for ear per plant with only one significant and negative SCA,L2 x L8 (-0.16) (Table 13).Indicates that this hybrid combination is poor for number of ears per plant.Similarresults were reported by (Berhanu, 2009) and (Bello and Olawuyi,2015).

They indicated the capacity of the crosses to produce hybrids having increased number of ears per plant.

Sixteen of the crosses showed positive SCA effects for ear diameter but none of them were significant (Table 13). On other hand,twenty of the crosses showed negative SCA effects, but only two of the crosses L3 x L9 (-0.21) and L4 x L5 (-0.26), showed significant and negative SCA effects for this trait.This indicates that none of these crosses were significantly good specific combinations for ear diameter.Amiruzzaman *et al*., 2010 found significant positiveand negative SCA effects for ear diameter.

Table 13. Estimates of specific combining ability effects (SCA) of 36 diallel crosses evaluated at Ambo and Kulumsa in 2017.

Crosses	**GY**	**DA**	**EPP**	**ED**
L1*L2	0.47 ^{ns}	-0.84 ^{ns}	0.04 ^{ns}	-0.032 ^{ns}
L1*L3	1.47*	-0.52 ^{ns}	0.22**	0.08 ^{ns}
L1*L4	-0.64 ^{ns}	1.34 ^{ns}	-0.03 ^{ns}	0.09 ^{ns}
L1*L5	1.23 ^{ns}	-0.45 ^{ns}	0.12 ^{ns}	-0.06 ^{ns}
L1*L6	-0.59 ^{ns}	0.55 ^{ns}	-0.11 ^{ns}	-0.036 ^{ns}
L1*L7	-1.27 ^{ns}	0.63 ^{ns}	-0.09 ^{ns}	-0.16 ^{ns}
L1*L8	-0.60 ^{ns}	0.38 ^{ns}	-0.05 ^{ns}	-0.0071 ^{ns}
L1*L9	-0.15 ^{ns}	-1.09 ^{ns}	-0.09 ^{ns}	0.13 ^{ns}
L2*L3	0.18 ^{ns}	-1.23 ^{ns}	0.0012 ^{ns}	0.10 ^{ns}
L2*L4	0.39 ^{ns}	0.13 ^{ns}	0.101 ^{ns}	-0.01 ^{ns}
L2*L5	-0.27 ^{ns}	-0.41 ^{ns}	-0.13 ^{ns}	-0.007 ^{ns}
L2*L6	-0.21 ^{ns}	-0.16 ^{ns}	0.07 ^{ns}	-0.035 ^{ns}
L2*L7	1.02 ^{ns}	0.66 ^{ns}	0.17*	-0.014 ^{ns}
L2*L8	-0.73 ^{ns}	0.91 ^{ns}	-0.16*	-0.007 ^{ns}
L2*L9	-0.86 ^{ns}	0.95 ^{ns}	-0.09 ^{ns}	0.0036 ^{ns}
L3*L4	-0.39 ^{ns}	0.95 ^{ns}	-0.13 ^{ns}	0.00 ^{ns}
L3*L5	-0.24 ^{ns}	-1.34 ^{ns}	-0.11 ^{ns}	0.08 ^{ns}
L3*L6	0.61 ^{ns}	0.66 ^{ns}	0.07 ^{ns}	0.08 ^{ns}
L3*L7	-1.33 ^{ns}	-0.02 ^{ns}	-0.09 ^{ns}	-0.03 ^{ns}
L3*L8	0.38 ^{ns}	0.73 ^{ns}	0.09 ^{ns}	-0.096 ^{ns}
L3*L9	-0.76 ^{ns}	0.77 ^{ns}	-0.05 ^{ns}	-0.21*
L4*L5	0.11 ^{ns}	-1.23 ^{ns}	0.102 ^{ns}	-0.26**
L4*L6	-0.28 ^{ns}	-0.73 ^{ns}	-0.09 ^{ns}	-0.04 ^{ns}
L4*L7	0.57 ^{ns}	0.34 ^{ns}	0.08 ^{ns}	0.11 ^{ns}
L4*L8	0.43 ^{ns}	0.34 ^{ns}	-0.04 ^{ns}	0.16 ^{ns}
L4*L9	-0.19 ^{ns}	-1.13 ^{ns}	0.00053 ^{ns}	-0.05 ^{ns}
L5*L6	0.18 ^{ns}	-0.52 ^{ns}	0.03 ^{ns}	0.014 ^{ns}

Table 13(continued)

L5*L7	0.04^{ns}	0.55^{ns}	-0.0063^{ns}	0.14^{ns}
L5*L8	-0.14^{ns}	0.30^{ns}	0.125^{ns}	-0.007^{ns}
L5*L9	-0.91^{ns}	3.09*	-0.128^{ns}	0.104^{ns}
L6*L7	-0.21^{ns}	0.05^{ns}	-0.09^{ns}	0.032^{ns}
L6*L8	0.15^{ns}	-0.19^{ns}	0.0087^{ns}	-0.04^{ns}
L6*L9	0.66^{ns}	0.34^{ns}	0.12^{ns}	0.025^{ns}
L7*L8	-0.33^{ns}	-0.88^{ns}	-0.10^{ns}	-0.04^{ns}
L7*L9	1.07^{ns}	-1.34^{ns}	0.12^{ns}	-0.03^{ns}
L8*L9	1.14^{ns}	-1.58^{ns}	0.13^{ns}	0.03^{ns}
SE(sij)	0.75	1.39	0.083	0.09

** Significant at 0.01 level of probability, * = significant at 0.05 level of probability, ns = non-significant, SE(gi)= standard error of general combining ability effects, GY= grain yield, DA= number of days to anthesis, EPP= number of ears per plant and ED= ear diameter.

4.4 Genotypic and Phenotypic Correlation

The values of estimated genotypic and phenotypic correlation coefficients between pair of characters in all possible combination are presented in Table 14.In this study, grain yield revealed positive and highly significant ($P<0.01$) phenotypic and genotypic correlation with number of ears per plant, ear length, number of kernels per row and thousand kernel weight. It had also highly ($P <0.01$) significant positive association with ear diameter at phenotypic level and had positive and highly significant genotypic correlation with plant height and ear height. Hence, the positive associations of the above-mentioned traits with grain yield indicated that these traits are important, and therefore, could be considered for indirect selection to improve grain yield, because grain yield can be simultaneously improved with a trait for which it showed strong relationship.

The selection for increasednumber of ears per plant, ear length, number of kernels per row,thousand kernel weight, ear diameter, plant height and ear height may result in simultaneousincrease in grain yield of maize. Similar results were reported by,Eleweanya*et al*. (2005), Berhanu (2009),Nzuve*et al*. (2014), Beyene (2016), Ziggiju and Legesse (2016). Another research work conducted by Hadji (2004) found strong correlation ofear height and plant height with grain yield, suggesting that, tall plants with high ear placement gave better yields than shorter plants with lower ear placement.This indicated that by increasing these attributes in growth parameter, especially plant height would help photosynthetic apparatus to synthesize more assimilates and hence production of higher yield.

Days to anthesis showed negative and highly significant ($p<0.01$) and significant ($p<0.05$) phenotypic and genotypic correlation with grain yield, respectively.Days to silking showed negative and significant association with grain yield only at phenotypic level. This suggests that the selection to improve yield of maize genotypes those used in current study may be useful through decreasing these traits.In line with this finding, Shashidhara (2008)also observed that, grain yield had negative association with days to anthesis at both genotypic and phenotypic level.In addition to this, Aminu and Izge (2012) reported that days to anthesis, ear height and plant height exhibited negative correlation with grain yield and suggested that these traits were not closely associated, and therefore, they may not be jointly selected.

The correlation among grain yield related traits were both negative and positive.Ear diameter showed positive and highly significant phenotypic association with rows per ear, kernels per row and thousand kernel weight. Increasing ear diameter can causeincrease in number of rows per ear, kernels per row and thousand kernel weightBeyene, (2016).It also revealed positive and significant genotypic association with thousand kernel weight.But it exhibited negative and highly significant phenotypic association with days to anthesis, days to silking, plant height and ear height. Negative and significant genotypic association with days to anthesis, days to silking and number of ears per plant was also observed.Ear length exhibited significant and positive genotypic association with anthesis silking interval and kernels per row. It showed positive and significant phenotypic association withrow per ear and kernels per row. In addition ear length had non-significant and negative phenotypic and genotypic association withother traits under study. In linewith the present finding, Muhammad *et al*. (2003)reported that, ear length had highly ($P < 0.01$) significant and positive genotypic and phenotypic association with number of kernels per row, ear height, plant height and number of days to maturity.

Number of rows per ear exhibited positive and significant phenotypic association with ear height, ear length and ear diameter. It revealed negative and significant phenotypic association with thousand kernel weight. But number of rows per ear showed non-significant positive and negative genotypic association with all the traits associated with it.The current finding is in line with the findings of Ziggiju and Legesse (2016). They reported that, number of kernel rows per ear exhibited positive and significant genotypic association with ear diameter and significant negative association with number of ears per plant.

Number of kernels per row showed positive and significant phenotypic association with anthesis silking interval, number of ears per plant, ear length, ear diameter and thousand kernel weight. It also exhibited positive and significant genotypic association with plant height, ear height and ear length. But number of kernels per row showed negative and significant phenotypic correlation with days to anthesis, days to silking, plant height and ear height. In addition, it had non-significant negative genotypic association with yield related traits. The current finding is in line with the findings of Kumar*et al*., 2011 and Praveen *et al*., 2014.

Days to anthesis exhibited positive and significant association at genotypic and phenotypic level with days to silking, plant height and ear height. It showed negative and significant genotypic association with ear diameter and thousand kernel weight and exhibited negative and highly significant phenotypic association with anthesis silking interval, ear diameter, number of kernel per row and thousand kernel weight. Similar with this finding, Zarei*et al*. (2012) observed that, days to anthesis had positive and significant association with number of days to maturity,plant height and ear height while studying eleven hybrid maize varieties.

Plant height showed positive and highly significant phenotypic correlation with days to anthesis, days to silking and ear height.Positive and highly significant genotypic association was also observed in between it and days to anthesis, days to silking, ear height and ears per plant and showed significant and positive genotypic association with number of kernels per row. Negative and highly significant phenotypic association was also observed with anthesis silking interval, ear diameter, kernel per row and thousand kernel weight.Generally, significant positive association among yield attributes indicates that, the improvement in one trait will cause improvement in the associated trait, which in turn will cause an increase in yield. Significant negative association among yield attributes indicates that decreasing these attributes, could consistently increase grain yield. The selection made to improve yield of maize genotype may be useful through decreasing these traits.

Table 14. Phenotypic (above diagonal) and genotypic (below diagonal) correlation coefficients of yield and yield related traits of 36 single crosses and four commercial hybrid checks evaluated at Ambo and Kulumsa.

Variable	**GY**	**DA**	**DS**	**ASI**	**PH**	**EH**	**EPP**	**EL**	**ED**	**RPE**	**KPR**	**TKW**
GY		-0.45**	-0.34**	-0.38**	-0.16*	-0.24**	0.63**	0.19**	0.33**	-0.04^{ns}	0.47**	0.52**
DA	-0.31*		0.95**	-0.23**	0.57**	0.47**	0.03^{ns}	-0.006^{ns}	-0.40**	0.11^{ns}	-0.24**	-0.70**
DS	-0.27^{ns}	0.98**		0.09^{ns}	0.48**	0.38**	0.09^{ns}	0.014^{ns}	-0.37**	0.09^{ns}	-0.16*	-0.63**
ASI	-0.15^{ns}	0.24^{ns}	0.41**		-0.33**	-0.30**	0.19**	0.06^{ns}	0.12^{ns}	-0.06^{ns}	0.28**	0.25**
PH	0.49**	0.47**	0.50**	0.28^{ns}		0.74**	0.08^{ns}	0.04^{ns}	-0.29**	0.13^{ns}	-0.24**	-0.47**
EH	0.43**	0.33*	0.35**	0.22^{ns}	0.78**		0.02^{ns}	0.09^{ns}	-0.29**	0.16*	-0.30**	-0.47**
EPP	0.56**	0.27^{ns}	0.29^{ns}	0.19^{ns}	0.41**	0.46**		0.07^{ns}	-0.15^{ns}	-0.04^{ns}	0.15*	-0.014^{ns}
EL	0.45**	-0.08^{ns}	-0.02^{ns}	0.30*	0.09^{ns}	0.20^{ns}	0.19^{ns}		-0.001^{ns}	0.18*	0.41**	0.08^{ns}
ED	0.16^{ns}	-0.37*	-0.38*	-0.18^{ns}	0.05^{ns}	-0.17^{ns}	-0.44**	-0.24^{ns}		0.26**	0.28**	0.42**
RPE	-0.08^{ns}	0.28^{ns}	0.26^{ns}	-0.018^{ns}	0.28^{ns}	0.16^{ns}	-0.12^{ns}	0.02^{ns}	0.20^{ns}		0.10^{ns}	-0.16*
KPR	0.39**	0.06^{ns}	0.09^{ns}	0.14^{ns}	0.32*	0.33*	0.19^{ns}	0.62**	-0.05^{ns}	0.21^{ns}		0.27**
TKW	0.40**	-0.78**	-0.77**	-0.21^{ns}	-0.23^{ns}	-0.17^{ns}	-0.29^{ns}	0.28^{ns}	0.42**	-0.25^{ns}	0.06^{ns}	

**=significant at 0.01 level of probability, *= significant at 0.05 level of probability, ns= non-significant, GY= grain yield, DA= days to anthesis, DS= number of days to silking, ASI= anthesis silking interval, PH=plant height, EH=ear height, EPP= number of ears per plant, EL= ear length, ED= ear diameter, RPE= number of kernel rows per ear, KPR= number of kernels per row and TKWT= 100-kernel weight.

5 SUMMARY AND CONCLUSIONS

To achieve higher productivity of maize, breeders should have information on the estimates of heterosis, combining ability of parental inbred lines and their performance in hybrid combinations. In addition, the ability to predict genotypic and phenotypicassociations for different traits would greatly enhance the efficiency of plant breeding programmes. The current study was conducted with the objectives of evaluating the performances of hybrids generated using diallel mating scheme and identifying inbred lines and cross combinations with good general and specific combining ability effects,respectively,for further use in hybrid maize breeding program. Determination of the relationship between yield and yield related traits and estimating the amount of standard heterosis were also among the major objectives of this study.Thirty-six single crosses resulted from diallel crosses of nineinbred lines were evaluated along with four commercial checks at Ambo and Kulumsa. The 40 entries were laid out in 5x8 (8 blocks that constitute 5 entries in each of the blocks) alpha lattice design with two replications.

Analyses of variance indicated significant mean squares due to genotypes were observed for grain yield, number of days to anthesis, number of days to silking, anthesis silking interval, plant height, number of ears per plants, thousand kernel weight and ear diameter at bothlocations.Across locationsanalyses of variance showed significant differences among genotypes for grain yield, anthesis date, silking date,anthesis-silking interval, plant height, number of ears per plant, thousand kernel weight and ear diameter.The significant differences observed among the genotypes for most of the traits studied indicated the presence of genetic variation among the materials studied, which is important for further improvement of the traits.Among the crosses, L4 x L8, L4 x L7, L1 x L3, L6 x L8 and L3 x L4at Ambo and L1 x L3, L3 x L8 and L7 x L9 at Kulumsa showed high grain yield,whileat across locations, the highest grain yield was depictedby crosses L1 x L3, L3 x L8, L4 x L8 and L8 x L9.This indicate the possibility of obtaining good hybrid (s)with desirable traits.

Results of diallelanalysesrevealedthat GCA of lineswere significant for all studied traits at each location and across the two locations. SCA mean squares were significant for days to anthesis, days to silking, anthesis silking interval and number of ears per plant at Ambo, for grain yield, plant height, number of ears per plant and thousand kernel weight at Kulumsa and at across location for grain yield, days to anthesis, number of ears per plant and ear diameter.Bothadditive and non-additive gene actions were involved in the inheritance of traits with high proportional contribution of GCA (additive gene action) for mostof the traits. Suggesting that the variation was mainly due to additive than non-additive gene effects.

Based on combining ability analyses,L3 and L8 were found to be the best general combiners for grain yield. These inbred lines with a high positive and significant GCA effects for grain yield were desirable parents for hybrid and or synthetic variety development, since they may contribute favorable alleles in the synthesis of new varieties. Lines with significant negative GCA effects for number of days to anthesis and silking were foundimplying the possibility of improvingearliness. Thus,L2, L4, L6, L7 and L8 showed negative and highly significant and significant GCA effects for both days to anthesis and silking.This indicatedthat the inbred lines had gene combinations that can enhance early maturity. For plant heightandear height, L1, L2 and L6 showed negative and significant GCA effects, which indicate shorter plant height and ear height, which are important for the development of genotypes resistant to lodging.

Inbred lines with significant and positive GCA effects were found fornumber of ears per plant, ear diameter and thousand kernel weight,suggesting the presence of divergence to improve these traits.Thus, for number of ears per plants, L3 and L9 showed positive and significant GCA effects.L1, L4 and L8showed significant and positive GCA effects for ear diameter. L6, L7 and L8 showed positive and significant GCA effects for thousand kernel weight.In combined analyses across locations, only one cross L1 x L3 showed significant and positive SCA effect. This hybrid could be included in further investigation of grain yield and related traits. Some combinations of inbred lines had SCA effects that were significantly higher or lower than what had been expected based on their parental performances. This deviation is usually attributed to genetic variation caused by non-additive gene effects such as dominance and different types of epistasis, which are related to heterosis.

The result of standard heterosis revealed the superiority of crosses over standard check(Kolba)for majority of the traits except for grain yield and thousand kernel weight.Positive heterosis was revealed for some of the crosses for number of ears per plant and ear diameter. This indicated thepossibility of increasing number of ears per plant, ear diameter andtraits related to them.Negative standard heterosis over Kolba for days toanthesis and silking was manifested by some crosses, indicating the crosses were earlier than the standard check; and hence, could escape terminal moisture stress than standard variety being cultivatedcommercially. Similarly, some of the crosses showed negative heterosis for plant height which is desirable as shorter statured crosses are preferred for lodging resistance. Cross L1 x L3 had the highest standard heterosis for grain yield than other crosses and revealed highest positive standard heterosis over Kolba for number of ears per plant.It had also positive and significant SCA effects for grain yield. Thisindicates the presence of substantial heterotic potential that could be exploited in maize breeding program andpossibility of developing desirable cross combinations and synthetic varieties through recombination of inbred lines with desirable traits of interest.

The result of phenotypic and genotypic correlation analyses for grain yield and grain yield related traits revealed that grain yield can be simultaneously improved with a trait for which it showed strong association.

From the study, it can be concluded that better performing inbred lines with desirable GCA, cross combinations with desirable SCAeffects and crosses with noticeable level of heterosis above the standard check for grain yield and other grain yield related traits were successfully identified. These genotypes constitute a source of valuable genetic materials that could be successively used for future breeding work in the development of maize cultivarswith desirable traits’ composition for highland sub-humid agro-ecology of Ethiopia.

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7 APPENDEX

Appendix Table 1. Mean grain yield and yield related traits of diallel crosses of 9 inbred lines and four commercial hybrid checks evaluated at Ambo in 2017.

	Traits								
Genotypes	**GY**	**DA**	**DS**	**ASI**	**PH**	**EH**	**EPP**	**ED**	**TKW**
L1*L2	7.49	89.00	89.00	1.15	223.50	113.00	1.50	4.35	327.70
L1*L3	8.37	94.00	96.50	1.26	230.00	110.50	1.71	4.40	253.50
L1*L4	6.88	90.00	91.00	1.20	216.50	107.00	1.26	4.80	326.40
L1*L5	7.38	94.00	96.00	1.24	239.00	116.50	1.28	4.50	277.55
L1*L6	5.82	89.00	92.00	1.28	205.00	108.00	1.10	4.45	338.25
L1*L7	5.88	90.50	92.00	1.22	198.50	108.00	1.03	4.25	355.65
L1*L8	7.80	91.00	91.00	1.14	219.00	104.50	1.33	4.70	333.05
L1*L9	6.58	93.00	96.00	1.28	233.00	126.50	1.23	4.75	278.60
L2*L3	7.91	92.50	94.00	1.22	233.50	122.00	1.66	4.15	294.95
L2*L4	7.11	89.00	90.00	1.19	227.50	112.50	1.45	4.40	291.75
L2*L5	6.10	95.00	96.50	1.22	230.50	111.00	1.12	4.30	337.40
L2*L6	6.18	90.00	89.50	1.13	203.00	106.00	1.45	4.20	270.15
L2*L7	7.24	90.50	91.00	1.17	227.50	114.00	1.40	4.15	344.55
L2*L8	7.91	91.00	89.00	1.04	219.00	114.00	1.33	4.45	320.65
L2*L9	5.49	96.00	96.50	1.18	215.50	119.00	1.29	4.50	243.65
L3*L4	8.00	94.00	96.00	1.24	251.50	134.00	1.31	4.50	307.90

A.Table1(contd)

L3*L5	5.65	98.50	100.00	1.22	255.00	145.00	1.28	4.40	238.40
L3*L6	7.42	94.50	94.50	1.15	219.50	123.00	1.66	4.15	275.90
L3*L7	5.95	93.00	96.50	1.30	228.00	129.50	1.31	4.15	262.15
L3*L8	7.77	96.00	98.50	1.26	228.50	135.50	1.55	4.35	297.30
L3*L9	6.53	98.50	100.00	1.22	242.50	140.00	1.62	4.00	182.60
L4*L5	6.15	91.50	95.00	1.30	204.50	123.50	1.19	4.15	288.80
L4*L6	6.21	90.00	89.50	1.13	223.50	115.50	1.22	4.45	307.05
L4*L7	8.67	89.00	92.00	1.28	227.00	125.50	1.46	4.55	337.35
L4*L8	9.57	88.50	87.00	1.07	258.00	131.50	1.41	5.00	330.90
L4*L9	6.99	94.00	95.50	1.22	248.50	122.50	1.38	4.40	262.40
L5*L6	4.71	93.00	93.00	1.15	229.00	125.00	1.05	4.35	304.65
L5*L7	6.44	95.00	97.00	1.24	241.00	126.00	1.29	4.65	323.75
L5*L8	6.97	95.00	96.00	1.20	266.00	107.00	1.43	4.65	290.60
L5*L9	4.60	106.00	106.00	1.15	249.00	128.00	1.10	4.55	229.70
L6*L7	6.77	90.00	90.00	1.15	214.00	108.00	1.31	4.35	398.35
L6*L8	8.27	89.50	88.50	1.10	220.00	126.00	1.62	4.50	408.50
L6*L9	6.51	93.50	95.50	1.24	213.00	118.50	1.65	4.30	289.85
L7*L8	7.75	88.50	90.50	1.24	212.50	125.50	1.34	4.70	332.35
L7*L9	5.93	95.00	97.00	1.24	247.00	141.00	1.24	4.30	312.15
L8*L9	7.64	93.50	94.50	1.20	254.00	139.00	1.55	4.50	269.80

A.table1(contd)

Argane	7.96	90.00	90.00	1.15	225.00	135.00	1.36	4.45	339.35
Kolba	11.24	88.00	90.00	1.24	278.00	160.50	1.60	4.40	366.20
Jibat	8.76	89.00	88.00	1.09	260.50	135.00	1.33	4.45	383.95
Wenchi	9.05	91.00	93.50	1.26	255.00	140.00	1.27	4.60	328.30
Mean	7.10	92.50	93.60	1.19	231.8	123.30	1.37	4.43	306.55
LSD$_{(0.05)}$	1.61	2.03	2.71	0.11	36.60	21.38	0.26	0.30	81.89
CV (%)	11.00	1.07	1.41	4.32	7.67	9.29	9.30	3.60	12.97
Min	4.60	88.00	87.00	1.04	198.50	104.50	1.03	4.00	182.60
Max	11.24	106.00	106.00	1.30	278.00	160.50	1.70	5.00	408.50

GY= grain yield, DA= number of days to anthesis, DS= number of days to silking, ASI= anthesis silking interval, PH= plant height, EH= ear height, EPP= number of ears per plant, EL= ear length, ED= ear diameter, RPE= number of kernel rows per ear, KPR= number of kernels per row, and TKWT =1000-kernel weight**.**

Appendix Table 2. Mean values of grain yield and yield related traits of diallel crosses and four commercial hybrid checks evaluated at Kulumsa in 2017.

	Traits								
Genotypes	**GY**	**DA**	**DS**	**ASI**	**PH**	**EPP**	**EL**	**ED**	**TKW**
L1*L2	10.11	85.50	88.00	1.26	176.00	1.24	18.00	4.70	430.50
L1*L3	11.93	89.50	92.50	1.28	191.50	1.76	17.50	4.60	359.45
L1*L4	8.85	86.00	89.50	1.30	179.50	1.17	14.50	4.95	400.25
L1*L5	10.67	91.50	94.50	1.28	218.50	1.48	16.50	4.65	394.00
L1*L6	8.36	85.00	87.00	1.24	170.00	1.29	16.00	4.60	416.40
L1*L7	8.19	86.50	89.00	1.26	185.50	1.34	15.00	4.60	361.30
L1*L8	8.69	85.00	88.00	1.28	196.50	1.24	15.50	4.95	407.50
L1*L9	8.41	92.50	95.00	1.26	204.50	1.38	15.50	4.65	373.45
L2*L3	10.01	89.50	92.50	1.28	205.00	1.57	16.00	4.55	363.25
L2*L4	10.57	84.50	87.00	1.26	183.50	1.43	15.50	4.80	395.95
L2*L5	8.86	90.50	93.00	1.26	203.00	1.34	15.50	4.60	376.90
L2*L6	8.69	82.50	85.00	1.26	167.50	1.50	15.50	4.50	430.55
L2*L7	10.87	86.50	89.00	1.26	190.50	1.67	15.50	4.65	413.15
L2*L8	8.23	86.00	88.00	1.24	185.50	1.22	15.50	4.85	443.15
L2*L9	7.98	93.50	95.50	1.24	210.00	1.53	15.50	4.30	309.70

A.table2(contd)

L3*L4	9.11	89.50	92.50	1.28	213.50	1.48	16.00	4.45	318.60
L3*L5	10.35	93.50	96.50	1.28	220.00	1.60	16.00	4.40	343.25
L3*L6	10.08	88.00	91.00	1.28	178.50	1.65	17.00	4.50	384.55
L3*L7	8.88	91.00	93.00	1.24	211.00	1.62	16.00	4.35	351.65
L3*L8	11.59	89.00	92.50	1.30	220.00	1.88	15.00	4.50	360.00
L3*L9	8.14	99.00	101.00	1.24	209.50	1.64	15.00	4.10	245.75
L4*L5	9.91	89.50	92.50	1.28	204.50	1.55	15.00	4.70	343.60
L4*L6	8.87	78.50	81.50	1.28	165.50	1.24	15.50	4.70	318.75
L4*L7	8.88	84.50	87.00	1.26	187.00	1.26	15.00	4.95	430.65
L4*L8	9.24	84.50	87.00	1.26	199.00	1.19	13.50	5.15	426.55
L4*L9	8.18	88.50	91.50	1.28	178.00	1.43	14.50	4.75	361.80
L5*L6	9.86	89.00	91.50	1.26	188.50	1.67	16.50	4.60	414.85
L5*L7	8.63	92.00	95.00	1.28	223.50	1.29	16.00	4.60	345.00
L5*L8	9.28	91.00	94.00	1.28	214.50	1.55	14.00	4.80	326.45
L5*L9	7.73	98.00	101.00	1.28	199.00	1.50	15.50	4.60	318.70
L6*L7	7.59	82.50	85.00	1.26	162.50	1.19	15.00	4.55	413.00
L6*L8	7.75	82.00	84.00	1.24	163.50	1.22	15.00	4.75	391.40
L6*L9	8.73	91.50	94.00	1.26	188.50	1.53	13.50	4.55	364.70
L7*L8	8.70	84.50	87.50	1.28	184.00	1.19	15.50	4.60	446.00
L7*L9	10.91	89.50	92.50	1.28	205.00	1.86	15.50	4.50	343.80

A.table2(cond)

L8*L9	10.87	90.00	92.00	1.24	217.00	1.71	15.00	4.90	332.75
Argane	11.85	85.50	89.00	1.30	220.00	1.59	18.00	4.55	427.75
Kolba	13.06	88.50	92.00	1.30	219.00	1.76	16.50	4.65	437.85
Jibat	10.89	87.00	90.00	1.28	224.50	1.55	16.50	4.70	449.90
Wenchi	11.80	86.00	89.50	1.30	215.00	1.81	17.00	4.40	438.05
Mean	9.53	88.20	90.90	1.27	197.00	1.48	15.60	4.63	380.30
LSD (0.05)	1.65	4.25	3.95	0.04	14.80	0.37	1.62	0.33	74.03
CV (%)	8.40	2.34	2.11	1.47	3.64	12.00	5.02	3.47	9.45
Min	7.60	78.50	81.50	1.24	162.50	1.17	13.50	4.10	245.80
Max	13.10	99.00	101.00	1.30	224.50	1.88	18.00	5.15	449.90

GY= grain yield, DA= number of days to anthesis, DS= number of days to silking, ASI= anthesis silking interval, PH= plant height, EH= ear height, EPP= number of ears per plant, EL= ear length, ED= ear diameter, RPE= number of kernel rows per ear, KPR= number of kernels per row, TKWT =1000-kernel weight**.**

Appendix Table 3. Mean monthly rain fall, air temperature and relative humidity of Ambo during 2017.

Month	Rainfall (mm)	Air temperature (^{o}C)			Relative humidity (%)
		Minimum	Maximum	Average	
January	5.50	8.30	26.30	17.30	47.00
February	60.90	10.98	27.07	19.03	56.30
March	11.90	12.03	28.37	20.20	47.70
April	29.30	12.40	28.50	20.45	54.70
May	145.70	12.11	25.79	18.95	50.40
June	134.70	11.70	24.68	18.17	53.90
July	205.80	11.90	22.19	17.05	79.50
August	144.10	11.47	21.88	16.68	72.10
September	209.60	10.73	22.80	16.77	61.60
October	6.20	9.81	25.24	17.52	47.90
November	18.00	8.67	25.43	17.05	54.50
December	0.00	7.70	24.80	16.58	46.70
Total	**971.70**	**127.75**	**303.072**	**215.74**	**672.30**
Mean	**80.98**	**10.65**	**25.26**	**17.98**	**56.025**

Source: *Ambo Agricultural Research Center, Weather Data, West shewa, Ambo, Ethiopia*

Appendix Table 4. Mean monthly rain fall, air temperature and relative humidity of Kulumsa during 2017.

Month	Rainfall (mm)	Air temperature (^{o} C)			Relative humidity (%)
		Minimum	Maximum	Average	
January	0.00	10.20	26.70	18.45	28.50
February	29.00	10.70	24.60	17.65	49.20
March	87.80	11.50	27.20	19.35	37.60
April	25.30	13.10	27.10	20.10	38.10
May	134.60	13.30	22.80	18.05	70.10
June	64.20	12.60	23.90	18.25	61.70
July	124.30	13.10	22.50	17.80	69.70
August	108.80	12.70	21.90	17.30	79.00
September	131.60	11.90	21.40	16.65	75.70
October	12.60	12.60	23.60	18.10	51.20
November	0.00	11.10	23.40	17.25	40.60
December	-	-	-	-	-
Total	**718.30**	**133.10**	**265.10**	**199.10**	**601.70**
Mean	**65.30**	**12.10**	**24.10**	**18.10**	**54.70**

Source: *Ambo Agricultural Research Center, Weather Data, West shewa, Ambo, Ethiopia*